

# Pesticide relevance and their microbial degradation: a-state-of-art

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**Abstract** The extensive use of pesticide causes imbalance in properties of soil, water and air environments due to having problem of natural degradation. Such chemicals create diverse environmental problem via biomagnifications. Currently, microbial degradation is one of the important techniques for amputation and degradation of pesticide from agricultural soils. Some studies have reported that the genetically modified microorganism has ability to degrade specific pesticide but problem is that they cannot introduce in the field because they cause some other environmental problems. Only combined microbial consortia of indigenous and naturally occurring microbes isolated from particular contaminated environment have ability to degrade pesticides at faster rate. The bioaugmentation processes like addition of necessary nutrients or organic matter are required to speed up the rate of degradation of a contaminant by the indigenous microbes. The use of indigenous microbial strains having plant growth activities is ecologically superior over the chemical methods. In this review, we have attempted to discuss the recent challenge of pesticide problem in soil environment

and their biodegradation with the help of effective indigenous pesticides degrading microorganisms. Further, we highlighted and explored the molecular mechanism for the pesticide degradation in soil with effective indigenous microbial consortium. This review suggests that the use of pesticide degrading microbial consortia which is an eco-friendly technology may be suitable for the sustainable agriculture production.

**Keywords** Pesticide · Pesticide degrading microorganism · Microbial degradation · Bioaugmentation · Indigenous · Biodegradation · Sustainable agriculture

## 1 Introduction

During the green revolution, more chemical fertilizers and pesticides were used to enhance the production of food grains needed to meet the needs of the ever expanding human population. Notwithstanding, the green revolution caused many environmental problems such as increased soil fertility loss, soil acidification, nitrate leaching, increased weed species resistance and loss of biodiversity (Tilman et al. 2002; Verma et al. 2013). The pesticides are a diverse group of inorganic and organic chemicals like herbicides, insecticides, nematicides, fungicides, and soil fumigants. In agriculture, these pesticides are applied

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to enhance crop yield and quality and to maximize economic returns by prevention of pest attack. The pesticides are bioactive, toxic substances, and it influences, directly or indirectly, soil fertility and health as well as agroecosystem quality (Lo 2010; Joergensen and Emmerling 2006). These chemicals affect the diversity of soil microbial communities, their metabolic activities, reproduction and growth. Plenty of the studies have discussed the effect of pesticides on soil organisms (e.g. Bunemann et al. 2006; Odukkathil and Vasudevan 2013), including on bacterial populations (Lo 2010; Johnsen et al. 2001).

Pest infestations deplete annual food production by an average of 45 % (Abhilash and Singh 2009). The use of chemical pesticides to control pests and disease vectors have enhanced agricultural yields and limited the spread of insect-borne diseases (e.g., malaria, dengue, encephalitis, filariasis, etc.) that affect human health (Bhatnagar 2001; Rekha and Naik 2006). Effective pest management is essential for maintaining high crop yields in tropical region because high temperatures and humidity in this region facilitate the rapid reproduction of pests, which exert crop loss from insects and diseases more severely (Kannan et al. 1992; Lakshmi 1993). Pesticide pollution of the local environment affects the lives of birds, wildlife, domestic animals, fish and livestock and thus disrupts the ecosystem structure and function through biomagnifications (Anonymous 1991). Unmannered application of pesticide affects the whole ecosystem by entering the residues in food chain and polluting the soil, air, ground and surface water (ICAR report 1967; UN/DESA 2008).

Various treatment methods (e.g. land filling of contaminated sites, recycling, pyrolysis and incineration) have been used for the removal and remediation of these chemicals from the contaminated sites. Phytoremediation has been used for removal of toxic chemical from soil and water. Currently, the pesticide remediation from agriculture fields is one of the important issue because such chemicals are very expensive and problematic as they form toxic chemicals by reaction of various organic and inorganic contents and element present in soils (Jain et al. 2005). Only efficient microbial technology is useful for pesticide removal/degradation from the agricultural soils. Microbial degradation (use of fungi, bacteria, actinomycetes and viruses) can effectively remove pesticides from the contaminated soil (organochlorines, organophosphates

and carbamates) through the enzymatic degradation (Porto et al. 2011). The biological degradation; involves the use of effective microorganism to degrade the complex pesticide into simple inorganic chemicals (Wood 2008). Moreover, this technology is less hazardous, environmentally friendly and economically viable and socially acceptable (You and Liu 2004). The indigenous soil microbial consortia are better and effective consortia for microbial degradation of pesticide than the non indigenous strains. Because, the indigenous strains grow very well and have higher adaptability in particular geographical region. Hence, these indigenous microbial consortia have potential to degrade the pesticide and also have plant growth promoting ability like production of plant growth hormones, biological nitrogen fixation, phosphate solubilization, hydrogen cyanide, siderophore and antagonistic properties for enhancing the sustainable agriculture.

The genetically modified indigenous microorganisms are also used for bioremediation because these organisms have particular genes, which are responsible for degradation of the specific pesticide (Sakamoto and Tsutsumi 2004). The natural microorganisms exposed to pesticides; develop resistance power though anti-catabolic processes to remove the toxic compounds. Since the knowledge on microbial bioremediation of pesticides is fragmented (Finley et al. 2010; Porto et al. 2011; Sakamoto and Tsutsumi 2004; You and Liu 2004; Wood 2008). Therefore, the objective of the present study was to elaborate the potential applications of various indigenous microorganisms in degradation and detoxification of pesticide in agricultural soils.

## 2 Pesticide relevance and problem

The increase in the demand for agro-products and changing regional climate has resulted in an increase in consumption and application rate of pesticide (Shetty et al. 2008). The rates of pesticides consumption in various countries depend on agricultural land. Some country showed higher consumption of total pesticide according to agricultural area. The World-wide top ten higher pesticide using countries are Italy (63,305 tone/y), Turkey (60,792.4 tone/y), Colombia (48,618.47 tone/y), India (40,379.24 tone/y), Japan (36,557 tone/y), Bolivia (31,566.76 tone/y), Ecuador

**Table 1** Worldwide higher pesticide (insecticide, herbicides, fungicides and bactericides) consuming countries with agricultural land area in year 2010

| Countries          | Worldwide higher consumption of pesticides in year 2010 (tones/year) |            |                             |                             | Worldwide area agricultural area (Sq km) |                         |
|--------------------|--|------------|-----------------------------|-----------------------------|--|-------------------------|
|                    | Insecticides   | Herbicides | Fungicides and bactericides | Total pesticide consumption | Total land area                          | Total agricultural area |
| Bangladesh         | 2,681.69   | 658.54     | 9,883.70                    | 13,223.93                   | 130,170                                  | 31,650                  |
| Bolivia            | 9,843.50   | 17,263.60  | 4,459.66                    | 31,566.76                   | 1,083,300                                | 369,650                 |
| Cameroon           | 3,467.28   | 3,470.20   | 2,457.46                    | 9,394.94                    | 472,710                                  | 96,000                  |
| Chile              | 7,071.00   | 7,234.00   | 3,727.00                    | 18,032                      | 743,530                                  | 157,430                 |
| Colombia           | 8,717.60   | 17,587.15  | 22,313.72                   | 48,618.47                   | 1,109,500                                | 425,030                 |
| Costa Rica         | 2,148.52   | 4,416.26   | 7,438.56                    | 14,003.34                   | 51,060                                   | 18,800                  |
| Dominican Republic | 609.43   | 3,849.66   | 1,323.83                    | 5,782.92                    | 48,320                                   | 24,470                  |
| Ecuador            | 7,689.61   | 14,394.76  | 9,118.73                    | 31,203.1                    | 248,360                                  | 749,770                 |
| El Salvador        | 750.97   | 11,007.37  | 85.41                       | 11,843.75                   | 20,720                                   | 15,293.4                |
| Germany            | 1,243.79   | 16,675.00  | 9,666.70                    | 27,585.49                   | 348,570                                  | 167,000                 |
| Guatemala          | 2,026.92   | 8,362.84   | 4,508.48                    | 14,898.24                   | 107,160                                  | 43,950                  |
| Honduras           | 314.00   | 2,860.90   | 1,877.60                    | 5,052.5                     | 111,890                                  | 32,200                  |
| Hungary            | 1,965.00   | 4,479.00   | 2,285.50                    | 8,729.5                     | 90,530                                   | 53,430                  |
| India              | 20,618.82  | 6,704.98   | 13,055.44                   | 40,379.24                   | 2,973,190                                | 1,797,590               |
| Italy              | 10,834.00  | 9,934.00   | 42,537.00                   | 63,305                      | 294,140                                  | 143,228                 |
| Japan              | 2,053.30   | 12,166.70  | 22,337.00                   | 36,557                      | 364,500                                  | 45,930                  |
| Myanmar            | 6,175.68   | 661.00     | 2,141.33                    | 8,978.01                    | 653,260                                  | 125,260                 |
| Netherlands        | 1,634.90   | 2,642.30   | 3,613.10                    | 7,890.3                     | 33,730                                   | 19,087                  |
| Norway             | 5.33   | 8,321.09   | 1,479.40                    | 9,805.82                    | 365,268                                  | 10,060                  |
| Peru               | 4,352.16   | 6,160.08   | 4,045.60                    | 14,557.84                   | 1,280,000                                | 214,700                 |
| Portugal           | 370.97   | 2,042.29   | 9,475.36                    | 7,249.2                     | 91,470                                   | 36,770                  |
| Romania            | 1,327.70   | 3,688.90   | 2,232.60                    | 26,506.74                   | 230,050                                  | 141,560                 |
| Turkey             | 8,215.57   | 745.59     | 17,545.58                   | 60,792.4                    | 769,630                                  | 390,120                 |
| Ukraine            | 8,531.50   | 40,910.60  | 11,350.30                   | 13,899.57                   | 579,320                                  | 412,670                 |
| United Kingdom     | 889.46   | 7,488.83   | 5,521.28                    | 13,223.93                   | 241,930                                  | 172,240                 |

Source: FAO (2010), World Bank (2010), Schreinemachers and Tipraqsa (2012)

(31,203.1 tone/y), Germany (27,585.49 tone/y), Romania (26,506.74 tone/y) and Chile (18,032 tone/y) (Table 1). The Worldwide top ten higher agricultural land are: India (1,797,590 sq.km), Ecuador (749,770 sq.km), Colombia (425,030 sq.km), Ukraine (412,670 sq.km), Turkey (390,120 sq.km), Bolivia (369,650 sq.km), Peru (214,700 sq.km), United Kingdom (172,240 sq.km), Germany (167,000 sq.km) and Chile (157,430 sq.km). Total annual pesticide consumption was depend on the total agricultural lands e.g. Turkey, Colombia, India, Bolivia, Ecuador, Germany and Chile showed higher pesticide consumption as well as agricultural area (Table 1).

Pesticides can be classified as either being readily degradable (non-persistent), or as being persistent. The non-persistent pesticides are: insecticides (methoxychlor, sevin, malathion), herbicides (paraquat, dalapon, dacthal, treflan) and fungicides (benlate, mancozeb, zineb, captan), and persistent pesticides are: insecticides (DDT, aldrin, dieldrin and chlordane), herbicides (simazine, turbacil, tordon) fungicides (PMAS, calo-clor, cadmium compounds) (Vargas 1975). Orgnochlorine (OC) insecticides (DDT, hexachlorocyclohexane, aldrin and dieldrin, etc.) and organophosphate insecticides (chlorpyrifos, acephate, diazinon, malathion and disulfoton etc.) are

most commonly used pesticides in developing countries of Asia because of their low cost and broad control spectrum and versatility against various pests (FAO 2005). The intense and frequent use of these chemicals has led to the persistence in soil due to lack of their timely degradation (Odukkathil and Vasudevan 2013). For example; metribuzin was in practice because of its easy transfer as a water soluble compound (Hernandez et al. 1998), and linuron for its persistence in the soil (Guzzella et al. 2006), and fluazinam due to its persistence and wide taxonomic range to inhibit phytopathogenic fungi (Kimyoji et al. 1995). Metribuzin (4-amino-6-tert-butyl-4,5-dihydro-3-methylthio-1,2,4-triazin-5-one) and linuron (3-(3,4-dichlorophenyl)-1-methoxy-1-methylurea) inhibit electron transport at the photosystem II receptor site, were used to control weeds in several crops, including potato (Tomlin 2002). Metribuzin is biodegraded rapidly in soil and its photodecomposition is also efficient in the soil surface as well as in water. Fluazinam (3-chloro-N-(3-chloro-5-trifluoromethyl-2-pyridyl)-a,a,a-trifluoro-2,6-dinitro-p-toluidine) has an uncoupling activity on mitochondrial oxidative phosphorylation and is used as a fungicide to protect the crops.

The World Health Organization (WHO 2004) provides an internationally accepted standard for hazard classification. Depending upon their intensity expressed in LD50 value those were (1) IA (Extremely), (2) IB (Highly hazardous), (3) II (Moderately hazardous) and (4) III (slightly hazardous). Currently, in India, there are registered 234 pesticides; among these, four belongs to WHO Class IA, 15 to WHO class IB and 76 to WHO Class II. They constituted 40 % of the registered pesticides. During 2005–2006 and 2009–2010, out of 15 pesticides; sulfur (fungicide, 16,424 mt), endosulfan (insecticide, 15,537 mt), moncozeb (provides, 11,067 mt) and phorate (insecticide, 10,763 mt) are highly used (Table 2) and the total consumption amounted 210,600 mt. According to the Directorate of Plant Protection, Quarantine and Storage, Government of India (2010); during 2005 to 2010, the highest use of pesticide (39,948 mt) has been reported in Uttar Pradesh as compared to other top six pesticide-consuming states of India during 2005 to 2010 (Fig. 1). In India, the average consumption of pesticide is lesser as compared to other developed countries, but the problem of pesticide residue in India is comparatively higher. Presently, the yearly

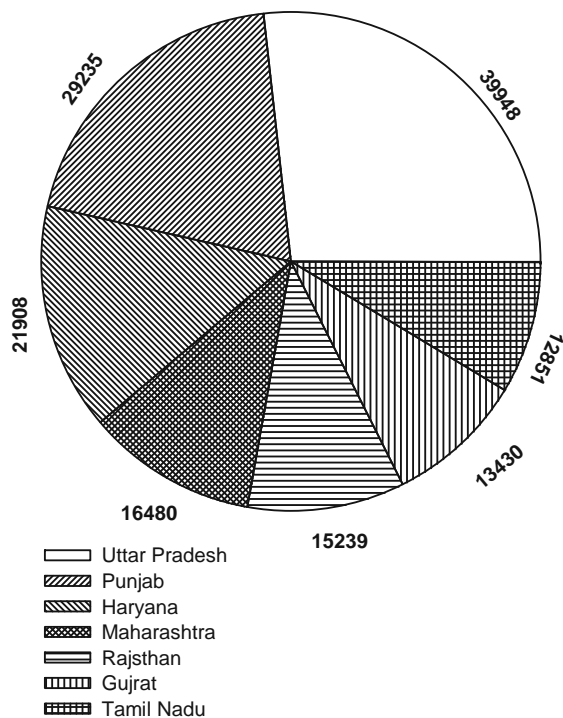
**Table 2** Most consumed pesticides in India (during 2005–2006 to 2009–2010)

| S.No. | Pesticide<br>(Technical Grade) | Quantity consumed<br>(metric tonnes) |
|-------|--------------------------------|--------------------------------------|
| 1     | Sulphur (fungicide)            | 16,424                               |
| 2     | Endosulfan (insecticide)       | 15,537                               |
| 3     | Mancozeb (fungicide)           | 11,067                               |
| 4     | Phorate (insecticide)          | 10,763                               |
| 5     | Methyl Parathion (insecticide) | 08408                                |
| 6     | Monocrotophos (insecticide)    | 08209                                |
| 7     | Cypermethrin (insecticide)     | 07309                                |
| 8     | Isoproturon (herbicide)        | 07163                                |
| 9     | Chlorpyrifos (insecticide)     | 07163                                |
| 10    | Malathion (insecticide)        | 07103                                |
| 11    | Carbendazim (fungicide)        | 06767                                |
| 12    | Butachlor (herbicide)          | 06750                                |
| 13    | Quinalphos (insecticide)       | 06329                                |
| 14    | Copper oxychloride             | 06055                                |
| 15    | Dichlorvos (insecticide)       | 05833                                |

*Source:* Total pesticides consumed during 2005–2006 to 2009–2010, as per official data of the Directorate of Plant Protection, Quarantine and Storage, Govt of India. ([www.indiaforsafefood.in/farminginindia.html](http://www.indiaforsafefood.in/farminginindia.html))

pesticide consumption in India is increasing due to rapid agricultural production (FAO 2010).

