Article

Bacterial megaplasmids and biodegradation: Solution to persistency of xenobiotics

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Abstract
Extra chromosomal material called plasmid has an important duty in the gradual change of bacterial sets of genes (genomes) by carrying out horizontal gene transfer processes. However, the origin and evolution of most plasmids remains vague, especially for plasmids that are greater than or equal to 100kb (megaplasmids). Tolerance is key for survival as vector-borne disease causing agents transmit between the arthropod and vertebrate, and temperature fluctuation is an environmental marker inducing change in gene expression of tick-borne spirochetes. The tumor-inducing Ti plasmid encodes ample of virulence functions for the crown gall agent *Agrobacterium tumefaciens*. This includes the *vir* genes which initiate genetic transformation of host cells and the catabolic genes needed to make use of the opines manufactured by infected plants. The tumor inducing plasmid also encodes, an opine-dependent quorum sensing system that tightly regulates Ti plasmid copy number and its conjugal transfer to other agrobacteria. Many natural *Agrobacteria* are avirulent, in the absence of the Ti plasmid. The load of harboring the Ti plasmid rests on the environmental context. Aside from infected hosts, plasmid costs are low but the benefit of the plasmid is also never available. Consequently, genotypes without plasmids are favored. On infected plants the expense of the tumor inducing plasmid can be very high, but balanced by the opine advantages, locally favoring plasmid bearing cells.

Keywords megaplasmids; xenobiotics; biodegradation

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1 Introduction

Extra chromosomal elements of finite size, usually stably inherited within a bacterial cell line and potentially capable of transfer between strains, species or genera is called plasmids. Frequently used methods in grouping of plasmids rely on nonconformity between closely related replicons. A major aspect concerns the growing interest in the role of plasmids in causing disease and host specificity and the possible advantages of plasmid-

borne positions for the genes involved. A range of plasmid-borne observable features, in addition to toxin and hormone synthesis confer several valuable qualities, such as heavy metal resistance (Overhage et al., 2005; König et al., 2004; Dib et al., 2008). The importance of mobile genetic elements and their implications with pathogenicity islands on plasmids and in the bacterial chromosome provide marker of possible evolutionary routes to the acquisition of disease-inducing capabilities. Extra chromosomal elements called plasmids were first discovered in enteric bacteria thereafter late 1950s onwards were increasingly recorded in relation to antibiotic resistance (Datta and Hughes, 1983; Hughes and Datta, 1983). Typing systems were made for plasmids, based on the observation that replicons sharing common replication functions were unable to stably co-exist, as independent plasmids, in the same cell: in general, when making choice for the acquisition of a second plasmid was applied to the culture, the related replicon was either displaced or recombined with the incoming plasmid to form a cointegrate. Conjugative plasmids, commonly present in bacterial cells (Gama et al., 2017; Shintani et al., 2015), can be transferred to other cells by conjugation. This process often requires sex pili to establish a mating pair by promoting cell aggregation (Cabezon et al., 2015).

Megaplasmids are extrachromosomal genetic elements in the size range of 100 kb and more. They are found in physiologically and phylogenetically different groups of bacteria and archaea. By definition, megaplasmids are not essential for the viability of their hosts under all growth conditions, but paradoxically many megaplasmids carry the genetic elements for the defining and characteristic traits of the organism in which they reside. Microbial megaplasmids broaden our knowledge of the extensively studied representatives, such as the catabolic plasmids of the pseudomonads, the rhizobial Sym plasmids, the Ti plasmids of the genus *Agrobacterium* and the giant enterobacterial virulence plasmids. It also presents snapshots of more recently disciphered megaplasmids. The contribution of extra chromosomal materials greater than 100kb (megaplasmids) to the biology of their hosts is described, highlighting the interactions between megaplasmid and chromosomal genes. Megaplasmids are the largest contiguous regions that can undergo HGT across bacterial cells (Romanchuk et al., 2014; Cooper et al., 2010).

