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Review on Microbial Degradation of Aromatic Hydrocarbons: Focus on Kinetics Modelling

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Abstract
Many anthropogenic activities produce huge quantities of chemical pollutants that find their ways into the natural environment. Those chemicals can either be of organic or inorganic sources, depending on their originating compounds. Over the years, there had been research findings regarding the application of microorganisms to provide solutions in the environment. This becomes imperative as salient issues in researches on microbial bioremediation will be understood. This review focused more on Kinetics modeling during biodegradation of aromatic hydrocarbons and their nature and effect on the environment coupled with the conventional remediation techniques. Kinetics modeling during bioremediation predicts microbial activities through their mechanism of actions towards the targeted contaminants. This gives better understanding of the rate of chemical degradation through different variable parameters. Modeling the cultivation of degrading organisms can highlight the inhibitory properties of the cells involved. Therefore, specific microbial growth rates can be modeled at various initial concentrations of the involving substrates. Such could be achieved using secondary models of Monod, Teissier, Aiba, Haldane, Yano and Luong. The models can reveal the substrate inhibitory effects to the reduction rate (as in the case of Monod) or inhibitory to the substrate rates like in the other models. Many studies were recently conducted on modeling microbial growth. Hence, utilization of those models are the best evidence that indicate when the substrates are toxic or inhibitory to the microbes. This provides better understanding on the future researches regarding the bioremediation effectiveness on scientific arguments.
Keywords: Environment, Pollutants, Microorganisms, Remediation, Modeling

INTRODUCTION

Environmental pollutants constitute large group of hazardous chemicals, which can be naturally occurring or from anthropogenicsource.Among the contributors from natural sources are oil seepage, forest fires and volcanic eruptions while anthropogenic sources involved industries, automobile discharges, incineration, coal, petroleum, agricultural practices and domestic wastes (Ravindra *et al.*, 2008). These sources deposit toxic organic and inorganic pollutants into the environment, many of which persist for a long duration because of their chemical complexity (Maliszewska, 1999). The persistence contributes immensely in the bioaccumulation of the pollutants within different ecosystems (Arulazhagan and Vasudevan, 2011). A certain proportion of the pollutants undergo natural transformations while others posedserious environmental challenge that critically affects public health (Bispo *et al.*, 1999; Lundstedt *et al.*, 2007; Yunusa and Umar, 2021).

The highest quantities of such organic materials are obtained from petroleum fractions Among the organic pollutants, are aromatic compounds that constituted assembled carbon structures in different benzene rings (Mishra *et al.*, 2001; Rubio-Clemente *et al.*, 2014; Umar, 2017). The complexity of these structures can be attributed to stable resonance within the conjugated π-electrons of the inert nucleus which allows them resist microbial degradation processes (Johnsen and Karlson, 2005; Desai and Vyas, 2006). The structure of aromatic compounds with single ring like phenol is simpler than those with many rings (Van Hamme *et al.*, 2003). Polycyclic aromatic compounds have low solubility in water but are readily soluble in fatty materials, which allowed them to be highly accumulative within animal's fatty cells thereby inducing mutation and cancer (Brandt and Watson, 2003). Many aromatic compounds are produced through incomplete combustion of organic matter and deposited into the environment through anthropogenic practices (Wong *et al.*, 2004; Chung *et al.*, 2007; IARC, 2010). thatrequired higher temperatures of refining (Connell, 2005). Many aromatic compoundscan

cause animal skin photosensitization associated with mild allergy, neurological disorders, kidney damage and body weight reduction (Patri*et al*., 2010).

Incidences of environmental pollutionsweredue to industrialization,transportation, minerals prospecting, refining, usage (Sany *et al*., 2014; Keshavarzifard and Zakaria, 2015; MohdRadzi *et al*., 2016). Public health related challenges are faced as a result of the frequency of the pollution occurrences and their severity to living ecosystems (Spinelliand Freitas, 2005; Akintunde *et al.,* 2015). High molecular weights polycyclic aromatic hydrocarbonsfor instance affect human life through the skin absorption into the bloodstream that eventually became converted into electrophilic derivatives that may result in cancer (Yunusa and Umar, 2021). This may affect the central nervous system through the blood circulation and causes peripheral neuropathy, and paralysis (Yunusa and Umar, 2021). The post-disposalbehavior of such pollutants gave further complications as unintended habitats are grossly affected (Oa and Lee, 2009; Park *et al.*,2010).

Microbial removal of environmental pollutants is reported to be the best technique due to the complete metabolic removal being associated with less expensive technology (Abdulsalam and Omale, 2009; Karamalidis*et al*., 2010). In this process, naturally occurring microbial cells are utilized because of their abundance, diversity, catabolic versatility and adaptations to critical conditions (Moraes*et al*., 2009). Bacteria are among the frequently utilized organisms as they can occupy suitable habitats in different environments as a result of them possessing broad enzymes spectrum that enables them catabolize the compounds as major substrates (Madigan *et al*., 1998). Such groups of organisms include the commonly studied bacteria like *Mycobacterium, Arthrobacter, Burkholderia, Sphingomonas,* and *Pseudomonas* (Kim *et al*., 2003; Seo, 2006; Baboshin *et al*., 2008).