In tropical countries; crop loss due to plague is severe because of high temperature and humidity, which facilitates the rapid multiplication of pests (Kannan et al. 1992; Lakshmi 1993). The intensive use of pesticides help for the protection of crops from pests (insects, mites, nematodes and rodents), plant pathogens (fungi, viruses and bacteria), and weeds reduced 30 % crop loss (Porto et al. 2011) and increase the sufficient food grain for the need of ever increasing human population (Acharya 2006). Among different pesticides; pyrethroids, organophosphates and chlorinated compounds (DDT, hexachlorocyclohexane, aldrin and dieldrin) are the most commonly used pesticides in the developing countries because of their low cost, easy availability in local markets and versatility against various pests (Porto et al. 2011). Polycyclic aromatic hydrocarbons (PAHs) form a group of compounds composed of two or more fused aromatic rings. These hydrophobic compounds display a high affinity for organic matter and particles, and accumulate in organic rich soil and marine sediments (Amellal et al. 2001).



**Fig. 1** The maximum pesticide-consuming states e.g. Uttar Pradesh, Punjab, Haryana, Maharashtra, Rajasthan, Gujarat and Tamil Nadu in India during 2005–2006 to 2009–2010. The values near each state is in MT (Data Source: Directorate of Plant Protection, Quarantine and Storage, Govt of India) ([www.indiaforsafefood.in/farminginindia.html](http://www.indiaforsafefood.in/farminginindia.html))

Carbamate pesticides are mainly used in the agriculture due to their broad activity spectrum, less toxic to human beings and easy degradation by the microorganism (Wolfe et al. 1978). On the other hand, the application of endosulfan as an insecticide, more than 99 % of it goes to misuse and remains in the environment as pollutants (Mahapatra 2008; Mahapatra and Panigrahi 2013). Organochloride pesticides are recalcitrant and resistant to biodegradation (Diaz 2004; Dua et al. 2002; Chaudhry and Chapalamadugu 1991). Because of indiscriminate and unplanned uses (EI-Bestway et al. 2000), long half-life, nondegradable nature, such poisonous chemical are continuously persisting in the soils of certain agroecosystems (You and Liu 2004; Gavrilescu 2005), contributed to loss of soil fertility, acidification, nitrate leaching and weed invasions (Tilman et al. 2002; Verma et al. 2013). It further enters into the food chain and pollutes the air, ground and surface water (ICAR 1967; Parsek et al. 1995; You and Liu 2004; UN/DESA 2008).

The farmers are not aware of the critical loads of these pesticides on the agricultural crops and soils, and they are used to spray pesticides for controlling the pest. Such pesticide load in soil causes negative consequences on the microbial flora and fauna (You and Liu 2004), which further causes the cascading effects on the agricultural ecosystem structure and function (Gavrilescu 2005). Further, such problem become more complicated due to extensive use of chlorinated pesticide, which is easily available in local markets of India, though banned in developed countries of the world (You and Liu 2004). Because of their unusually long half life and non-biodegradable nature, these poisonous chemicals are likely to persist in the environment and inter into the food chain and cause serious health hazards (Parsek et al. 1995).

Humans are exposed to pesticides by different routes of exposure, such as; inhalation, ingestion and dermal contact (Rekha and Naik 2006). Increasing incidence of cancer (Porto et al. 2011), mutagenicity and circulatory problem (Sinha et al. 1995, 1997), chronic kidney diseases, suppression of the immune system, sterility among males and females (Colosio et al. 2009; Jekanovic and Prostran 2009), endocrine disorders, neurological (IARC 1986; Vaccari et al. 2006; Porto et al. 2011) and behavioral disorders, especially among children, have been attributed by the chronic pesticide poisoning (Agnihotri 1999). Pesticide pollution to the local environment so affects the lives of birds, wildlife, domestic animals, fish and livestock and more pesticide load in environment enhances the resistance ability of microbial strains of soils. Thus, increased amount of pesticides disrupt the whole ecosystem through biomagnifications (Anonymous 1991). Persistent organic pollutants (POPs) are chemicals that remain persistent in the environment for long periods, become widely distributed geographically, accumulate in the fatty tissue of living organisms and are toxic to humans and wildlife (United Nations Environment programs 2011). The Stockholm Convention seeks to restriction as well as elimination of production and releases of nine organochlorine pesticides, viz: aldrin, chlordane, DDT, dieldrin, endrin, heptachlor, hexachlorobenzene, mirex, toxaphene (Stockholm Convention 2009) and Endosulfan (Stockholm Convention 2011). These chemicals are highly hazardous to organism because of their higher degree of halogenations, inclination to bioaccumulation in the lipid component, and resistance to natural



degradation (Weber and Varbelow 2013; Torres et al. 2013a, b; Weber and Varbelow 2013; Abhilash et al. 2013).

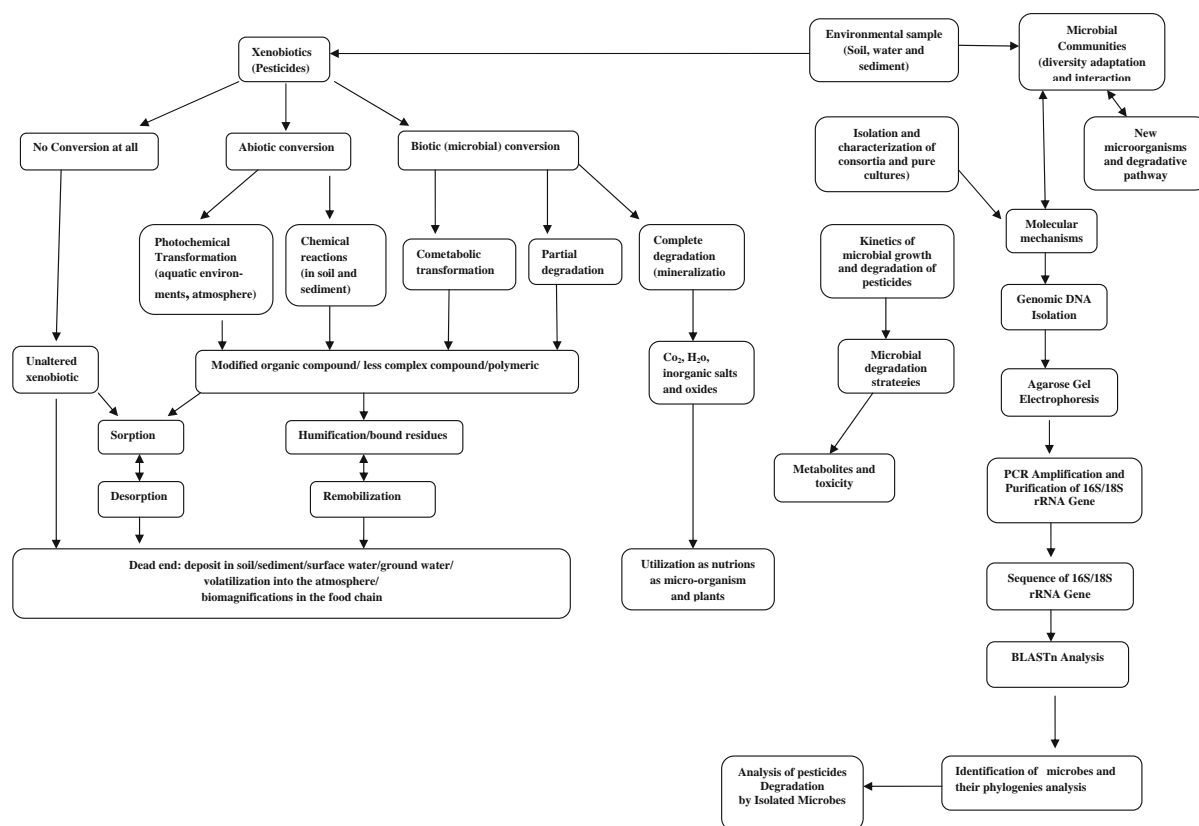
### 3 Microbial degradation of pesticides

Soil microbes perform substantial role in litter degradation (Schneider et al. 2010), promotion of plant growth (Hayat et al. 2010), nutrient cycling (Van Der Heijden et al. 2008) and the degradation of pollutants and pesticides (Pino and Penuela 2011; Zhao et al. 2009). Such functions are significant to the farmers and society; therefore, the applications of pesticide which hamper the ecosystem services need to be minimized. The effect of pesticide on the activity of soil microbes has been observed by testing the efficiency of carbon utilization and nitrification. The success of the nitrification test against the pesticide side effect is likely due to the fact that no soil fungi are known to be involved in the nitrification process and that only few species of bacteria are able to perform the process. Recently, the expressed functional genes (*amoA* and *amoB*) involved in the nitrification process have been used to quantify the effect of pesticides on nitrification. One other microbial-driven ecosystem function that has been found to be affected by pesticide use is the degradation of pesticides by increasing the pesticide degrading microbial populations (Bælum et al. 2008; Lancaster et al. 2010). In mRNA quantification study the process of nitrification has been shown too susceptible against certain pesticides, and the nitrification rate was linked with the quantity of mRNA transcript. Other molecular sequencing study suggested that the microbial community structures are influenced by pesticides (Jacobsen and Hjelmsø 2014).

For minimization of soil pollution and soil toxicant in agricultural fields, various treatment methods (i.e., filling of contaminated land sites, recycling, pyrolysis and incineration) have been used (Wang et al. 2005). The physico-chemical remedial strategies to clean up sites containing these compounds are neither cost effective nor adequate enough (Jain et al. 2005). Therefore, biological method would be one of the promising methods to exploit the ability of microorganisms for removal of pollutants from the contaminated sites. This alternative treatment strategy (bioremediation) could be effective, minimally

hazardous, economical, environment-friendly, and versatile (Finley et al. 2010; Porto et al. 2011). The microbial based (with the help of fungi, bacteria, actinomycetes and viruses) degradation may ease the pesticide problem (Finley et al. 2010) which is a natural process (Kosaric 2001), does not produce toxic intermediates (Pieper and Reineke 2000; Furukawa 2003) more effective technology, less hazardous and environment-friendly (You and Liu 2004; Wang et al. 2005). Soil microorganisms collectively decompose various xenobiotic compounds and return the item to the mineral salts which are utilized by plants (Fig. 2). Hence, they play an important role in the dissipation of xenobiotic pesticides in the soil. Microorganisms especially bacteria, due to their continuous exposure to such environmental stress, develop a genetically determined system against toxicant (Parsek et al. 1995). The highly diverse microbial communities present in fresh and marine water, sewage and soils are able to transform a wide range of organic chemicals. Compared to chemical methods, the microorganisms that survive in the environment, utilize the pesticides for obtaining the energy seem to be the best candidates for bioremediation of pesticide present in soil or water (Fig. 2).

Pesticide degradation may be carried out by one or more ways described as biotransformation, biomineralization, bioaccumulation, biodegradation, bioremediation and cometabolism (Shakoori et al. 2000; Park et al. 2003; Finley et al. 2010). Microbial degradation involves the use of effective microorganism for the enzymatic breakdown of toxic pesticides (organochlorines, organophosphates and carbamates) into a nontoxic compounds or it may be defined as; microbial mediated degradation of complex organic compound (pesticide) into simple inorganic chemicals on the contaminated sites; soil, ground water, sludge's, industrial water system and gas (You and Liu 2004; Wood 2008; Finley et al. 2010; Porto et al. 2011). Thus, the microorganisms which play substantial role in the in situ removal and detoxification of these toxicants from the concerned environment are of special significance (Desaint et al. 2000; Wang et al. 2005; Wood 2008). Large number of bacterial strains; viz. *Arthobacter* (Aislabie et al. 2005; Patil et al. 1970), *Pseudomonas* (Singh et al. 2003; Lakshmi et al. 2008; Liming et al. 2014), *Ralstonia* (Hay and Focht 2000), *Rhodococcus* (Zaitsev et al. 1995; Park et al. 2003), *Bacillus* (Anwar et al. 2009; Zhu et al. 2010;



**Fig. 2** Microbial degradation of pesticide affected by various environmental factor and characterization of pesticide degrading microbes

Liu et al. 2012; Fawzy et al. 2014), *Nocardiopsis* (Pravin et al. 2012), *Cryptococcus* (Evy et al. 2012) and *Acetobacter* (Shakoori et al. 2000) and *Alcaligenes* (Padmanabhan et al. 2003; Yang et al. 2005) have been isolated from different parts of the world with amazing property to degrade xenobiotic contaminants are listed in Table 3. These microorganisms are appropriately termed as nature's biodegraders and/or scavengers because they recycle most natural waste materials into harmless compounds. The endogenous microbes remove pollutants from soils by their extraordinary ability to use a wide variety of xenobiotics as sole energy and carbon source (Siddique et al. 2003). Such microorganisms are highly adaptable and have the capability to degrade the recalcitrant compounds through evolution of new genes, which encode enzymes that can use these compounds as their primary substrates (Suenaga et al. 2001).