2 Benefits of Plasmids

2.1 Pathogenicity and host specificity

The genes involved in causing disease and host specificity comprise of two main groups, those termed avirulence (*avr*) and virulence (*vir*) genes (Ashbolt et al., 2013; Broaders et al., 2013; Warnes et al., 2012; Vivian and Gibbon, 1997; Vivian *et al*., 1997; Vivian and Arnold, 2000), and those involved with a type III protein secretion system, the `harp' (*hrp*) genes (Bogdanove et al., 1996; Lee, 1997; Galan and Collmer, 1999). It is obvious that the type III secretion system, also present in many animal pathogens, determines the production of a pilus-like structure, which is believed to deliver certain protein products, including *Avr* proteins, inside plant cells (Roine et al., 1997; Taira et al., 1999). In contrast, those *avr* genes that have been described are evenly divided between plasmid and chromosomal locations (Vivian and Gibbon, 1997). Avirulence genes have been discovered in conferring the ability to induce an HR in plant hosts that carry a matching gene for resistance (R), the so-called gene for gene theory (Grad et al., 2012; Sørensen et al., 2005; Baltrus et al., 2011).

2.2 Toxins

Phytopathogenic bacteria produce different types of toxins that has adverse effect on the host plant, often causing chlorosis and stunting. The genetic determinants for one of these, coronatine, are found on plasmids. However, among a majority of strains of *Pseudomonas syringae* examined, the genes were chromosomal (Cuppels and Ainsworth, 1995). The toxin is a polyketide, coronafacic acid, coupled by an amide bond to a cyclopropyl amino acid, coronamic acid. Production is thermo regulated, in a manner that is constant with its

expression during plant infection, which is optimal at 18°C (Palmer and Bender, 1993; Ullrich and Bender, 1994).

2.3 Copper and antibiotics

Bordeaux mixture, primarily a fungicide based on copper plus lime, whose accidental discovery is recounted by Schumann (1991), has been used to control plant disease in crops for over 100 years. Plasmid-borne resistance to copper has been found in several phytopathogenic bacteria, including *X. campestris pv. vesicatoria* pathogenic on pepper (*Capsicum annuum*), in *Ps. syringae pv. syringae* pathogenic to ornamental fruit trees. The genes specifying resistance to copper appear to be widely conserved among the two genera (Voloudakis et al., 1993) and are generally located on large plasmids, with the exception of a walnut (*Juglans regia*) pathogen, *X. campestris pv. juglandis*, in which they are chromosomal (Lee et al., 1994). Resistance to streptomycin, which has been used since the late 1950s to control disease in fruit orchards, was detected in the pathogen *Ps. syringae pv. papulans* and a number of other Gram-negative bacteria present in apple (*Malus* sp.). Common fluorescent epiphytic bacteria, which were not associated with disease, were found to transfer streptomycin resistance efficiently to the pathogen, *Ps. syringae pv. papulans*, in the laboratory, suggesting that these bacteria may provide a reservoir for streptomycin resistance (Huang and Burr, 1999).

3 Megaplasmids

Megaplasmids play a key role in the ecology and evolution of bacterial populations as they frequently carry genes conferring traits such as antibiotic resistance, pathogenesis, and the ability to break down nutrients (Turner et al., 2002; Slater et al., 2008; Rankin et al., 2011). These independently replicating genetic materials are primarily distinguished from chromosomes by the defining attribute of carrying only non-essential genes. In toting up they tend to be smaller than bacterial chromosomes and often code conjugative systems that allow for their horizontal spread to other bacterial cells (Thomas and Nielsen, 2005; Harrison et al., 2010). For the reason that they often confer phenotypes that are beneficial in particular environments, megaplasmids and their horizontal transport have a significant role in structuring bacterial communities and in determining the evolution of bacterial populations (Slater et al., 2008).