There are instances where the environment is found to be contaminated with complex mixtures of both organic and inorganic pollutants like aromatic hydrocarbons and hazardous heavy metals. In such situations, microorganisms may face difficulties in removing such pollutants due to the challenges in transporting the organic pollutants into the microbial cells for mineralization resulting from the inhibitory effects of the heavy metals (Sandrin and Maier, 2003; Pereira *et al*., 2007; Srogi, 2007; Cao *et al*., 2008; Ibarrolaza *et al*., 2009). The heavy metals usually alter the structural permeability of the microbial cell membranes and prolong the cells' acclimatization time before consuming the organic substrate (Maliszewska and Smreczak, 2003; Sandrin and Maier, 2003; Zhang *et al*., 2011; Bashir *et al.,* 2014). This makes the pollutants to inhibit the microbial growth by substituting the main enzymes' functional groups with heavy metals ions (Yunusa and Umar, 2021).

Therefore, before initiating bioremediation of contaminated environments via the use of microorganisms, it is important to perform exhaustive background checks on the intrinsic features of the contaminated sites. Such an investigation should involve the elucidation of the extent of contaminated area, sampling parameters, locations, collection procedures and analytical methods to be used (Umar and Bashir, 2014).

The release of organic and inorganic pollutants allows their widespread into various soil, air and water environments (Umar, 2017). Within the water environment, hazardous chemicals attach themselves to the suspended particles before settling down the sediments and entering the food chain of the ecosystem (Rubio-Clemente *et al*., 2014). Once deposited in the soil environment, such pollutants became adsorbed to the soil particles with a very minute quantity being dissolved and transported into surface water and down the groundwater via runoff (Bossert and Bartha, 1984; Zhang *et al*., 1998; Birgül *et al*., 2011; Vela *et al*., 2012; Chizhova *et al*., 2013).

STRATEGIES FOR REMEDIATING ENVIRONMENTAL POLLUTANTS

Physical removal approach

- **Adsorption**:This involved attaching the aromatic compoundsinto the adsorbentdue to surface energy (IUPAC, 1990). The other atoms in the surface of the adsorbents through physio-sorption, van der Waals attraction, and chemio-sorption or electrostatic attraction fill bonding requirements of the constituting atoms (Ferrari *et al*., 2010). Adsorption can be applied to activated charcoal, and water purification processes through the selective transfer of adsorbates from the fluid phase to the surface of insoluble, rigid particles suspended in a vessel or packed in a column (Czeleje*t al*., 2016). Materials employed as adsorbents are spherical pellets moldings or monolithshaving the capacity to resist abrasion and thermal stability. Adsorbents can also be hydrophilic, polar, oxygen-containing compounds such as silica gel and zeolites (Cussler, 1997).

- **Photolysis:** This involved photon-mediated breakdown of the aromatic compounds due to mixed chemical interactions which results in the photodecomposition of the targeted contaminants (Thyrhaug *et al.*, 2016). The source of the photon need not only be visible light as all photons have enough energy that can interfere with chemical bonds. The reactions involve electromagnetic wave energy equivalent to or greater than those of visible light, as a photon's energy is inversely proportional to its wavelength. Thus, Ultraviolet light, x-rays, gamma rays and visible light itself can bring about photolysis (Thyrhaug *et al.*, 2016). Hence, photolysis is utilized in remediating contaminated environments by applying those radiations to breakdown pollutants molecules.
- **Ozonation:** The process can be utilized during the precipitation of iron and manganese from water and detoxifications of urea and cyanides to cyanates (Horvath *et al.*, 1985). Recent advances elucidate the effects of acute and chronic ozone exposure on human health (EPA, 2015). Among such effects include the impairment of the respiratory, cardiovascular and central nervous systems which may lead to premature death and problems in human reproductive health and development (EPA, 2015).

Degradation of Petroleum hydrocarbons

Bioremediation can completely transform pollutants into non-hazardous products with fewer effects in an environmentally friendly manner (Declercq *et al.*, 2012). This review gives much emphasis on organic pollutants as they constituted larger percentage of the entire global pollutants that destabilize living ecosystems (Umar *et al.*, 2016; 2017; 2018a; 2018b; 2019; 2020a; 2020b). Additionally, many inorganic pollutants are degraded through the physicochemical approaches as explained in the above paragraphs. Many organic structures are susceptible to enzymatic attacks which are simply obtainable from microorganisms (Yunusa and Umar, 2021). The microorganisms involved required nutrient sources and other favorable culture conditions to convert the target pollutant within the cellular biomass into an intermediate and metabolic precursor (Yunusa and Umar, 2021). The process had been reported since 19th century, but further researches could provide broad perspectives into the matter (Borden *et al.*, 1986). Recognition of the target substrate by the aerobic microbes is aided by the enzymes and facilitated by chemical transformations thorough hydroxylation (Desai and Vyas, 2006). Anaerobic microbes on the other hand, can only reduce the target substrate bonds thereby simplifying its complexity nature (Desai and Vyas, 2006).