The pesticide degrading genes of soil bacteria reside on plasmids (anti-catabolic plasmid) and

encode the pollutant-degrading enzymes (Laemmli et al. 2000). These catabolic plasmids have been reported from different species of *Pseudomonas*, *Alcaligenes*, *Actinobacter*, *Cytophaga*, *Moraxella*, *Klebsiella* and *Arthrobacter* (Sayler et al. 1990). *Pseudomonas aeruginosa* MRM6, *Pseudomonas aeruginosa* SFM4 and *Acromobacter xylosoxidans* ES9 dégradé the endosulfan (a broad range of pesticide). The bacteria *Clostridium sporogenes* and *Bacillus coli* produce trace amounts of benzene and mono-chlorobenzene from lindane and can further metabolize it by producing the CO<sub>2</sub> from sub-merged soils. *Pseudomonas putida* and *Acinetobacter* have ability for dehalogenate the chloro-aromatic compounds (Vollmer et al. 1998). A group of brown-rot fungi (*Gloeophyllum trabeum*, *Fomitopsis pinicola*, and *Daedalea dickinsii*) degrades the DDT. *Mucor circinelloides* and *Galactomyces geotrichum* isolated from cattle manure compost (CMC) (Purnomo et al. 2010a) and *Pleurotus ostreatus*, from spent mushroom

**Table 3** Pesticide degrading microorganisms have various type pesticides degrading ability

| Pesticide                      | Organism   | Nature of study  | Reference                                   |
|--------------------------------|--|--|---|
| Acibenzolar-S-methyl<br>Aldrin | <i>B. pumilus</i> SE34   | Biodegradation of soil-applied pesticides by selected strains of plant growth-promoting rhizobacteria (PGPR) and their effects on bacterial growth   | Myresiotis et al. (2012)                    |
|                                | <i>Trichoderma viride</i> , <i>Micrococcus</i> 204, <i>Bacillus</i> sp. 458  | Comparison of insecticide degradation by soil microorganisms   | Patil et al. (1970)                         |
|                                | <i>Aspergillus niger</i>   | Evaluation: biotransformation by microorganism   | Korte and Porter (1970)                     |
| Atrazine                       | <i>Bacillus</i> , <i>Micromonospora</i> , <i>Mycobacterium</i> , <i>Nocardia</i> , <i>Streptomyces</i> , <i>Thermoactinomyces</i> and <i>Pseudomonas</i> | Epoxidation of aldrin to exo-dieldrin by soil bacteria   | Ferguson and Korte (1977)                   |
|                                | <i>Pseudomonas fluorescens</i>   | Removal of Aldrin, using activated carbon <i>Pseudomonas fluorescens</i> free cell cultures  | Erick et al. (2006)                         |
|                                | <i>Arthrobacter nicotinovorans</i>   | Characterization of <i>Arthrobacter nicotinovorans</i> HIM, an atrazine-degrading bacterium  | Aislabie et al. (2005)                      |
| Chlorpyrifos                   | <i>Cryptococcus laurentii</i>  | Biodegradation of atrazine by <i>Cryptococcus laurentii</i> isolated from contaminated agricultural soil   | Evy et al. (2012)                           |
|                                | <i>Pleurostostreatus</i> INCQS 40310   | Optimized atrazine degradation by <i>Pleurostostreatus</i> INCQS 40310-an alternative for impact reduction of herbicides used in sugarcane crops   | Pereira et al. (2013)                       |
|                                | <i>Pichia kudriavzevii</i> strain Atz-EN-01  | Atrazine degradation in liquid culture and soil by a novel yeast <i>Pichia kudriavzevii</i> strain Atz-EN-01 and its potential application for bioremediation  | Evy et al. (2013)                           |
| Chlorpyrifos                   | <i>Raoultella planticola</i>   | Atrazine biodegradation by a monoculture of <i>Raoultella planticola</i> isolated from a herbicides wastewater treatment facility  | Swissa et al. (2014)                        |
|                                | <i>Micrococcus</i> sp  | Bacterial degradation of chlorpyrifos in pure culture and in soil  | Mallick et al. (1999)                       |
|                                | <i>Pseudomonas</i> sp  | Effects of soil pH on the biodegradation of chlorpyrifos and isolation of a chlorpyrifos-degrading bacterium   | Singh et al. (2003)                         |
|                                | <i>Enterobacter</i> strain B-14  | Biodegradation of chlorpyrifos by <i>Enterobacter</i> strain B-14 and its use in the bioremediation of contaminated soil   | Singh et al. (2004)                         |
|                                | <i>Alcaligenes faecalis</i> DSP3   | Isolation and characterization of a chlorpyrifos and 3, 5, 6- trichloro-2-pyridinol degrading bacterium  | Yang et al. (2005)                          |
|                                | <i>Serratia</i> sp. and <i>Trichosporon</i> sp.  | Mineralization of chlorpyrifos by co-culture of <i>Serratia</i> and <i>Trichosporon</i> sp.  | Xu et al. (2007)                            |
|                                | <i>Klebsiella</i> sp.  | Biodegradation of chlorpyrifos by <i>Klebsiella</i> sp. isolated from an activated sludge sample of waste water treatment plant in Damascus  | Ghanem et al. (2007)                        |
|                                | <i>Sphingomonas</i> sp.  | Isolation of a chlorpyrifos-degrading bacterium, <i>Sphingomonas</i> sp. strain Dsp-2, and cloning of the mpd gene   | Li et al. (2007)                            |
|                                | <i>Paracoccus</i> sp. TRP  | Biodegradation of chlorpyrifos and 3,5,6-trichloro-2-pyridinol by a newly isolated <i>Paracoccus</i> sp. strain TRP  | Xu et al. (2008)                            |
|                                | <i>Pseudomonas aeruginosa</i><br><i>Verticillium</i> sp. DSP   | Biotransformation of chlorpyrifos and bioremediation of contaminated soil<br>Fungal degradation of chlorpyrifos by <i>Verticillium</i> sp. DSP in pure cultures and its use in bioremediation of contaminated soil and pakchoi | Lakshmi et al. (2008)<br>Fang et al. (2008) |



Table 3 continued

| Pesticide | Organism  | Nature of study   | Reference                     |
|-----------|---|---|-------------------------------|
| DDT       | <i>Pseudomonas nitroreducens</i> PS-2   | Rhizosphere remediation of chlorpyrifos in mycorrhizospheric soil using ryegrass  | Korade and Fulekar (2009)     |
|           | <i>Bacillus pumilus</i> C2A1  | Biodegradation of chlorpyrifos and its hydrolysis product 3,5,6-trichloro-2-pyridinol by <i>Bacillus pumilus</i> strain C2A1  | Anwar et al. (2009)           |
|           | <i>Bacillus licheniformis</i> ZHU-1   | Isolation and application of a chlorpyrifos-degrading <i>Bacillus licheniformis</i> ZHU-1   | Zhu et al. (2010)             |
|           | <i>Acremonium</i> sp. GFRC-1  | Fungal degradation of chlorpyrifos by <i>Acremonium</i> sp. strain (GFRC-1) isolated from a laboratory-enriched red agricultural  | Kulshrestha and Kumari (2011) |
|           | <i>Synechocystis</i> sp. strain PUPCCC 64   | Chlorpyrifos degradation by the cyanobacterium <i>Synechocystis</i> sp. strain PUPCCC 64  | Singh et al. (2011)           |
|           | <i>Pseudomonas stutzeri</i> B-CP5   | Isolation, characterization and fingerprinting of some chlorpyrifos-degrading bacterial strains isolated from Egyptian pesticides-polluted soils  | Awad et al. (2011)            |
|           | <i>Micrococcus luteus</i> NCIM 2103, <i>Bacillus subtilis</i> NCIM 2010 and <i>Pseudomonas aeruginosa</i> NCIM 2036       | Detoxification of chlorpyrifos by <i>Micrococcus luteus</i> NCIM 2103, <i>Bacillus subtilis</i> NCIM 2010 and <i>Pseudomonas aeruginosa</i> NCIM 2036   | Bhumbar et al. (2011)         |
|           | <i>Bacillus cereus</i>  | Bacterial degradation of chlorpyrifos by <i>Bacillus cereus</i>   | Liu et al. (2012)             |
|           | <i>Trichoderma harzianum</i> and <i>Rhizopus nodosus</i>  | Studied the biodegradation of chlorpyrifos by soil fungi  | Harish et al. (2013)          |
|           | <i>Azospirillum lipoferum</i> and <i>Paenibacillus polymyxa</i>   | To compare the capability of <i>Paenibacillus polymyxa</i> and <i>Azospirillum lipoferum</i> to degrade chlorpyrifos  | Romeh and Hendawi (2014)      |
|           | <i>Bacillus</i> sp. SMF5, <i>Penicillium</i> sp. F09-T10-1 and <i>Streptomyces thermocarboxydus</i> strain A-B            | Biodegradation of chlorpyrifos by microbial strains isolated from agricultural wastewater   | Fawzy et al. (2014)           |
|           | <i>Cellulomonas fimi</i> and <i>Phanerochaete chrysosporium</i>   | Biodegradation of chlorpyrifos by co-culture of <i>Cellulomonas fimi</i> and <i>Phanerochaete chrysosporium</i>   | Barathidasan et al. (2014)    |
|           | <i>Trichoderma viride</i>   | Degradation of DDT by a soil fungus <i>Trichoderma viride</i>   | Matsumura and Boush (1968)    |
|           | <i>Trichoderma viridae</i> , <i>Pseudomonas</i> sp., <i>Micrococcus</i> sp., <i>Arthrobacter</i> sp., <i>Bacillus</i> sp. | Screened DDT contaminated soil for DDT residues and toxicity to microorganisms, microbial biomass and dehydrogenase activity. Isolated two unicellular green algae and three di-nitrogen-fixing cyanobacteria and were tested for their ability to metabolize DDT | Patil et al. (1970)           |
|           | <i>Terrabacter</i> sp.  | Isolated a <i>Terrabacter</i> sp. strain from a 1-1-1-trichloro-2,2-bis(4-chlorophenyl) ethane residue-contaminated agricultural soil and studied the biotransformation of DDE  | Aislabie et al. (1999)        |
|           | <i>Pseudomonas acidovorans</i> M3GY   | Cometabolism of 1, 1-dichloro-2,2-bis (4-chlorophenyl) ethylene by <i>Pseudomonas acidovorans</i> M3GY grown on biphenyl  | Hay and Foch (1998)           |
|           | <i>Ralstonia eutropha</i> strain A5   | Transformation of 1,1-dichloro-2,2-(4-chlorophenyl) ethane (DDD) by <i>Ralstonia eutropha</i> strain A5   | Hay and Focht (2000)          |
|           | <i>Eubacterium limosum</i>  | Reductive dechlorination DDT by human intestinal bacterium <i>Eubacterium limosum</i> under anaerobic conditions  | Yim et al. (2008)             |
|           | <i>Azoarcus</i>   | Biodegradation of DDT by stimulation of indigenous microbial populations in soil with cosubstrates  | Ortiz et al. (2013)           |

Table 3 continued

| Pesticide        | Organism   | Nature of study   | Reference                       |
|------------------|--|---|---------------------------------|
| Diazinon         | <i>Serratia marcescens</i> DI101   | Biodegradation of diazinon by <i>Serratia marcescens</i> DI101 and its use in bioremediation of contaminated environment  | Abo-Amer (2011)                 |
|                  | <i>Serratia liquefaciens</i> and <i>Serratia marcescens</i>  | Isolation of Bacterial for Degradation of Selected Pesticide  | Hussaini et al. (2013)          |
|                  | <i>Pseudomonas aeruginosa</i> S1, <i>Bacillus amyloliquefaciens</i> S2, <i>Bacillus pseudomycoides</i> S4 and <i>Bacillus licheniformis</i> S5 | Diazinon decomposition by soil bacteria and identification of degradation products by GC-MS   | Tamer and El-Naggar (2013)      |
|                  | <i>Pseudomonas peli</i> BG1, <i>Burkholderia caryophylli</i> BG4 and <i>Brevundimonas diminuta</i> PD6   | Degradation of the organophosphorus insecticide diazinon by soil bacterial isolate  | Mahmuddin et al. (2014)         |
|                  | <i>Flavobacterium</i> sp.  | In situ enhanced bioremediation of dichlorvos by a phyllosphere <i>Flavobacterium</i> strain  | Ning et al. (2012)              |
| Dichlorovos      | <i>Proteus vulgaris</i> , <i>Vibrio</i> sp., <i>Serratia</i> sp. and <i>Acinetobacter</i> sp.  | Biodegradation of dichlorovos (organophosphate pesticide) in Soil by Bacterial Isolates   | Agarry et al. (2013)            |
|                  | <i>Bacillus</i> sp.  | Dieldrin degradation by soil microorganisms   | Matsumura and Boush (1967)      |
| Dieldrin         | <i>Pseudomonas</i> sp.   | Breakdown of dieldrin in the soil by a microorganism  | Matsumura et al. (1968)         |
|                  | <i>Arthobacter</i> sp., <i>Bacillus</i> sp.  | Evolution of CO <sub>2</sub> from soil incubated with dieldrin-14C  | Jagnow and Halder (1972)        |
|                  | <i>Phlebiabrevispora Nakasone</i> TMIC33929(strain YK543)  | Bioconversion of dieldrin by wood-rotting fungi and metabolite detection  | Kamei et al. (2010)             |
|                  | <i>Mucor racemosus</i> strain DDF  | Biodegradation of dieldrin by a soil fungus isolated from a soil with annual endosulfan applications  | Kataoka et al. (2010)           |
| Difluorobenzenes | <i>Cordyceps militaris</i> KS-92 and <i>Cordyceps brongniartii</i> ATCC66779   | Biodegradation of Dieldrin by <i>Cordyceps</i> Fungi and Detection of Metabolites   | Xiao and Kondo (2013)           |
|                  | <i>Rhodococcus opacus</i> GM-14  | Utilization of halogenated benzenes, phenols, and benzoates by <i>Rhodococcus opacus</i> GM-14  | Zaitsev et al. (1995)           |
|                  | <i>Rhodococcus</i> strain MS111  | Degradation of alkanes and highly chlorinated benzenes, and production of biosurfactants, by a psychrophilic <i>Rhodococcus</i> sp. and genetic characterization of its chlorobenzene dioxygenase | Rapp and Gabriel-Jürgens (2003) |
|                  | <i>Labrys portucalensis</i>  | Degradation of difluorobenzenes by the wild strain <i>Labrys portucalensis</i>  | Moreira et al. (2012)           |