3.1 Types of megaplasmids

(1) Ti plasmid

The genus *Agrobacterium* carry a plasmid that is accountable for transfer of its DNA to plant cells and is named consequently as tumour inducing plasmid (pTi or simply Ti). Ti plasmids of *Agrobacterium* are classified according to the type of amino acid metabolites called opines they manufacture. Basically, there are four different kinds of opines so extreme assumed to be synthesized by *Agrobacterium* strains: octapine (pTi A6), succinamopine (pTi Bo546), nopaline (pTi C58), and leucinopine (EU 6) (Chang et al., 1983). The basic organization of Ti-plasmid is identical in all the types with the foremost difference being present in the T-DNA, the part that is transferred to plants and codes for enzymes that synthesize the opines. Other differences are with orientation to insertion elements (IS) and recurring sequences current in the non-T-DNA part of the plasmid. Homology studies among Ti plasmids discovered both homologous and non-homologous sequences and are considered as evolutionary mosaics with non-homologous sequences acquired during parallel transfer of DNA (Otten et al., 1992). Ti plasmids fit in to group of repABC replicons with reverence to their replication origin. This replicon is present in most of α-proteobacteria (Suzuki et al., 2000). The first two genes of repABC cassettes, repA and repB are implicated in active partitioning, whereas the third repC, encodes a replication initiator protein (Pappas, 2000). repABC replicons are huge, low copy number plasmids that are stable and generally do not function outside the class of α-proteobacteria. Nevertheless, the copy number of Ti-plasmids fluctuates depending on plant signals that are dependable for initiation of its virulence genes. The so

called plant inducers such as phenols, low down Ph before the creation of tumors in the plants and quorum signals secreted by the *Agrobacteria* after development of tumors increases the reproduction number of Ti plasmids. Reciprocal dwindle in copy number to the basal level is brought about by diverse novel mechanisms such as protein repressors at the operator site of the repABC promoter site and also by the antisense RNA (Pappas, 2000).

Infection of a plant host involves its genetic makeover in which a large fragment or segments of Ti plasmid-borne genes (the transferred or T-DNAs) are replicated from the plasmid via a conjugation-like instrument, delivered into the plant cell via a type IV discharge system, and incorporated into the host plant's genome (Escobar and Dandekar, 2003; Brencic and Winans, 2005). Ti plasmid virulence genes are only uttered when pathogenic *A. tumefaciens* cells stumble upon a specific set of environmental circumstances (plant-created phenolics, sugars, low pH, and restraining phosphate) most pinpointing of wounded plant tissue (Winans, 1990). Following makeover, the plant host cell machinery directs the appearance of T-DNA genes, principal to T-DNA proscribed production of the plant hormones auxin and cytokinin, ensuing in accelerated splitting up of transformed plant cells (Drummond et al., 1977; Garfinkel et al., 1981). This gives rise to the most noticeable indicator of crown gall disease tumor development. Less conspicuously, but arguably of primary importance for the pathogen, the plant's expression of T-DNA genes also results in the production and liberate of a suite of inimitable metabolites that are largely termed opines (Brencic and Winans, 2005). Opine catabolic genes passed on the Ti plasmid permit the pathogen to catabolize the plant created opines, providing a key advantage of pathogenesis to the infecting bacteria (Guyon et al., 1993; Savka and Farrand, 1997; Platt et al., 2012b). Hairy root infection caused by Ri plasmid bearing *A.* rhizogenes also involves T-DNA transfer that causes plants to produce opines, nonetheless rather than cause tumor development this disease stimulates the development of adventitious roots. Countless Ri and Ti plasmid T-DNA genes show homology, such as the Ti encoded auxin biosynthesis genes, iaaM and iaaH, and the corresponding Ri encoded aux1 and aux2 genes. However, several Ri plasmid T-DNAs genes show limited or no homology to genes established on Ti plasmid T-DNAs. These genes, such as rolA, rolB, and rolC, function in motivating meristem construction, a key feature distinctive hairy root and crown gall diseases (Britton et al., 2008).