Table 3 continued

| Pesticide    | Organism  | Nature of study   | Reference                      |
|--------------|---|---|--------------------------------|
| Endosulfan   | <i>Bacillus subtilis</i> MTCC1427   | Biodegradation of soil-applied endosulfan in the presence Biosurfactant   | Awasthi et al. (1999)          |
|              | <i>Staphylococcus</i> sp. and <i>Bacillus</i> strains   | Endosulfan mineralization by bacterial isolates and possible degradation pathway identification   | Kumara and Philipa (2006)      |
|              | <i>Pseudomonas aeruginosa</i>   | Effect of tween 80 added to the soil on the degradation of endosulfan by <i>Pseudomonas aeruginosa</i>  | Jayashree and Vasudevan (2007) |
|              | <i>Anabaena</i> sp. ATCC 7210   | Biodegradation of Endosulfan by <i>Anabaena</i>   | Shivaramaiah (2010)            |
|              | <i>Pseudomonas fluorescens</i>  | Biodegradation of endosulfan isomers in broth culture and soil microcosm by <i>Pseudomonas fluorescens</i> isolated from soil                 | Giri et al. (2014)             |
| Endrin       | <i>Nocardioopsis</i> species MJ435  | Degradation of organophosphate pesticide in liquid culture by marine isolate <i>Nocardioopsis</i> species                                     | Dudhagara et al. (2012)        |
|              | <i>Alcaligenes faecalis</i> JBW4  | Biodegradation of organochlorine pesticide endosulfan by bacterial strain <i>Alcaligenes faecalis</i> JBW4                                    | Kong et al. (2013)             |
|              | <i>Staphylococcus</i> , <i>Micrococcus</i> , <i>Bacillus</i> , <i>Pseudomonas</i> , <i>Mucor</i> , <i>Penicillium</i> , <i>Aspergillus fumigates</i> , <i>Candida</i> | Bioremediation of Endosulfan contaminated Soil  | Mohanasrinivasan et al. (2013) |
|              | <i>Klebsiella</i> sp. M3  | Biodegradation of Endosulfan in Broth Medium and in Soil Microcosm by <i>Klebsiella</i> sp. M3  | Singh and Singh (2014)         |
|              | <i>Trichoderma viride</i> 12, <i>Pseudomonas</i> sp. 27, <i>Micrococcus</i> 204, <i>Arthrobacter</i> sp. 278, <i>Bacillus</i> sp. 4                                   | Comparison of insecticide degradation by soil microorganisms  | Patil et al. (1970)            |
| Fenitrothion | <i>Flavobacterium</i> sp.   | Hydrolysis of selected organophosphorus insecticides by two bacterial isolates from flooded soil  | Adhya et al. (1981)            |
| Glyphosate   | <i>Burkholderia</i> sp. strain NF100  | Involvement of two plasmids in fenitrothion degradation by <i>Burkholderia</i> sp. strain NF100   | Hayasu et al. (2000)           |
|              | <i>Penicillium citrinum</i>   | Biotransformation of 6-nitrochrysene  | Pothuluri et al. (1998)        |
| HCN          | <i>Pseudomonas aeruginosa</i> and <i>Bacillus megaterium</i>  | Phyto-Microbial Degradation of Glyphosate in Riyadh Area  | Al-Arfaj et al. (2013)         |
|              | <i>Pseudomonas aeruginosa</i> WH-2  | Aqueous phase partitioning of hexachlorocyclohexane (HCH) isomers by biosurfactant produced by <i>Pseudomonas aeruginosa</i> WH-2             | Sharma et al. (2009)           |
|              | <i>Sphingomonas</i> sp. NM05  | Surfactant biodegradation of hexachlorocyclohexane (HCH) isomers by <i>Sphingomonas</i> sp. NM05  | Manickam et al. (2012)         |
| Heptachlor   | <i>Phanerochaete chrysosporium</i>  | Biodegradation of Heptachlor by <i>Phanerochaete chrysosporium</i> ME 446   | Arisoy and Kolankaya, (1998)   |
| Methomyl     | <i>Phlebia</i> sp.  | Metabolism of Organochlorine Pesticide Heptachlor and its Metabolite Heptachlor Epoxide by White-rot Fungi, Belonging to Genus <i>Phlebia</i> | Xiao et al. (2011)             |
|              | <i>Stenotrophomonas maltophilia</i> M1  | Degradation of methomyl by the novel bacterial strain <i>Stenotrophomonas maltophilia</i> M1  | Mohamed (2009)                 |

Table 3 continued

| Pesticide                               | Organism  | Nature of study  | Reference                      |
|---|---|--|--------------------------------|
| Methyl parathion                        | <i>Pseudomonas</i> sp.  | Isolation of a methyl parathion-degrading <i>Pseudomonas</i> sp. that possesses DNA homologous to the opd gene from a <i>Flavobacterium</i> sp.                          | Chaudry et al. (1988)          |
|   | <i>Bacillus</i> sp.   | Effect of yeast extract on the degradation of organophosphorus insecticides by soil enrichment and bacterial cultures  | Sharmila et al. (1989)         |
|   | <i>Pseudomonas fluorescens</i>  | Organophosphate utilization by the wild-type strain of <i>Pseudomonas fluorescens</i>  | Zboinska et al. (1992)         |
|   | <i>Plesiomonas</i> sp. strain M6  | Isolation of methyl parathion-degrading strain M6 and cloning of the methyl parathion hydrolase gene   | Cui et al. (2001)              |
| Monocrotophos (MCP)                     | <i>Stenotrophomonas maltophilia</i> M1  | Degradation of methomyl by the novel bacterial strain <i>Stenotrophomonas maltophilia</i> M1   | Mohamed (2009)                 |
|   | <i>Cyanobacteria</i>  | Biodegradation and Utilization of Organophosphorus Pesticide Malathion by <i>Cyanobacteria</i>   | Ibrahim et al. (2014)          |
|   | <i>Pseudomonas</i> sp. strain WBC-3   | Bioaugmentation of a methyl parathion contaminated soil with <i>Pseudomonas</i> sp. strain WBC-3   | Wang et al. (2014)             |
|   | <i>Arthrobacter atrocyaneus</i> MCM B-425 and <i>Bacillus megaterium</i> MCM B-423        | To study biomineralization of monocrotophos (MCP) and identify the metabolites formed during biodegradation  | Bhadbhade et al. (2002)        |
|   | <i>Paracoccus</i> sp. M1  | Isolation of a monocrotophos-degrading bacterial strain and characterization of enzymatic degradation  | Jia et al. (2007)              |
|   | <i>Aspergillus niger</i> MCP1   | Isolation and characterization of monocrotophos degrading activity of soil   | Jain et al. (2012)             |
| Parathion                               | <i>Pseudomonas stutzeri</i> MTCC 2300   | Microbial degradation of monocrotophos by <i>pseudomonas stutzeri</i>  | Barathidasan and Reetha (2013) |
|   | <i>Flavobacterium</i> sp. ATCC27551   | Degradation of Parathion by bacterial strain <i>Flavobacterium</i> that degrade parathion ATCC27551  | Sethunathan and Yoshida (1973) |
|   | <i>Bacillus</i> sp. and <i>Pseudomonas</i> sp.  | Degradation of parathion by bacteria isolated from flooded soil  | Siddaramappa et al. (1973)     |
|   | <i>Pseudomonas stutzeri</i>   | Parathion utilization by bacterial symbionts in a chemostat  | Daughton and Hsieh (1977)      |
| PCBs                                    | <i>Arthrobacter</i> spp., <i>Bacillus</i> spp   | Biologically induced hydrolysis of parathion in soil: kinetics and modelling   | Nelson et al. (1982)           |
|   | <i>Desulfomonile tiedjei</i> , <i>Desulfotobacterium</i> , <i>Dehalobacter restrictus</i> | Polychlorinated biphenyls and their biodegradation   | Borja et al. (2005)            |
| Polycyclic aromatic hydrocarbons (PAHs) | <i>Arthrobacter</i> sp. strain GLP-1  | Isolation and characterization of a mutant of <i>Arthrobacter</i> sp. strain GLP-1 which utilizes the herbicide glyphosate as its sole source of phosphorus and nitrogen | Pipke and Amrhein (1988)       |
|   | <i>Arthrobacter atrocyaneus</i> MCM B-425 and <i>Bacillus megaterium</i> MCM B-423,       | Biomineralization of an organophosphorus pesticide, Monocrotophos, by soil bacteria  | Bhadbhade et al. (2002)        |
| Propamocarb hydrochloride               | <i>B. amyloliquefaciens</i> IN937a <i>B. pumilus</i> SE34                                 | Biodegradation of soil-applied pesticides by selected strains of plant growth-promoting rhizobacteria (PGPR) and their effects on bacterial growth                       | Myresiotis et al. (2012)       |
| Thiamethoxam                            | <i>B. amyloliquefaciens</i> IN937a, <i>B. pumilus</i> SE34 <i>B. subtilis</i> FZB24       | Biodegradation of soil-applied pesticides by selected strains of plant growth-promoting rhizobacteria (PGPR) and their effects on bacterial growth                       | Myresiotis et al. (2012)       |
| 2,4-Dichlorophenoxy acetic acid         | <i>Aspergillus niger</i>  | Metabolism of 2,4-Dichlorophenoxyacetic Acid ('2,4-D') by <i>Aspergillus niger</i> van Tiegh   | Faulkner and Woodcock (1964)   |
|   | <i>Cupriavidus pinatubonensis</i> JMP134  | Simultaneous assessment of the effects of an herbicide on the triad: rhizobacterial community, an herbicide degrading soil bacterium and their plant host                | Kraiser et al. (2012)          |

waste (SMW), degrade the DDT (Purnomo et al. 2010b). Several pesticides were degraded through amide or ester hydrolysis mediated by the soil microorganism. Pentachlorobenzene was reduced to pentachloroaniline by specific microbes (Chacko et al. 1966).

Seo et al. (2007) reported five distinct bacterial strains (C3, C4, P1-1, JS14, and JS19b1) for degradation of polycyclic aromatic hydrocarbons (PAH). P1-1 can degrade carbophenothion, chlorfenvinphos, diazinon, fonofos, and pirimiphos-methyl. JS14 can transform chlorfenvinphos and diazinon. JS19b1 can break down diazinon, pirimiphos-methyl, and temephos. Other genera *Burkholderia* (Kang et al. 2003), *Pseudomonas* (Prabha and Phale 2003), *Sphingomonas* (Ye et al. 1996; Van Herwijnen et al. 2003) and *Stenotrophomonas* as Gram negative and *Mycobacterium* and *Rhodococcus* as Gram positive were so isolated and characterized for biodegradation of PAHs varying from two-ring PAHs to five ring PAHs (Beate et al. 1993; Moody et al. 2004). *Arthrobacter*, *Agrobacterium*, *Burkholderia*, *Enterobacter* (Cui et al. 2001; Johnsen et al. 2005; Bhadbhade et al. 2002; Pipke and Amrhein 1988) *Plesiomonas* and *Pseudomonas* (Horne et al. 2002a, b) have ability to degrade of a highly toxic and powerful inhibitory acetylcholinesterase organophosphorus pesticides (OPS) such as chlorpyrifos (Singh et al. 2003), coumaphos, diazinon, fenitrothion monocrotophos and parathion (Cui et al. 2001) (Table 3). Barragan-Huerta et al. (2007) isolated *Pseudomonas aeruginosa*, *P. putida*, *Stenotrophomonas maltophilia*, *Flavimonas oryzihabitans*, and *Morganella morganii* from coffee beans and identified as pesticide-degrading microorganism. *P. aeruginosa* and *F. oryzihabitans* have ability to degrade the DDT and endosulfan (Barragan-Huerta et al. 2007). Degradation of methomyl by the novel bacterial strain *Stenotrophomonas maltophilia* M1 observed by Mohamed (2009). Ortiz-Hernández and Sánchez-Salinas (2010) isolation *Stenotrophomonas maltophilia*, *Proteus vulgaris*, *Vibrio metschnikouii*, *Serratia ficaria*, *Serratia* spp. and *Yersinia enterocolitica* from agricultural soils and characterized as tetrachlorvinphos {phosphoric acid, ethenyl dimethyl ester 2-chloro-1-(2,4,5-trichlorophenyl)} degrading bacteria.

Matsumura and Boush (1966) isolated various microorganisms from the agricultural soils of northern Ohio, which have the ability for degradation of

malathion through the action of a carboxylesterase. The cleavage of the aromatic ring is a common reaction when soil microorganisms degrade pesticide which is not usually encountered in higher animals. Thomas and Parkins (1995) categorized atrazine degraders into two groups; one degrades the side chains and other degrades the rings. Few microorganisms can condense or conjugate pesticides (Burchfield and Storrs 1957). Several recent studies have been reported that the different microbial strains have different potential for pesticide degradation in lab and field condition (Table 3). Ibrahim et al. (2014) reported that Cyanobacteria showed significant degradation of malathion. Similarly Liming et al. (2014) observed that the *Pseudomonas* sp. strain WBC-3 showed efficient degradation of methyl parathion (Table 3). The *Burkholderia* spp., *Achromobacter* spp., *Alcaligenes* spp., *Ralstonia* spp., and *Rhodanobacter* spp. bacterial species have the ability for rapid degradation of aromatic hydrocarbons (Bacosa et al. 2010, 2013). The degradation of n-hexadecane by a microbial consortium in the presence of electric field in soil has been evaluated up to 53.7 %, and it can be enhanced by 20.3 % without electric field. The mechanism of n-hexadecanoic acid what supposed to be intracellular  $\beta$ -oxidation (Yuan et al. 2013). Thus, the availability of such microbes under pesticide stress may provide efficient, cheaper and environmentally friendly solution for bioremediation of xenobiotic contaminated soil (Pallud et al. 2004).

#### 4 Molecular approaches for pesticide degradation

The microbial degradation of pesticide involves various types of enzyme. These methods are based on various types of genes coded with plasmid or chromosomal DNA. Pesticidal degradative genes in microbial strains have been found to be located on plasmids, transposons, and/or on chromosomes. Current studies have provided clues to the evolution of degradative pathways and the organization of catabolic genes, thus making it much easier to develop genetically engineered microbes for the purpose of pesticide degradation. Genetically engineered microorganisms have substantial ability to degrade the pesticide because they secrete various specific enzymes which have a specific catabolic gene into plasmids. The recombinant DNA studies have made it

possible to develop DNA and RNA probes that are being used to identify microbes from diverse environmental communities with a unique ability to degrade pesticides (Kumar et al. 1996). With the help of quantitative measurements of soil DNA and RNA; Bælum et al. (2008) inferred that the repeated application of the soil herbicide MCPA (2-methyl-4-chlorophenoxyacetic acid) resulted in an increased population of microorganisms that could degrade the compound. Similarly, Lancaster et al. (2010) applied five rounds of the herbicide glyphosate to soil and found that the microbial biomass incorporated the herbicide faster after four rounds of applications.

#### 4.1 Mechanism of enzyme based pesticide degradation by microbes

Pesticide degradation is a process that involves the complete rupture of an organic compound into inorganic constituents of pesticide by pesticide degrading microbes. The biodegradation involves transferring the substrates and products within a well-coordinated microbial community, a process referred to as metabolic cooperation under natural environments (Abraham et al. 2002). Enzyme based pesticide degradation process is an innovative treatment technique for removal of pesticide from polluted environments. Fungi and bacteria are considered as the extracellular enzyme-producing microorganisms for degradation of pollutant. White rot fungi have been used as promising bioremediation agents, especially for compounds not readily degraded by bacteria. The production and secretion of extracellular enzymes in microbes by environmental effects could be of interest. Some of these extracellular enzymes are involved in lignin degradation, such as lignin peroxidase, manganese peroxidase, laccase and oxidases. Several microbial strains that degrade pesticide have been listed in Table 4. Transferases, isomerases, hydrolases and ligases enzymes are responsible for the biodegradation of the pesticides. These enzymes catalyze metabolic reactions including hydrolysis, oxidation, addition of an oxygen to a double bond, oxidation of an amino group ( $\text{NH}_2$ ) to a nitro group, addition of a hydroxyl group to a benzene ring, dehalogenation, reduction of a nitro group ( $\text{NO}_2$ ) to an amino group, replacement of a sulfur with an oxygen, metabolism of side chains, ring cleavage.

The metabolism of pesticides involves three phase process; in first phase process the initial properties of a parent compound are transformed through oxidation, reduction, or hydrolysis to generally produce a more water-soluble and usually a less toxic product than the parent, in second phase process involves conjugation of a pesticide to a sugar or amino acid, which increases the water solubility and reduces toxicity compared with the parent pesticide, and in third phase process helps in conversion of second phase metabolites into secondary conjugates, which are also non-toxic. In these processes fungi and bacteria are involved producing intracellular or extra cellular enzymes including hydrolytic enzymes, peroxidases, oxygenases, etc. (Van Herwijnen et al. 2003; Ortiz-Hernández et al. 2011).

Hydrolases are a broad group of enzymes which helps in pesticide biodegradation. It catalyzes the hydrolysis of several major biochemical classes of pesticide (esters, peptide bonds, carbon-halide bonds, ureas, thioesters, etc.) (Scott et al. 2008). Organophosphate hydrolases (OPH or Phosphotriesterase) enzyme isolated from *Pseudomonas diminuta* and *Flavobacterium* sp. (Table 4). The first isolated phosphotriesterase belongs to the *Pseudomonas diminuta* strain MG, this enzyme encoded by a gene called *opd* (organophosphate-degrading) and shows a highly catalytic activity towards organophosphate pesticides. These enzymes specifically hydrolyze phosphoester bonds, such as P–O, P–F, P–NC, and P–S (Ortiz-Hernández et al. 2003). Other microbial enzymes such as organophosphorus hydrolase (OPH; encoded by the *opd* gene), methyl-parathion hydrolase (MPH; encoded by the *mpd* gene), and hydrolysis of coroxon (HOCA; encoded by the *hocA* gene), were isolated from *Flavobacterium* sp. (Sethunathan and Yoshida 1973), *Plesimonas* sp. strain M6 (Cui et al. 2001) and *Pseudomonas moteilli* (Horne et al. 2002a, b), respectively.

Esterase have been cloned and proteins have sequenced from several microorganism, e.g. two ferulic acid esterases from *Aspergillus tubingensis*, a cephalosporin esterase from the yeast *Rhodospiridium toruloides*, a chrysanthemic acid esterase from *Arthrobacter globiformis*, and several other esterase from *Pseudomonas fluorescens* strain. These enzymes used for biodegradation of various types of organophosphate, and other herbicide and insecticide. Cytochrome P450 oxidoreductases helps in degradation of



**Table 4** Pesticide degrading enzyme of various microbial strains and their co factors

| Enzyme                         | Cofactor requirements                 | Source organism(s)  | Documented target pesticide(s)                            | Current bioremediation strategies employed      |
|--------------------------------|---------------------------------------|---|---|---|
| <b>Oxidoreductases</b>         |                                       |   |   |   |
| Gox                            | Flavin (FAD)                          | <i>Pseudomonas</i> sp LBr;<br><i>Agrobacterium</i> strain T10 | Glyphosate  | In plant  |
| <b>Monooxygenases</b>          |                                       |   |   |   |
| Esd                            | Flavin and NADH                       | <i>Mycobacterium</i> sp.                                      | Endosulfan and Endosulfate                                | Not yet in use                                  |
| Ese                            | Flavin (FMN)                          | <i>Arthrobacter</i> sp  | Endosulfan and Endosulfate                                | Not yet in use                                  |
| Cyp1A1/1A2                     | Heme and NADH                         | Mammalian (Rat)   | Atrazine, Norfl urazon and Chlortoluron                   | In plant  |
| Cyp76B                         | Heme and NADH                         | <i>Helianthus tuberosus</i>                                   | Linuron, Chlortoluron and Isoproturon                     | In plant  |
| P450                           | Heme and NADH                         | <i>Pseudomonas putida</i>                                     | Hexachlorobenzene and Pentachlorobenzene                  | Transgenic <i>Sphingobium chlorophenolicum</i>  |
| <b>Dioxygenase</b>             |                                       |   |   |   |
| TOD                            | Fe <sup>2+</sup> and NADH             | <i>Pseudomonas putida</i>                                     | Trifl uralin herbicides                                   | Not yet in use against Pesticides               |
| E3                             | None                                  | <i>Lucilia cuprina</i>  | Synthetic pyrethroids and phosphotriester insecticides    | Not yet in use                                  |
| <b>Phosphodiesterases</b>      |                                       |   |   |   |
| PdeA                           | None                                  | <i>Delftia acidovorans</i>                                    | Organophosphorus compounds                                | Free-enzyme bioremediation                      |
| <b>Phosphotriesterases</b>     |                                       |   |   |   |
| OPH                            | Fe <sup>2+</sup> and Zn <sup>2+</sup> | <i>Agrobacterium radiobacter</i>                              | Insecticides phosphotriester                              | Free-enzyme bioremediation                      |
| OpdA                           | Fe <sup>2+</sup> and Zn <sup>2+</sup> | <i>Pseudomonas diminuta</i><br><i>Flavobacterium</i> sp.      | Parathion, methyl parathion, malathion, coumaphos, others |   |
| <b>Phosphonatase</b>           |                                       |   |   |   |
| Phn                            | None                                  | <i>Escherichia coli</i><br><i>Sinorhizobium meliloti</i>      | Organophosphorus compounds                                |   |
| <b>Haloalkane dehalogenase</b> |                                       |   |   |   |
| LinB                           | None                                  | <i>Sphingobium</i> sp.; <i>Sphingomonas</i> sp                | Hexachlorocyclohexane ( $\beta$ - and $\delta$ - isomers) | Bioaugmentation with <i>Sphingobium indicum</i> |
| AtzA                           | Fe <sup>2+</sup>                      | <i>Pseudomonas</i> sp. ADP                                    | Chloro-s-triazine herbicides                              | In plant and GM bacteria                        |
| TrzN                           | Zn <sup>2+</sup>                      | <i>Nocardioideis</i> sp.                                      | Chloro-s-triazine herbicides                              | Not yet in use                                  |
| LinA                           | None                                  | <i>Sphingobium</i> sp.; <i>Sphingomonas</i> sp.               | Hexachlorocyclohexane ( $\gamma$ - isomer)                | Bioaugmentation with <i>Sphingobium indicum</i> |

Table 4 continued

| Enzyme    | Cofactor requirements          | Source organism(s)              | Documented target pesticide(s)                       | Current bioremediation strategies employed |
|-----------|--------------------------------|---------------------------------|--|--|
| TfdA      | $\alpha$ -ketoglutarate and Fe | <i>Ralstonia eutropha</i>       | 2,4-dichlorophenoxyacetic acid and pyridyl-oxyacetic | Not yet in use                             |
| DMO       | NADH and a Rieske Fe-S centre  | <i>Pseudomonas maltophilia</i>  | Dicamba  | Not yet in use                             |
| C-P-lyase |                                |                                 |  |  |
| Glp A&B   | None                           | <i>Pseudomonas pseudomallei</i> | Organophosphorus compounds                           | Not yet in use                             |
| ND        |                                |                                 |  |  |
| hocA      | None                           | <i>Pseudomonas monteilii</i>    | Organophosphorus compounds                           | Not yet in use                             |
| mpd       | None                           | <i>Pseudomonas</i>              | Organophosphorus compounds                           | Not yet in use                             |

Source: Singh and Walker (2006), Scott et al. (2008), Riya and Jagatpati (2012)

atrazine, norflurazon and chlortoluron from soils. Cytochrome CYP76B1 isolated from *Helianthus tuberosus* was cloned into tobacco and Arabidopsis. This enzyme has capability to catalyse the oxidative dealkylation of phenylurea herbicides such as linuron, chlortoluron and isoproturon (Didierjean et al. 2002). Prokaryotic cytochrome P450 s isolated from *Pseudomonas putida* (Chen et al. 2002) and *Sphingobium chlorophenolicum* have great potential to degrade chlorinated pentachlorobenzene and hexachlorobenzene (Yan et al. 2006). Toluene dioxygenases (TOD) enzyme isolated from *P. putida* F1 that is highly used as degradation of toluene, polychlorinated hydrocarbons, ethylbenzene and p-xylene (Table 4).

Haloalkane dehalogenases (Dh1A) enzyme encoded gene *LinB* isolated from *Xanthomonas thobacter autotrophicus* GJ10; haloacetate dehalogenase (DehH1) from *Moraxella* sp.B; and 2-hydroxymuconic semialdehyde hydrolase (DmpD) from *Pseudomonas* sp. CF600 which is responsible for degradation of hexachlorocyclohexane (HCN). Oxidoreductase is an enzyme that catalyses oxidation and reduction reaction. It is important enzyme like glyphosate oxidase (GOX) for glyphosate degradation. This enzyme is a flavoprotein amine oxidase from *Pseudomonas* sp. LBr that catalyses the oxidation of glyphosate to form aminomethylphosphonate (AMPA) and releases the keto acid glyoxylate (Scott et al. 2008).

*Mycobacterium tuberculosis* ESD strains secrete endosulfan monooxygenase II enzyme which degrade the beta-endosulfan to the monoaldehyde and hydroxyether but transforms alpha-endosulfan to the more toxic endosulfan sulfate. Alternatively, hydrolysis of endosulfan in some bacteria (*Pseudomonas aeruginosa*, *Burkholderia cepacia*) yields the less toxic metabolite endosulfan diol (Kumar et al. 2007). Endosulfan can spontaneously hydrolyze to the diol in alkaline conditions, so it is difficult to separate bacterial from abiotic hydrolysis. *Phanerochaete chrysosporium* and *T. versicolor* have ability to degrade simazin, dieldrin and trifluralin pesticides independently by laccase activity (Magan and Fragueiro 2005).

#### 4.2 Mechanism of catabolic based pesticide degradation by microbes

The pesticide has been degraded by various microbial strains for detoxification of pollutant that may be used

as energy source. The ubiquitous nature of microbes on the earth has capability to catalyze the mechanism of pesticide degradation (Paul et al. 2005). The microbes degrade toxic material because they have some specific genes in their genetic material (chromosomal or plasmid DNA) (Table 5). First catabolic plasmid DNA was isolated from *Pseudomonas putida* as CAM plasmid. This plasmid controls the oxidation of the naturally occurring terrene and camphor (Rheinwald et al. 1973). Such catabolic plasmid with encoded gene degrades the synthetic molecules. The plasmid (pJP1) encoded with gene degrades the notorious organochlorine herbicide 2, 4-D (Pemberton and Fisher. 1977). The intensively studied 2,4-D plasmid (pJP4) isolated by *Ralstonia eutropha* strains JMP134 have very broad host range and one or more clusters of degradative genes have been encoded for the degradation of the organochlorines 2,4-D and 3-chlorobenzoate (3-CBA) (Pemberton and Schmidt 2001). In certain cases these catabolic gene clusters occur within transposable elements and therefore each one move unfettered among plasmids and the main chromosome. *Ralstonia eutropha* (Tn4371), *Burkholderia cepacia* (Tn5530), *Pseudomonas putida* (Tn4654) and *Alcaligenes* sp. (Tn5271) have various transposon for degradation of biphenyl 4-chlorobiphenyl, 2,4-D, Toluene, 3-Chlorobenzoate and Carbofuran, respectively (Table 5). The evolution of microbial genes involved in the biodegradation of xenobiotic molecules could be a powerful and positive development in the fight against environmental pollution.

#### 4.3 Catabolic bio-degradation pathway and its operon system

Catabolism of aromatic compounds in bacteria has revealed that the various enzymes (e.g. monooxygenase, dehydrogenase, hydrolase, oxygenase and isomerase etc.) involve for conversion of toxic chemical of pesticide into various intermediate product such as protococatechuate and (substituted) catechols (Clarke 1984; Gibson and Subramanian 1984; Reineke 1984; Fewson 1988; Reineke and Knackmuss 1988; Commandeur and Parsons 1990; Chaudhry and Chapalamadugu 1991). These dihydroxylated intermediates (protocatechuate and catechols) are directly enter into one of two possible pathways, either a meta cleavage-type or an ortho cleavage-type pathway which supply

central metabolic routes such as the tricarboxylic acid cycle (Harayama et al. 1989; van der Meer et al. 1992) (Fig. 3). The aromatic ring fission catalysed by dioxygenases enzyme of these pathways occurs between the hydroxyl groups (intradiol or ortho cleavage), or adjacent to one of the hydroxyls (extradiol or meta cleavage) (Fig. 3). Meta cleavage pathways such as; the lower pathway on plasmid pWWO, pNAH7 and VI150 (from a *Pseudomonas* strain that uses phenol, cresols and 3,4-dimethylphenol as sole carbon and energy sources) show homology for similar cleavage. Such meta-cleavage pathways degrade the methylated catecholic substrates. The TOL plasmid pWW0 isolated from the *Pseudomonas putida* has various gene and encodes a set of enzymes involved in the conversion of toluene and xylenes to their carboxylic acid derivatives. TOL plasmids are self-transmissible and contain two or more operons which encode enzymes required for the degradation of methylbenzenes, such as toluene, xylenes, and 1, 2, 4 trimethylbenzene, via methylbenzoates (Williams and Worsey 1976; Frantz and Chakrabarty 1986; Burlage et al. 1989; Harayama et al. 1989; Assinder and Williams 1990; Harayama and Rekik 1990; Saint et al. 1990). The pathways of TOL degradation consist two parts: first one is upper pathways that have skill to convert toluene and xylene into carboxylic acid derivatives (Harayama et al. 1989) and second one is a lower (or meta-cleavage) pathway transfer the carboxylic acid to the precursors of Krebs cycle intermediates (Harayama and Rekik 1990).