Numerous pathogenic and avirulent strains of *A. tumefaciens* carry a different type of agrobacterial megaplasmid. Like the Ti plasmids, these At plasmids vary extensively in their gene construction and concerto, though they also distribute regions of homology. Non-essential for pathogenesis, the At plasmids have acknowledged considerably less concentration than Ti plasmids. For this rationale, they were conventionally referred to as cryptic plasmids as they were beforehand uncharacterized relative to the Ti plasmids. Although superfluous for virulence, the full sequence of the best characterized At plasmid, pAtC58, reveals the presence of genes implicated in a collection of functions as well as, but not limited to, chemotaxis, iron uptake, DNA damage revamp, heat shock, and catabolism (Goodner et al., 2001; Wood et al., 2001; Slater et al., 2009). One set of At plasmid genes that has established particular concentration are the blcABC genes, previously named attKLM, because of their primarily proposed, but later refuted role in addition (Matthysse et al., 2008).

(2) Ri Plasmid

It shares far-reaching efficient homology with the Ti–plasmid. Ri–plasmid, like the latter, has a separate piece(s) of DNA which is transferred to plant genome during infection (Chilton et al., 1982; White et al., 1982; Willmitzer et al., 1982). Transmit of the DNA (T-DNA) to the plant genome is mediated by a further piece on the plasmid renowned as the virulence (*vir*) region. The T-DNA bestows on the plant cells the competence to develop in the nonattendance of exogenous plant hormones. The T-DNA also bestows on the changed tissue the aptitude to manufacture customized amino acids (opines), which, in turn, are utilized only by the rabble-rousing bacteria as the carbon, nitrogen and energy foundation. The *Agrobacterium* species thus institute a

inimitable ecological niche by genetically engineering the host plant a highly sophisticated parasitism. DNA sequences homologous to the T-DNA of Ri plasmids were reported in some unreconstructed plant species (Spano et al., 1982; White et al., 1982, 1983; Tepfer, 1984). Large plasmids were shown to be there in strains of *A. rhizogenes* (Schell et al., 1976; Currier and Nester, 1976; White and Nester, 1980a). These strains are recognized to manufacture at slightest two classes of opines. One such class is represented by opines of agropine assembly, and the additional class being the agrocinopine group. All strains of *A. rhizogenes* are recognized to manufacture agrocinopine and all or a few opines of the agropine group. The strains which produce partner the agropine type opines (agropine, mannopine, agropinic acid and mannopinic acid) are identified as the agropine type strains, while the strains which manufacture all agropine type opines exclusive of agropine are known as the mannopine type strains (Petit et al., 1983; Tempe et al., 1984; Tepfer and Tempe, 1981; White et al., 1982; Willmitzer et al., 1982). Two T-DNA regions have been recognized in agropine Ri-plasmids. The two tDNAs are alienated from each other by about 15 Kb of non-transferred DNA. The right T–DNA (TR) contains genes homologous to the T–DNA from Ti–plasmids (Riseuleo et al., 1982; Willmitzer et al., 1982; Huffman et al., 1984; Jouanin, 1984). Most important among these are the genes homologous to the tms1 and tms2 of the Ti–plasmid. These genes are implicated in auxin biosynthesis in *A. tumefaciens*.

(3) Catabolic megaplasmids

The huge dimension of catabolic plasmids is attributable to the fact that they often have the full set of plasmid transfer genes as well as the anthology of catabolic genes/operons required for (complete) degradation of chemical compound(s), linked with copious transposons and/or IS elements or their bits and pieces. Catabolic modules are classically inserted into the plasmid backbone at supplementary sites, that is, where the backbone can be disrupted devoid of cost to the plasmid's customary functions. Similar to plasmid backbone gene association, catabolic pathway gene organization should perk up (clustering of genes that code for degradation pathways) in anticipation of gene expression is optimized in terms of maximal degradation competence and regulatory flexibility; the most well-conserved catabolic pathways are those that are most strongly clustered (Thomas 2000). As more sequences from bacterial genomes and catabolic plasmids are made available, it must be promising to trace at least some stages of the progress of the different genetic preparations. Plasmid genome progression comparisons, specially those of the promiscuous IncP plasmids, designate that catabolic plasmids contain multifaceted genetic histories ensuing from transposition and recombination procedures (Dennis, 2005) .

4 Megaplasmids and Biodegradation

Microbial biodegradation is the basis of all biogeochemical cycles. The probable of soil and water bacteria to degrade a variety of kinds of environmental pollutants, as well as man-made chemicals (xenobiotics) which have only lately been introduced into nature, is very large. New metabolic pathways are incessantly developing, which enable these microorganisms to use compounds that they have not encountered earlier than. To continue to exist, bacteria must swiftly become accustomed to changing environmental stimuli such as transient nutrient resources, and also exposure to xenobiotics, toxic chemicals, or abnormally elevated amounts of natural chemical compounds (oil spills, etc.). As the result of this adaptation, bacteria obtain novel catabolic abilities. Mobile genetic elements (MGEs), acquired via horizontal (lateral) gene transfer (HGT), play a main role in such adjustment. MGEs – transferable (mega) plasmids, (conjugative) transposons, integrons, genomic islands, or phages. (Hacker and Carniel, 2001; Nojiri et al., 2004; Osborn and Boltner, 2002) . MGEs supply a location where catabolic and anabolic genes can be assembled from the prokaryotic horizontal gene pool to provide the answer to environmental stresses (Thomas and Smalla, 2000). Beside biodegradation genes/operons, MGEs also carry determinants for resistance to antibiotics, heavy metals and emission, symbiosis and virulence,

bacteriocin manufacture, and enlarged mutation frequencies. Soil is a chemically multifaceted environment, in part due to the wide range of compounds produced by plants, and additional intricacy is introduced by decomposition and soil biogenesis. Many compounds of plant origin are chemically related, although they are usually present at concentrations that individually do not support bacterial growth. Thus, the alternative, potentially successful spirited strategy for soil bacteria is to use the varied compounds simultaneously, rather than swiftly act in response to transient nutrient resources. This strategy may underlie selective pressure for large genomes having manifold chromosomes and/or (mega) plasmids, which code numerous paralogous catabolic genes. Two examples are *Rhodococcus sp*. RHA1 and *Burkholderia xenovorans* LB400. As these two organisms are phylogenetically extremely diverse, this suggests the primeval origin of this catabolic capacity (McLeod et al., 2006). Catabolic plasmids hold genes encoding the enzymes requisite for the degradation and exploitation of chemical compounds. Typically, these plasmids have squat copy numbers and they are moderately large (from 50 kb up to megaplasmids of more than 1 Mb). Although the catabolic plasmids described to date are more often than not circular, linear catabolic plasmids have been isolated from gram positive bacteria. The first plasmids implicated in the degradation of xenobiotic compounds were described more than 30 years ago. At the present time, the list of catabolic plasmids is rising incessantly due to enormous sequencing.

4.1 Aromatic catabolic traits conferred by megaplasmids in gram negative bacteria

The best deliberate and most likely the most ubiquitous microbial strategy for aerobic degradation of aromatic compounds involves two critical steps: first, hydroxylation of adjacent carbon atoms of the aromatic ring and second, the ring cleavage of the ensuing catecholic intermediates (Dagley, 1986). In the case of phenol degradation, the aromatic ring is first monohydroxylated by phenol hydroxylase (PH, phenol 2-monooxygenase) at ortho location to the preexisting hydroxyl group. The next step is catalyzed by either catechol 1,2-dioxygenase (C12O, initiating the ortho conduit leading to structure of succinyl-CoA and acetyl-CoA) or catechol 2,3-dioxygenase (C23O, initiating the meta pathway principal to structure of pyruvate and acetaldehyde). Two diverse types of PHs have been recognized: single-component (sPH) and multicomponent (mPH). In plasmid pEST1026 , the pheBA operon codes for C12O and sPH, required for phenol degradation by its host strain (Kivisaar et al., 1990). Bacteria convey a range of enzymes for the preliminary attack of dissimilar aromatic compounds – benzoate, toluene, benzene, xylenes, cresols, naphthalene, salicylate, mandelate, aniline, and others. These marginal (upper) pathways convey about a convergence of numerous diverse aromatic compounds to a partial number of ring cleavage substrates such as gentisate, catechol, protocatechuate, hydroquinone, etc., which are further degraded by mid (lower) pathways (Dagley, 1986). In the normal hosts of the plasmids pDK1, pWW0, pWW53, and pNL1, degradation of toluene and xylenes is mediated by the xyl genes, the pathway takings via catechol or its methylated derivatives and C23O as the ring fission enzyme (Burlage et al., 1989; Romine et al., 1999; Shaw and Williams, 1988; Tsuda and Genka, 2001).