The TOL plasmid pWW0 bears one operon (xylCMABN) of upper-pathway which encodes for secretion of benzaldehyde dehydrogenase (xylC), xylene monooxygenase (xylMA), benzyl alcohol dehydrogenase (xylB) enzymes and the gene xylN is an outer membrane porin involves in m-xylene uptake. These enzymes oxidize methylbenzenes to methylbenzoates (Harayama et al. 1986, 1989) that is the upper pathway, while the “lower-pathway” includes meta operon having 13 genes. These genes encoded by the operon (xylXYZLTEGFJQKIH) are responsible for conversion of methylbenzoates to pyruvate, acetaldehyde, and acetate via (methyl) catechols (Franklin et al. 1983; Harayama and Rekik 1990) (Fig. 4). The gene xylXYZ (benzoate dehydrogenase), xylT (ferredoxin) xylE (catechol 2,3-oxygenase), xylG (2-hydroxymuconic semialdehyde dehydrogenase), xylF (2-hydroxymuconic semialdehyde), xylJ (2-Oxopent-

**Table 5** Pesticide degrading gene found in plasmid/chromosome of various microbial strains

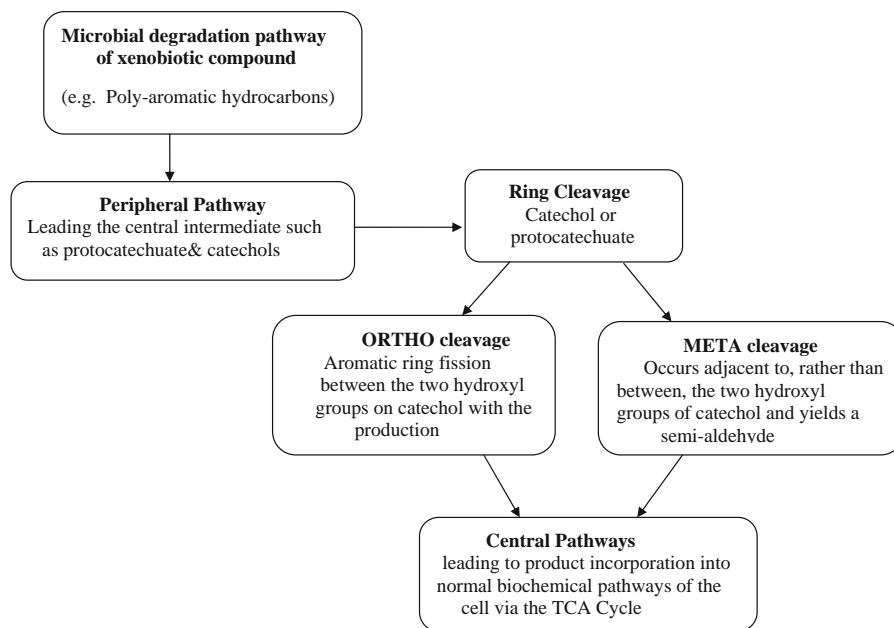
| Bacterium                                   | Substrate degraded   | Gene  | Location                | Reference   |
|---|--|---|-------------------------|---|
| <i>Alcaligenes eutrophus</i>                | 2,4-D  | <i>tfdA/tfdB/tfdC/tfdD/tfdE/tfdF/tfdR</i>                     | Plasmid and Chromosomal | Don and Penberton (1981)                                    |
| <i>Alcaligenes</i> sp.                      | PCB  | <i>bphA/bphB/bphC/bphD</i>                                    | Plasmids                | Shields et al. (1985)                                       |
| <i>Alcaligenes faecalis</i>                 | Phenanthrene   | <i>phnAa/phnAc/phnAd/</i>                                     | Plasmid                 | Habe and Omori (2003), Chauhan et al. (2008)                |
| AFK2  |  | <i>phnB/phnC/phnD/phnE/</i>                                   |                         |   |
|   |  | <i>phnF/phnG phnH/phnI</i>                                    |                         |   |
| <i>Arthrobacter keyseri</i> 12B             | Phthalate  | <i>ptrD/ptrA/ptrB/ptrC/ptrAa/phnAb/</i><br><i>phnAc/PhnAd</i> | Plasmid                 | Vamsee and Phale (2008)                                     |
| <i>Burkholderia</i> PS12                    | 1,2,4,5-tetrachlorobenzene   | <i>tecAB</i>  | Plasmids                | Beil et al. (1999)  |
| <i>Comamonas</i>                            | Paratoluenesulfonicacid  | <i>tsa</i>  | Plasmid                 | Tralau et al. (2001)  |
| <i>testosterone</i> T-2                     |  |   |                         |   |
| <i>Nocardioideis</i> KP7                    | Phenanthrene   | <i>phd</i>  | Chromosome              | Habe and Omori (2003)                                       |
| <i>Pseudomonas putida</i>                   | Napthalene   | <i>pahA/pahAb/pahB/pahC/pahD/pahE/</i><br><i>pahF</i>         | Chromosome              | Habe and Omori (2003), Chauhan et al. (2008)                |
| <i>Sphingomonas</i> sp. P2                  | Biphenyl, Napthalene, Phe naphthalene, Anthacene, Dibenzofuran, Fluorene, Fluoranthene, Pyrene | <i>ahd, bph, nah, xyl,</i>                                    | No report               | Pinyakong et al. (2000, 2003)                               |
| <i>Sphingobium yanoikuyae</i> B1            | Toluene, Xylene, Biphenyl, Napthalene  | <i>bph/nap/xyl</i>  | Chromosome              | Gibson et al. (1973), Zylstra and Kim (1997), Gibson (1999) |
| <i>Sphingobium yanoikuyae</i> Q1            | Toluene, Xylene, Biphenyl, Napthalene,   | <i>bph</i>  | Chromosome              | Furukawa et al. (1983)                                      |
| <i>Sphingobium</i> sp. LB126                | Fluorene   | <i>fld</i>  | No report               | Bastiaens et al. (2000), Wattiau et al. (2001)              |
| <i>Sphingobium agrestis</i> HV3             | Toluene, Napthalene  | <i>cnp</i>  | Plasmid                 | Klipi et al. (1980), Yrjala et al. (1997)                   |
| <i>Sphingomonas paucimobilis</i> Var.EPA505 | Pyrene   | <i>pbhD</i>   | Chromosome              | Kanally and Harayama (2000)                                 |
| <i>Sphingobium indicum</i> B90A             | HCH  | <i>linA/linA2/linX1</i>                                       | Chromosome              | Malhotra et al. (2007)                                      |
| <i>Sphingomonas paucimobilis</i> Var.EPA505 | Pyrene   | <i>linB/linC/linX2/linX3</i>                                  | Chromosome              | Kanally and Harayama (2000)                                 |
| <i>GMMs degrading organic compound</i>      |  | <i>pbhD</i>   | Chromosome              |   |
| <i>Burkholderia cepacia</i> L.S.2.4         | Toluene  | pTOD plasmid  | Plasmid                 | Barac et al. (2004)   |

Table 5 continued

| Bacterium   | Substrate degraded    | Gene                     | Location | Reference             |
|---|-----------------------|--------------------------|----------|-----------------------|
| <i>Burkholderia cepacia</i> VM1468                                    | Toluene               | pTOM-Bu61 plasmid        | Plasmid  | Taghavi et al. (2005) |
| <i>Escherichia coli</i> AtzA  | Atrazine              | Atrazine chlorohydrolase | Gene     | Strong et al. (2000)  |
| <i>Pseudomonas fluorescens</i> HK44                                   | Naphthalene           | luxCDABE                 | Gene     | Sayler et al. (2000)  |
| <i>Pseudomonas putida</i> KT2442(Pnfl42::TnMo-d-OTc)                  | Naphthalene           | pNF142 plasmid, gfp      | Plasmid  | Filonov et al. (2005) |
| <i>Pseudomonas fluorescens</i> F113rif <sup>brm</sup> BP 1::gfp-mut 3 | Chlorinated biphenyls | Operon bph, gfp          | Plasmid  | Boldt et al. (2004)   |

4-enoate hydratase), xylQ (acetyl dehydrogenase), xylK (4-Hydroxy-2-oxovalerate aldolase), xylII (4-Oxalocrotonate decarboxylase) and xylH (4-Oxalocrotonate tautomerase) encoded by respective enzymes are the part of meta cleavage pathway (Fig. 4). Catabolic pathways are controlled by specific regulatory proteins, which recognize inducer molecules and interact with promoter-operator regions of the catabolic operons. In the TOL-encoded pathways, xylR and xylS coordinately regulate the full transcription of the xyl operons (Spooner et al. 1986; Nakazawa et al. 1990). xylR is responsible for activation of regulatory gene while the xylS only activate the lower pathway for the degradation of toluene and xylene polyaromatic hydrocarbon (Holtel et al. 1990).

The modified ortho cleavage pathways helps for catabolism of chlorobenzoates, chlorobenzene and chlorophenoxyacetate which produce chlorinated catechol intermediates. These are dealt with plasmid-borne gene (Harwood and Parales 1996); tfd pathway for the degradation of 2,4-D carried by pJP4 plasmid which was isolated from the bacterial strains *Alcaligenes eutrophus* JMP134 (*Ralstonia eutropha*). The size of plasmid is 88 kb which is a self-transmissible broad—host—range, catabolic plasmid. The five operons are responsible for ortho-cleavage pathway. The largest operon is tfdCDEF and tfdCIIDIEIIFII which contain genes of a modified ortho cleavage pathway (Fig. 5). tfdA, tfdB and tfdBII also encode enzymes, while tfdK encodes a transporter protein involved in the uptake of 2,4-D (Pemberton and Schmidt 2001). The *tfdA* gene encodes a dioxygenase that converts 2, 4-D to 2, 4-dichlorophenol (Fukumori and Hausinger 1993). The *tfdB* gene encodes a 2, 4-dichlorophenol monooxygenase that hydroxylates 2, 4-dichlorophenol to 3, 5-dichlorocatechol (Perkins et al. 1990). Two different gene clusters, *tfdCIDIEIFI* and *tfdDIICIEIIFII*, encode enzymes for the catabolism of chlorocatechols to 3-oxoadipate (Fig. 5). The enzymes from both modules are active during degradation of 2, 4-D (Leveau et al. 1999; Laemmli et al. 2000) and 3-CB (Pelrez-Pantoja et al. 2000). Two identical regulatory genes, *tfdR* and *tfdS* control the whole function of operons (Matrubutham and Harker 1994). According to Genthner et al. (1989) the order of degradability of monochlorophenol was meta > ortho > para. Themel et al. (1996) reported anaerobic dehalogenation of 2-chlorophenol, a common intermediate of polychlorophenol degradation, by mixed



**Fig. 3** Microbial degradation pathway of xenobiotic compound

bacterial cultures. Masunaga et al. (1996) proposed dechlorination pathway of chlorophenols in contaminated sediment (Table 6).

## 5 Genetically modified microbes (GMMs) for pesticide degradation

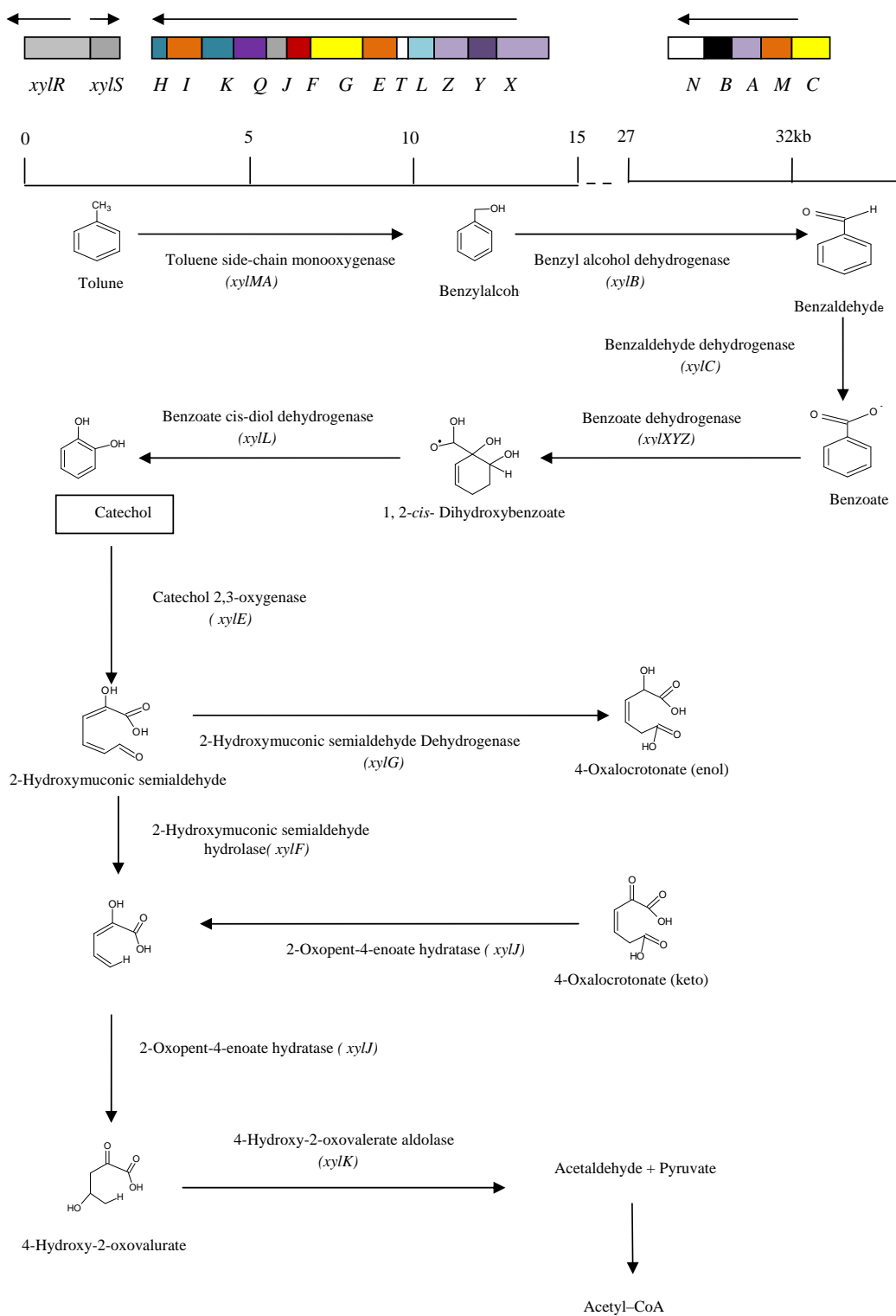
For more than a century, microbes have been consciously introduced into the environment for specific purposes. The scientists have attempted to produce microbes or plants with enhanced capability to degrade toxic compounds and organic pollutants in the environment. Biodegradation is largely considered as a less expensive alternative to physical and chemical disposal of pollutants (Amarger 2002). Current knowledge on microbial genetics allows us to construct new strain with exciting capabilities. Such genetically modified microorganisms (GMMs) have been postulated to be applicable in agriculture for effective degradation of pesticides, control of plant pathogen (biocontrol), and to improve plant growth (biofertilizers) (Amarger 2002). Wasilkowski et al. (2012) stated that the combination of conventional microbiology, biochemistry, ecology and genetic engineering is a very effective tools and techniques

for in situ bioremediation. Several reports showed that GMMs had higher tendency to crumble of various organic pollutant as compared with natural or indigenous strains (Cases and de Lorenzo 2005).

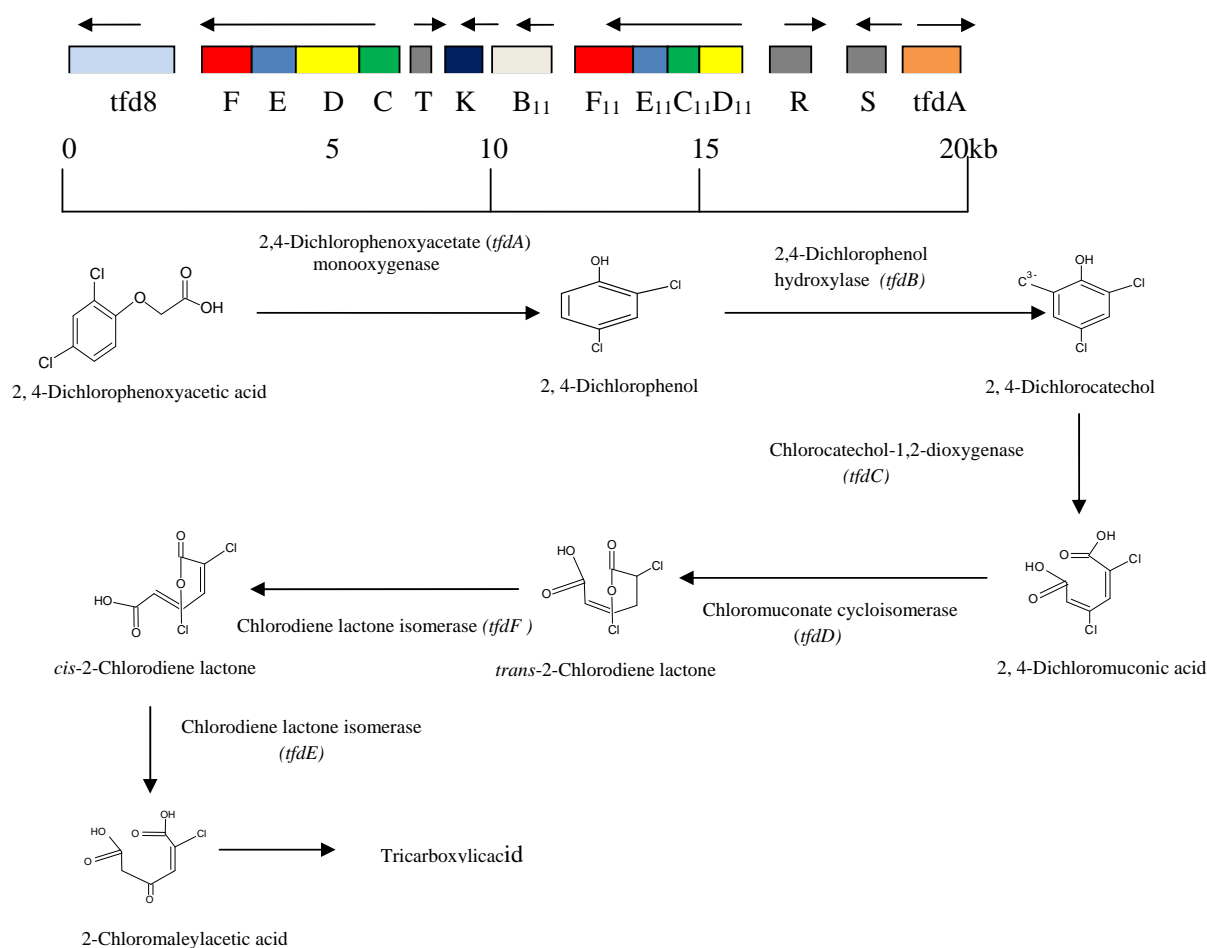
Kuritz and Wolk (1995) reported that the two cyanobacteria have natural ability to degrade a highly chlorinated aliphatic pesticide and lindane (gamma-hexachlorocyclohexane). Studies have shown that such abilities may be enhanced by genetic engineering to degrade another chlorinated pollutant, 3-chlorobenzoate. The genetically engineered *E. coli* degrades organophosphate pesticides with surface-expressed organophosphorus hydrolase (Mulbry and Kearney 1991; Chen and Mulchandani 1998). A novel approach to convalescing the capability of soil microbes to degrade 2,4-D was by natural conjugative transfer of plasmids encoding degradation ability (Top et al. 1998). *E. coli* with plasmids were introduced to 2,4-D contaminated soil and transfer of the plasmids to indigenous soil bacteria established, with augmented consumption of 2,4-D.

When GMMs are introduced in field condition, then, so many biotic and abiotic factors affect their survival in nature. Among the physiological factors; high clay content, high pH and relatively high moisture content can have a positive effect on





**Fig. 4** Meta-cleavage pathway of organic pollutant (e.g. Toluene). Adopted from Pemberton and Schmidt (2001)



**Fig. 5** Ortho-cleavage pathway for degradation of pesticide (e.g. 2,4-Dichlorophenoxy). Adopted from Pemberton and Schmidt (2001)

**Table 6** Few examples of catabolic transposons

| Bacterium                              | Phenotype (substrate degraded) | Transposon      | Reference                  |
|--|--------------------------------|-----------------|----------------------------|
| <i>Pseudomonas</i> sp. (pP51)          | Chlorobenzene (CB)             | Tn5280          | Van der Meer et al. (1991) |
| <i>Alcaligenes</i> sp. strain BR60     | Chlorobenzoates                | Tn5271          | Nakatsu et al. (1995)      |
| <i>P. putida</i> ML2 (pHMT112)         | Benzene                        | Tn5542          | Tan (1999)                 |
| <i>R. eutropha</i> NH9 (pENH91)        | 3CBA                           | Tn5707          | Tan (1999)                 |
| <i>P. putida</i> mt-2 (pWWO)           | Toluene, xylene                | Tn4651          | Tsuda et al. (1999)        |
| <i>P. putida</i> mt-2 (pWWO)           | Toluene, xylene                | Tn4653          | Tsuda et al. (1999)        |
| <i>P. putida</i> MT53 (pWW53)          | Toluene, xylene                | Tn4656          | Tsuda et al. (1999)        |
| <i>P. putida</i> G7 (NAH7)             | Naphthalene                    | Tn4655          | Tsuda et al. (1999)        |
| <i>R. oxalatica</i> A5                 | Biphenyl/4-chlorobiphenyl      | Tn4371          | Merlin et al. (1999)       |
| <i>Ralstonia eutropha</i> A5           | (Chloro)biphenyl               | Tn4371          | Springael et al. (2001)    |
| <i>P. putida</i> KF715                 | Biphenyl/salicylate            | bph-sal element | Nishi et al. (2000)        |
| <i>Pseudomonas</i> sp. B13             | Chlorocatechol                 | clc element     | van der Meer et al. (2001) |
| <i>Burkholderia cepacia</i> 2a (pIJB1) | 2,4-dichlorophenoxyacetate     | Tn5530          | Poh et al. (2002)          |

microbial survival (Da and Deng 2003; Heijnen et al. 1988; Van Elsas et al. 1986). Factors that negatively affect the number of introduced microbes include; dry periods, presence of competing microorganisms, and predation by protozoa and lysis by bacteriaophage (Ashelford et al. 2000; Eberl et al. 1997; Johansen et al. 2002). On the other hand, GMMs could evolve and adapt to the prevailing environmental conditions via natural selection. Velicer (1999) reported that the evolutionary adaptation of microorganism to degrade the herbicide 2,4-dichlorophenoxyacetic acid could result in increased competitive fitness to use succinate as a substrate. Although an innumerable of different GM strain has been constructed for bioremediation but their successful applications in the field are rare (Haro and de Lorenzo 2001; Morrissey et al. 2002; Van Limbergen et al. 1998). Moreover, difficulties to scale up the laboratory experiments, low bioavailability of compound, and legislative problems with applying GM strain have precluded wide-scale use.

Halden et al. (1999) studied that the degradation of 3-phenoxybenzoic acid in soil and could increase GMM survival and 3-phenoxybenzoic acid degradation six orders of magnitude by adding phosphate and nitrogen. An example of a field scale remediation is the study of Strong et al. (2000), *P. fluorescens* HK44 with a lux gene fused to a naphthalene-degradative pathway and it was the first GM strain approved for field release in the US (Ripp et al. 2000; Strong et al. 2000). *P. fluorescens* HK44 having pUTK21 plasmid, which was made by transposon Tn4431 insertion into NAH7 plasmid from *P. fluorescens* 5R. This transposon originated from *Vibrio fischeri* which having luxCDABE gene cassette (Sayler and Ripp 2000). The other GMM strain e.g. *P. putida* KT2442 (pNF142::TnMod-OTc) have ability to degrade naphthalene in soil (Filonov et al. 2005). *P. putida* KT2442 has been constructed by three strains of *Escherichia coli* S17-1 with pTnMod-OTc plasmid (carrying tetracycline resistance gene), *Pseudomonas* sp. 142NF (pNF142) able to degrade naphthalene and *P. putida* KT2442 with *gfp* gene localized in chromosome. Other study, Lipthay et al. (2001) reported the degradation of 2,4-dichlorophenoxyacetic acid (2,4-D) by bacteria *Ralstonia eutropha* and *Escherichia coli* HB101 carrying pRO103 plasmid which having gene encoding 2,4-dichlorophenoxyacetic acid/2-oxoglutaric dioxygenase. GMM *R. eutropha* (pRO103) showed significant degradation of 2,4-D in soil.

Similarly, Rodrigues et al. (2006) developed two genetically modified strains *Rhodococcus* sp. RHA1 (pRHD34::fcb) and *Burkholderia xenovorans* LB400 (pRO41) for degradation of mixture of PCBs and Aroclor 1242 in soil. A combined inoculation of microorganism and its host plant by providing extra nutrients could enhance microbial survival and activity (Brazil et al. 1995). Such use of a dual microorganism-plant system, in which the plant supports microbial growth and the microorganism performs the bioremediation is known as rhizoremediation (Kuiper et al. 2004; Yee et al. 1998).

The GMMs have been used for successful bioremediation of pollutants in soil and water under laboratory scale; however, field applications are limited. Long term field studies are now needed to evaluate their effectiveness. Transfer of genetic material from GMOs to indigenous micro-organisms can have an environmental impact as it alters genotypic diversity. Its genotypic diversity results in unanticipated changes in the phenotypic expression of the recipient micro-organism(s) that may have a harmful impact on the environment (Doyle et al. 1995). According to Singh et al. (2011); application of GE bacteria based remediation of various heavy metal pollutants is in the forefront due to eco-friendly and lesser health hazards compared to physico-chemical based strategies, which are less eco-friendly and hazardous to human health. *P. putida* SM1443 carrying a 2,4-D degradative plasmid pJP4 was used as the donor strain. The bioaugmented aerobic granule system with *P. putida* SM1443 gained 2,4-D degradation ability faster and maintained a more stable microbial community than the control in the presence of 2,4-D under fed batch test (Quan et al. 2010). Nancharaiah et al. (2008) first studied bioaugmentation of aerobic microbial granules with *P. putida* carrying a TOL plasmid in batch tests and observed a significant increase in the degradation of benzyl alcohol. Therefore, the GMMs can be applied not only in degradation of pesticide and toxic compounds but also in promotion of plant growth. Generally, plant growth-promoting bacteria (PGPB) are not competent for promotion of plant growth in the existence of various toxic compounds (Cases and de Lorenzo 2005; Davison 2005; Pimentel et al. 2011). Due to this, Yang et al. (2011) attempted to design genetically modified bacteria strain P13 which have ability to promote maize growth as well as degrade phenol. This strain

had been development by recombination of *Pseudomonas aeruginosa* SZH16 and *Pseudomonas fluorescens* by horizontal gene transfer methods.

In Indian scenario; each technology developer is required to have their own Institutional Bio Safety Committee (IBSC) which must include at least one member appointed by the Department of Biotechnology (DBT). The IBSC's formulate requests for approval for testing, which goes to the Research Committee on Genetic Modification (RCGM). This is the responsibility of DBT and includes representatives from the Ministries of Health, Science and Technology (the parent Ministry for DBT) and Agriculture. The RCGM can approve field trials and other tests and reviews reports on these tests for further action. Approvals for commercial releases must come from the Genetic Engineering Approval Committee (GEAC) which is chaired by the Ministry of the Environment and includes representatives from the Ministries of Health, Science and Technology and Agriculture. To date; India has approved Bt cotton for commercial use in India (March 2002). There is still some discussion within India, on how to treat applications for food approvals in respect to imported commodities. Since this happens rarely in India, hence, the system is not yet defined completely.

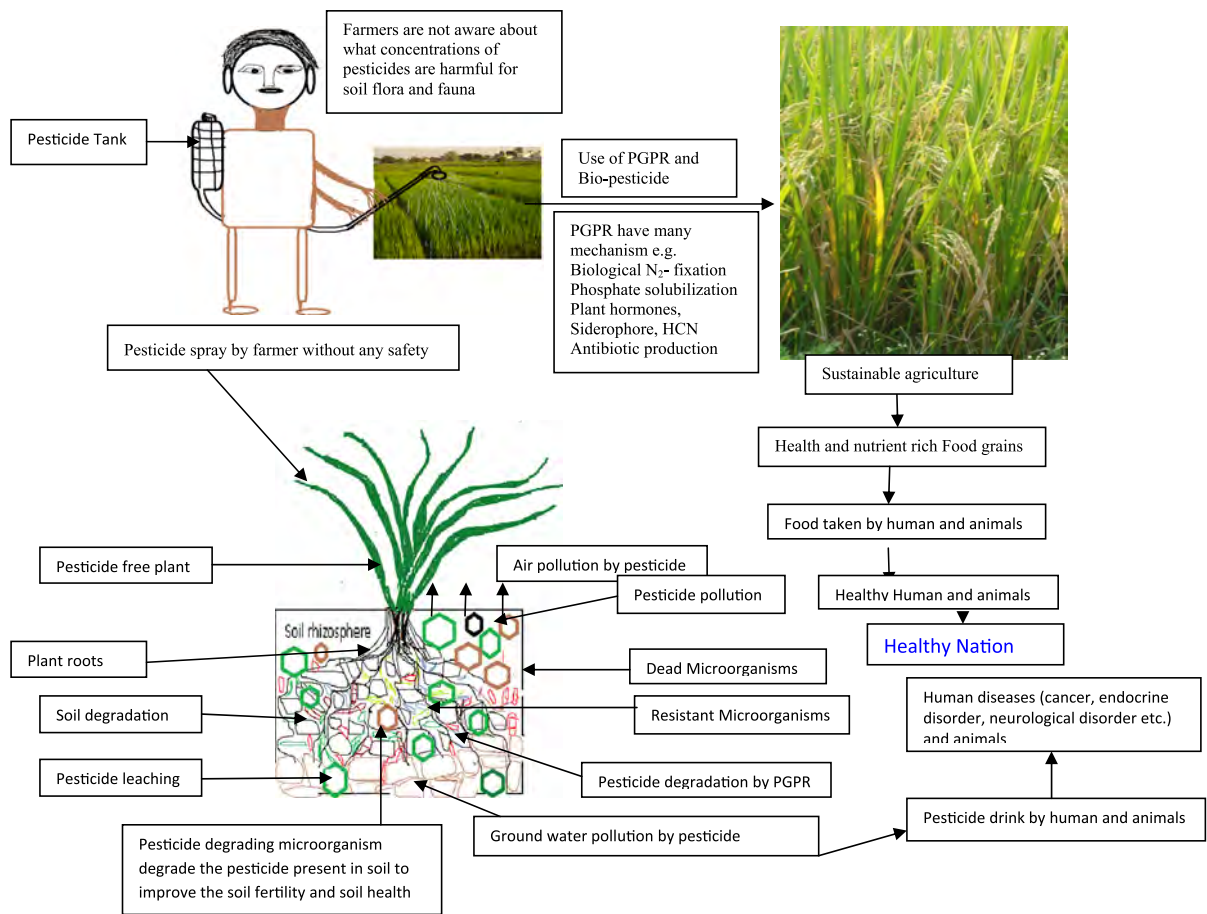
## 6 Role of indigenous microbes for pesticide degradation and plant growth promotion

The indigenous microbes are native microorganism which is isolated from the local environmental sample. These microbes have capability to grow very fast in certain environment and perform their potential for pesticide degradation and plant growth promotion ability. The bioaugmentation (introduction of specific competent microorganisms) has been well thought-out a valuable tool for increasing the rate and extent of biodegradation of pesticide pollution (Coppotelli et al. 2008). The combined inoculation of competent and indigenous microbes directly isolated from the same soil is often called as bioaugmentation (Phelps et al. 1994; Otte et al. 1994). Many studies have shown that biotic and abiotic environmental factors influence the effectiveness of bioaugmentation (Mrozi and Piotrowska-Sege 2010). Therefore, it would be more practical when using bioaugmentation to use autochthonous

microorganisms (Hosakawa et al. 2009). Autochthonous bioaugmentation (ABA) is defined as a bioaugmentation technology that uses microorganisms indigenous to the site (soil, sand and water) to be decontaminated (Ueno et al. 2007).