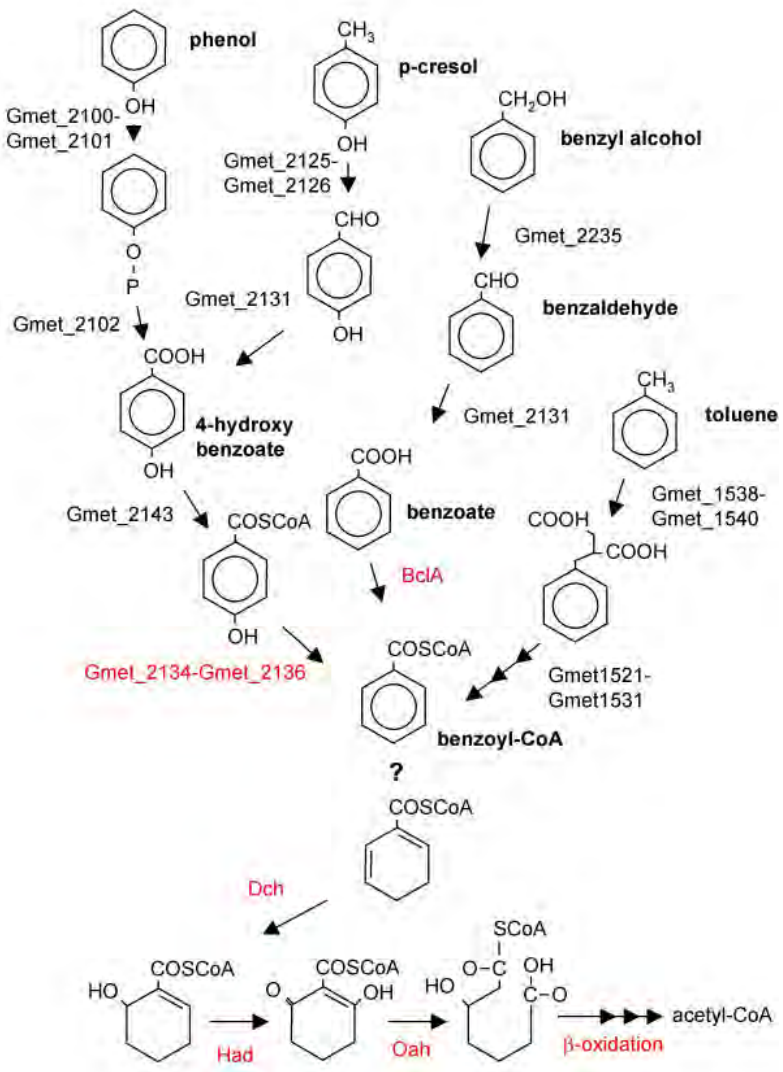

Fig. 1 Aromatic biodegradation pathways implied by catabolic genes and operons positioned on megaplasmids.

4.2 Degradation of chloroaromatics mediated by megaplasmids

Degradation of chloroaromatic compounds using oxygen appears to be governed by comparable principles (Schlomann, 1994) chloro substituted catechols as mid inter-mediates are transformed to β-ketoadipate in a series of reactions comparable to the catechol ortho-cleavage pathway, chosen as the customized ortho pathway. In *P. putida* AC867, 3-chlorobenzoate degradation leads to the formation of chlorocatechol, which is further degraded by chlorocatechol 1,2-dioxygenase, chloromuconate. cycloisomerase, and dienelactone hydrolase implied by the clcABD operon present in the plasmid pAC27 (Chatterjee and Chakrabarty, 1984). The host strain of the plasmid pP51, *Pseudomonas sp*. strain P51, is able to use di and trichlorobenzene(s) as sole carbon and energy sources. The tcb genes, accountable for this phenotype, are positioned in two regions of pP51. The upper-pathway gene come together tcbAaA-bAcAdB, converting chlorobenzoates to the individual chlorocatechol, is comparable in dimension, organization, and functional characteristics to sets of genes for other bacterial multicomponent dioxygenases, such as the toluene degradation genes todC1C2BA on the *P. putida* F1 chromosome (Zylstra *et al*. 1988), the biphenyl degradation genes bphA1A2A3A4B on the Burkholderia xenovorans LB400 megaplasmid (Mondello, 1989), the xylene/toluene degradation genes

xylXYZ on the plasmid pWW0 (Harayama et al., 1986), or the abovementioned bed catabolic genes of pHMT112. The herbicide 2,4-dichlorophenoxyacetic acid (2,4-D) is degraded by several bacteria belonging to different phylogenetic groups. The best-studied 2,4-D degradation genes are tfd -like, and the majority extensively studied tfd genes are to be found on the 88 kb IncP-1 plasmid pJP4 of *Ralstonia eutropha* JMP134 (Trefault et al., 2004). The marginal pathway implicit by the tfdA and tfdB / tfdB II genes is accountable for converting 2,4-D and 3-chlorobenzoate to the individual chlorocatechol, the latter is further degraded by the customized ortho-pathway encoded by the isofunctional tfdCDEF and $tfdD_{II}$ $C_{II}E_{II}F_{II}$ operons.

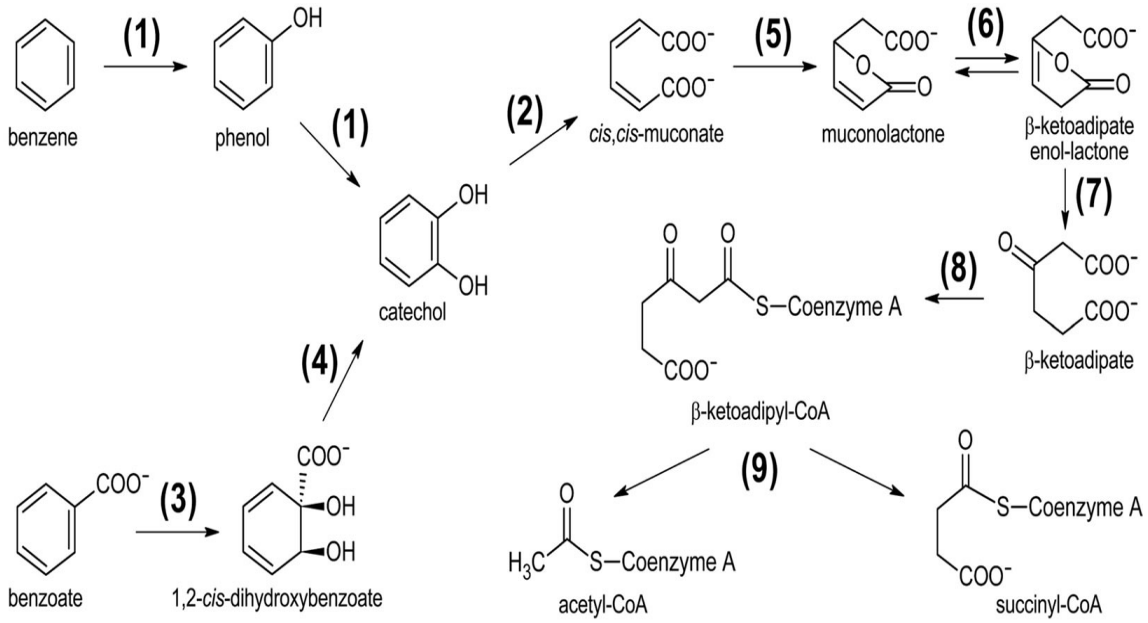

Fig. 2 Degradation of phenol.