In India, farmers use the pesticide for crop production but they are not known about their toxic effects for environmental pollution as well as loss of soil fertility and health (Fig. 6). For minimization of soil pollution and soil toxicant in agricultural field, degradation of pollutants with indigenous microbial consortia could be very useful because they easily survive and multiply in same environmental condition (Wang et al. 2005). Large numbers of bacteria that are able to degrade carbamate pesticides have been isolated from soil around the world (Desaint et al. 2000). Isolation of indigenous bacteria capable of metabolizing organophosphate compounds has received considerable attention because such bacteria provide an environmentally friendly method of detoxification (You and Liu 2004; Wang et al. 2005; Wood 2008). Large numbers of indigenous microorganisms have been used in many studies for the removal and detoxification of toxicants from the certain environments (Desaint et al. 2000; Wang et al. 2005). The use of various microorganisms to enhance the rate of biodegradation as well as plant growth promoting activities (production, plant growth hormones biological nitrogen fixation, phosphate solubilization, hydrogen cyanide, siderophore and antagonistic properties) are well documented in various studies (Glick 1995; Vessey 2003; Sakamoto and Tsutsumi 2004; Verma et al. 2012; Isaac et al. 2013) (Fig. 6).

The indigenous microbial strains e.g. *Pseudomonas*, *Marinobacter* *Salinibacterium* and *Brevibacterium* are able to colonize plant root system and promote plant growth, thus, referred to plant growth promoting microbes. These isolated bacteria from polluted sediment samples degraded the phenanthrene, naphthalene, phenanthrene, and pyrene (Isaac et al. 2013). Archetypical naphthalene and catechol dioxygenase genes were found in two isolates belonging to genus *Pseudomonas* (*Pseudomonas monteilii* P26 and *Pseudomonas xanthomarina* N12) which degrades the polycyclic aromatic hydrocarbons (Isaac et al. 2013). Pesticide degrading microorganism is an effective indigenous plant growth promoting microorganism (PGPM), which is generally free-living, soil-borne bacterium, isolated from the rhizosphere, when



**Fig. 6** Schematic diagram of pesticide application by the unaware farmers in agricultural crops and its effect on soil flora and fauna as well as soil, water and air pollution. The pesticide

residue has been degraded by pesticide degrading microorganism to enhanced sustainable agriculture

applied to seeds or crops, enhanced the growth of the plant through suppression of plant disease (bioprotectants), improved nutrient acquisition (biofertilizers), production phytohormones (biostimulants) and acting as biopesticides (Vessey 2003) (Fig. 6). The direct mechanisms of plant growth by pesticides include the provision of phosphorus solubilization and its uptake by plants, biological nitrogen fixation, sequestration by siderophores, production of plant hormones like auxins, cytokinins and gibberellins and Lowering of ethylene levels in plant (Verma et al. 2012) (Fig. 6). The indirect mechanisms used by PGPM include; production of useful antibiotic against pathogenic microorganisms, reduction of iron availability to phytopathogens in the rhizosphere, synthesis of fungal cell wall lysis enzymes and competition with

detrimental microorganisms for sites on plant root (Glick 1995). Yu et al. (2006) investigated the impact of the fungicide chlorothalonil ( $1.5 \text{ mg kg}^{-1}$ ) on soil micro-organisms by enumerating bacteria, fungi and actinomycetes using the most probable number method, and by measuring acid phosphatase, alkaline phosphatase, urease, catalase, and invertase activities.

According to Wang et al. (2007) an endophytic bacterium *Bacillus cepacia* strain FX2 isolated from a corn plant (*Z. mays*) has ability to degrade toluene and phenol because this possess a large plasmid encoding the catechol 2, 3-dioxygenase (C23O), a key enzyme in the degradation pathway of monocyclic aromatic compounds. Wang et al. (2010) conducted greenhouse and field trials to investigate the potential applications of strain FX2 to important crop plants (CORN and

wheat). The study showed increased plant growth and biomass. Cultivable endophytic bacteria is a indigenous or native microbes which able to grow on toluene as the only source of carbon and containing a C23O gene were found in the plants inoculated with strain FX2 but not in their non-inoculated controls. Many strains of these bacteria were often reported to be isolated from different plants, able to promote host plant growth, produce antifungal metabolite, degrade organic pollutants and possess C23O genes (Nejad and Johnson 2000; Sessitsch et al. 2004; Taghavi et al. 2005; Kavino et al. 2007; Mendes et al. 2007; Wang et al. 2007). Furthermore, a greater number of phosphate-solubilizing and siderophore producing endophytic bacteria were found in the corn and wheat inoculated with strain FX2 than in their controls. Phosphorus is one of the major essential macronutrients for biological growth and development and phosphate-solubilizing microorganisms may therefore play an important role in supplying phosphate (Wang et al. 2007; Taghavi et al. 2005) to plants in a more environmentally-friendly and sustainable manner (Rodrigues et al. 2006; Khan et al. 2007). Production of siderophores by bacteria becomes important in the suppression of plant pathogens and induction of systemic resistance in plants (Compant et al. 2005). Wang et al. (2010) reported that the horizontal gene transfer (HGT) required for the efficient degradation of a pollutant by the endophytic population might not only contribute to pollutant degradation, but also have other beneficial effects on plant, such as growth promotion and disease suppression. HGT, associated with an endophytic bacterium containing a transferable plasmid carrying the genetic information encoding the desired metabolic properties, is very important for agronomic and environmental applications in crop plants.

### 6.1 Field studied of pesticide degradation by microbial consortium

Ghazali et al. (2004) isolated consortium first (*Pseudomonas aeruginosa* strains S4.1, S53 and *Bacillus* sp. strain S3.2) and consortium second (*Pseudomonas aeruginosa* strains S4.1, S53, *Bacillus* sp. strain S3.2, 113i, O63 and *Micrococcus* sp) from hydrocarbon-contaminated soils. Consortium second was more efficient for removing the medium- and long-chain alkanes in the diesel-contaminated soil as compared to

consortium first under field condition. A potent polycyclic aromatic hydrocarbons (PAHs) degrading microbial consortium of five fungi (*Phanerochaete chrysosporium*, *Cunninghamella* sp., *Alternaria alternata* (Fr.) Keissler, *Penicillium chrysogenum*, and *Aspergillus niger*) and three bacteria (*Bacillus* sp., *Zoogloea* sp., and *Flavobacterium* sp.) were isolated from PAH contaminated which has great potential to PAH degradation under field condition (Lin et al. 2004; Su et al. 2006). Abbondanzi et al. (2005) conducted an experiment to determine PAHs concentration and changes in microbial populations in brackish sediments. Abbondanzi et al. (2005) suggested that the PAH degrading bacteria degraded the PAHs (phenanthrene, anthracene and fluoranthene) in MPN tubes with increasing concentration of microbial population after incubation in optimal conditions.

Chemical analyses and microbiological counts suggested a potential for PAHs biodegradation by natural occurring populations of sediment microorganisms, thus indicated an “optimal range” in sediment PAHs concentrations, outside of which the natural selection of the indigenous microflora did not occur. Chirnside et al. (2007) isolated indigenous microbes (*Alcaligenes xylosoxydans* subsp. *denitrificans*, *Alcaligenes xylosoxydans* subsp. *xylosoxydans*, *Pseudomonas putida*, *Pseudomonas marginalis*, and *Providencia rustigianii*) from 100-year-old pesticide-contaminated mix-load site from Pennsylvania. The selective microbial consortium (SMC) was identified by fatty acids methyl ester (FAME) analysis and they showed ability to degrade herbicides, atrazine (2-chloro-4-ethylamino-6-isopropylamino-S-triazine) and alachlor (2-chloro-20, 60-diethyl-N-[methoxymethyl]-acetanilide) under field condition. Jacques et al. (2008) isolated microbial consortium (five bacteria: *Mycobacterium fortuitum*, *Bacillus cereus*, *Microbacterium* sp., *Gordonia polyisoprenivorans*, *Microbacteriaceae* bacterium, Naphthalene-utilizing bacterium; and a fungus identified as *Fusarium oxysporum*) from a PAHs contaminated land farm site to degrade and mineralize different concentrations (0, 250, 500 and 1,000 mg kg<sup>-1</sup>) of anthracene, phenanthrene and pyrene in soil. The microbial consortium degraded on an average, 99, 99 and 96 % of the different concentrations of anthracene, phenanthrene and pyrene in the soil, in 70 days, respectively.

Kim et al. (2009) observed that the bacteria of three species (*Acinetobacter baumannii*, *Klebsiella oxytoca*,



and *Stenotrophomonas maltophilia*) have ability to degrade phenylephrine (PHE) which was isolated from sludge of a pulp wastewater treatment plant. When a single microorganism was used, phenanthrene degradation efficiency was very low (48.0, 11.0, and 9.0 % for *A. baumannii*, *K. oxytoca*, and *S. maltophilia* respectively, after 360 h cultivation) but in mixed consortia of *A. baumannii* and *S. maltophilia* degraded ~ 80.0 % of phenanthrene and reduced lag time to 48 h as compared to the 168 h of pure *A. baumannii* culture. The results showed that the mixed cultures of microorganisms may be effective in bioremediation, even if the microorganisms in the cultures have low degradation activity in pure culture. Alisi et al. (2009) recorded 75 % degradation of diesel hydrocarbons and complete degradation of n-C12–20 at 42 days due to inoculation of native microbial strains. *Sphingobium chlorophenolicum* strain C3R was isolated from a PAH contaminated soil by enrichment cultures with *phenanthrene* as sole carbon and energy source (Andreoni et al. 2004). *S. chlorophenolicum* strain C3R was effective pesticide degrading microbes for degradation of phenanthrene in agricultural soil co-contaminated by metals and mixtures of PAHs. These C3R strain persisted in inoculated microcosms as monitored by the DGGE analysis and out competed some indigenous bacteria (Colombo et al. 2011). Silva et al. (2009) isolated the microbial (3 *Bacillus* strains B1F, B5A and B3G; *Chromobacterium* sp. 4015; and *Enterobacter agglomerans* sp. B1A) and fungal strains (*Achremonium* sp., *Verticillium* sp. and *Aspergillus* sp.) and developed different types of microbial consortium of native and non native microbes for degradation of PAHs (naphthalene, phenanthrene, anthracene, pyrene, dibenzo[a]anthracene, benzo[a]pyrene). Their experiment suggested that the native microbial consortia rapidly degraded the PAHs from soil as compared to other treatments combinations.

Fagervold et al. (2011) established that the polychlorinated biphenyl (PCB) dehalorespiring bacteria had a considerable effect on the dehalogenating activity of PCB 151 (2,20,3,5,50,6-hexachlorobiphenyl) and Aroclor 1260, in sediment microcosms, inoculated with two indigenous PCB dehalorespiring microorganisms (DEH10 and SF1), and non-indigenous strain (*Dehalobium chlorocoercia* strain DF-1). In different treatments of microbial combinations, the numbers of dechlorinators increased approximately

100- and 1,000-fold with PCB 151 and Aroclor 1260, respectively. These observations indicate that bioaugmentation with PCB dehalorespiring microorganisms is a potentially tractable approach for in situ treatment of PCB impacted sites (Fagervold et al. 2007). Madueño et al. (2011) isolated and characterized indigenous soil bacteria of PAH-degrading strains (1A, 22A, 22B and 36). The results suggested that the strain 22B was more resistant to C-starvation and drying conditions and this strain was highly suitable for bioaugmentation in PAH-contaminated soils of Central Patagonia, due to its adaptation to the usual environmental conditions.

## 7 Challenges of microbial degradation of pesticides

The main problem of popularization and use of microbial consortia for degradation of pesticides in soil is; its unavailability and effectiveness. The specific microbial strain for degradation of specific pesticide is unavailable in the local market for the farmers because all microbial strains do not degrade all types of pesticides which need further research. Other significant aspects are; the effective pesticide degrading microorganism and biopesticide preparations are sensitive to heat, desiccation and ultraviolet radiations (Chakoosari 2013). These conditions reduce the effectiveness of the biopesticides. Special formulation of biopesticide and pesticide degrading microbial consortia in non toxic carrier material are essential for the long term storage at normal temperature.

## 8 Futures prospective

The approaches like integrated nutrient and pest management are necessary to increase sustainable agricultural productivity and conservation of natural resources (Matson et al. 1997). In India; agricultural development, planning and policy are most important objective. In agricultural development; pesticides have gain importance as a plant protection agent for boosting food production. The pesticides are being used indiscriminately resulting in sever environmental contaminations. To reduce the toxic effects of pesticide in soil and water, genetically modified

microorganism could be important bio-inoculants which may be used as effective biodegrading agent. Such microorganisms survive in the environment and utilize the pesticide for obtaining their energy, hence, will be a suitable candidate for bioremediation of pesticides-contaminated soil or water (Glick 2003). This technique is cheaper, effective and natural to combat the residual problem. These isolates have the potential to clean up the environment from pesticide pollutant and minimize the toxic effects of pesticides from the soil and water (Matson et al. 1997; Glick 2003). Further, these pesticide degrading microorganisms have ability to promote plant growth and yield due to production of phytohormones, ammonia, siderophore. The biological nitrogen fixation and phosphate solubilization have the antagonistic activity against phytopathogenic microorganism. These pesticide degrading microorganisms improve the soil health and fertility and thus, enhance the sustainable agriculture.

## 9 Conclusion

In current scenario, farmers are using higher dose of pesticides and chemical fertilizers in unmanaged manner for higher production of grain yield. Due to which; pesticides and chemical fertilizers pollute the water, soil and air, and cause many human diseases. Biodegradation that involves the capabilities of microorganisms in the removal of pollutants would be the most promising, relatively efficient and cost-effective technology. Effective and indigenous microbial consortia contribute significantly for the removal of toxic pesticides. These pesticides degrading microbial consortium being an effective biofertilizer could minimize use of chemical fertilizer up to 20–30 %. The use of an effective and indigenous microbial consortium as a tool for pesticide degradation on the contaminated sites is needed to adopt in practice at larger scale. These genetically modified microbial strains may develop more effective strains for pesticide degradation by genetic engineering technology and expression of enzymes. These effective microbial consortia need to be grown in large quantity by bioreactors for large scale field application. Conclusively, it is economically viable; and enhances the quality of life for farmers and society as a whole.

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