4.3 Aromatic catabolic traits conferred by megaplasmids in gram positive bacteria

Actinomycetales are an order of gram positive bacteria that live in a broad range of environments, as well as soil and water. The representatives of two genera *Rhodococcus* and *Arthrobacter* are amongst the most recurrently isolated aerobic bacterial genera. They are metabolically and ecologically varied and have the capability to survive in environmentally harsh situation for unlimited periods of time. They have been shown to degrade a wide range of organic compounds. Their assimilatory abilities have been accredited to a variety of enzymatic behavior on the one hand and to cell walls rich in mycolic acids on the other. The latter apparently smooth the progress of the uptake of hydrophobic compounds (Gurtler et al., 2004). The *Rhodococcus sp*. RHA1 is a powerful PCB-degrading soil actinomycete that catabolizes a broad variety of compounds and has one of the largest bacterial genomes consisting of a linear chromosome (7.804 Mb) and three linear plasmids – 1.123 Mb (pRHL1), 443 kb (pRHL2), and 332 kb (pRHL3) (McLeod et al., 2006). *Rhodococcus erythropolis* strain BD2 harbors a linear 210-kb plasmid pBD2 moving the ipb genes for isopropylbenzene degradation (Stecker et al., 2003), the individual degradation pathway goes during 3-isopropylcatechol. The deduced proteins of this degradation pathway are 94–100% indistinguishable to RHA1's biphenyl degradation pathway enzymes determined by pRHL1 bph genes, therefore demonstrating that the individual operons have been disseminated among gram positive soil bacteria via linear-plasmid-mediated HGT. *Arthrobacter keyseri* strain

12B harbors a 130 kb catabolic plasmid pRE1 bearing the pht operon that encodes the exchange of phthalate to protocatechuate (Eaton, 2001). Phthalate (benzene-1,2-dicarboxylate) is a mid midway in the bacterial degradation of phthalate esters (used as plasticizers) as well as of certain fused-ring polycyclic aromatic hydrocarbons (found in fossil fuels). Gram negative bacteria transform phthalate through protocatechuate as well, but the enzymes of these pathways are not intimately related even though they catalyze similar reactions.

4.4 Naphthalene-degradative plasmid Nah7

Catabolic plasmids such as SAL (for salicylate), TOL (for toluene), and CAM (for camphor) were discovered in the 1970s. A self-transferable plasmid with the genes requisite for naphthalene degradation from *P. putida* G7, designated NAH7, was reported in 1973 by Dunn and Gunsalus (1973). NAH7 was assigned to the IncP-9 inaptness group of plasmids from Pseudomonas strains on the basis of its incompatibility with another IncP-9 plasmid (White and Dunn 1978) and its close association with the TOL plasmid pWW0 from *P. putida* mt-2 (Benson and Shapiro 1978 ; Greated *et al*., 2002) for both the backbone and catabolic genes (Lehrbach et al., 1983; Harayama et al., 1987) . Since its discovery, the biochemistry and genetics of the degradation pathway determined on NAH7, as well as those on pWW0, have been carefully investigated by numerous researchers. The information thus obtained has provided the foundation for studies of PAH degradation. Nevertheless, only lately have the absolute nucleotide sequences of these plasmids been resolute (Greated et al., 2002; Sota et al., 2006).

5 Conclusion

Bacterial degradation of PAHs and heteroaromatics has been at length studied for a long period; in the last decade, in order on the degradation pathways, genes, and enzymes has enlarged swiftly. For PAH degradation, Several current studies have attempted to characterize the degradation system for PAHs with four or additional rings. In fact, the metabolic pathways for pyrene, fluoranthene, benzopyrene, and others have been proposed recently (Kanaly and Harayama, 2000). The isolation of innovative xenobiotic degrading bacteria followed by genetic analyses will supply new examples of catabolic plasmids. In addition, recent genome wide research has provided information on the incidence of plasmids with unknown functions. However, it ought to be noted that the action of xenobiotic degradation conferred by catabolic plasmids might be reliant on the host cell. Although the catabolic gene(s) on plasmids is distributed amid a variety of bacterial strains via horizontal gene transfer, previous purposeful investigations of the xenobiotic-degrading systems conferred by catabolic plasmids have frequently been passed out using a single (in many cases, an original host) or a constrained number of host bacterial cell back-grounds in optimal laboratory conditions.

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