The commonly removal approach of polycyclic aromatic hydrocarbons involved the oxygenation of the targeted compound into dihydrodiol intermediate with the help of dioxygenase enzymes (Mishra *et al.*, 2001). The process involved the initial activation of the enzymes using NADPH or NADP co-factor which increases their reactivity and makes the targeted substrate lose their resonance stability. This allowed the aerobic organisms attach the oxygen molecules onto the targeted organic structure and make them less complex for the subsequent utilization by the microbes as carbon source (Mishra *et al.*, 2001). Further hydroxylation breaks the pollutant structure into the products that can enter the tri-carboxylic acid (TCA) cycle and produce adenosine tri phosphate (ATP) energy for the cells functioning (Umar, 2017). The end product is usually water and carbon dioxide for plants utilization (Khanna *et al.*, 1998).

Mechanisms of Microbial actions during Biodegradation

Metabolites recognition during biodegradation provides better understanding on the cellular metabolic pathways and dynamics approach undergone by the microbes involved (Kitano, 2002; Goodacre *et al.*, 2004; Nicholson *et al.*, 2004; Tao *et al.*, 2007; Lu *et al.*, 2014). For instance, during the biodegradation of phenanthrene, intermediates called 3,4-dihydroxyphenanthrene and phthalic acid are produced through dioxygenation of C_3 and C_4 (Umar *et al.*, 2016; 2017; 2018a; 2018b). The TCA cycle is the ultimate destination of those products, and its byproducts are thought to be beneficial (Seo*et al.*, 2009).The most commonly bacteria involved are members of the gram-negative group of the genera *Pseudomonas*, *Alcaligenes*, *Acinetobacter*, *Arthrobacter*, *Mycobacteria* and *Sphingomonas*, to *Corynebacterium*, *Rhodococcus*and *Nocardia* (Ahn *et al.*, 1999; Stingley *et al.*, 2004). Recent researches had shown that genus *Enterobacter* is very efficient in degrading aromatic structures (Umar *et al.*, 2016; 2018a; 2018b).The bacteria are rampantly prevalent on used vehicle lubricants contaminated soil with population size up to 10^8 cells/gram (Umar *et al.*, 2016).

The mechanisms through which these organisms performs their functions involved bonds breakage at the meta-position (extradiol cleavage), or at the ortho-position (intradiol

cleavage) of the targeted compound (Mishra *et al.*, 2001). Intradiol cleavage involved hydroxylation of carbon atoms while extradiol cleavage involved the adjacent carbon atoms hydroxylation (Mishra *et al.*, 2001). In the extradiol cleavage, catechol 2,3-dioxygenase, 1,2-dihydroxynaphthalene dioxygenase and 2,3-dihydroxybi-phenyl dioxygenase are encoded by the nahH, nahC and BphCs genes respectively (Harayama and Rekik, 1989). Each of those enzymes possessed four matching subunits of 32 kDa with Fe^{2+} cofactor (Kimbara *et al.*, 1989; Hirose *et al.*, 1994). The expression of αα, αß and ßß subunits within catechol 1,2-dioxygenases is thought to confer on bacteria ability to efficiently carryout intradiol cleavage (Nakai *et al.*, 1990).

KINETICS MODELING

Different models were used to describe biodegradation of organic pollutants which provide better degradation understanding (Loginova *et al.*, 2009). In this approach, microbial growth rate would be associated with the concentration of the organic substrate. Numerous mathematical models (primary) have been put forward to explain the microbial growth and metabolism of the substrates (Loginova *et al.*, 2009).Microbial growth usually exhibits a known pattern, in which the specific growth rate starts initially at zero at a lag time (λ), followed by the exponential phase, where an acceleration in a certain time period leads to a maximal value for the growth rate (μ_{max}). The growth curves eventually plateau entering a stage of which the rate becomes zero, where an asymptote (*A*) is normally achieved in form of stationary phase. Eventually, in the death phase, the growth rate becomes negative (Zwietering *et al.*,1990). The lag period is thought to occur as the bacteria prepared for growth after acclimatizing to their new environment (Baranyi and Roberts 1994). In secondary modeling, μ_{max} helps in determining the effects of both dependent and independent parameters as microbial activity (μ_m) equalizes the slope of the line at the exponential phase (Zwietering *et al.*,1990; Fujikawa, 2010). The most studied method involved the sigmoidal curve and linear regression while nonlinear regression can be used to describe the entire set of data producing constants such as μ_{max}, λ and *A*(Johnsen *et al.*,2013). Primary Equations involving Logistic (Zwietering *et al.*,1990), Gompertz (Gompertz, 1825), Richards (Richards, 1959), Schnute (Zwietering *et al.*,1990), Baranyi-Roberts (Baranyi, 1995), Von Bertalanffy (Babák *et al.*, 2012), Buchanan three-phase (Buchanan, 1993) and Huang (Huang, 2013) are the primary kinetics modeling (Equations 1 to 8).

Modified Logistic =
$$y=\frac{A}{\left\{1+\exp\left[\frac{4\mu_m}{A}(\lambda-t)+2\right]\right\}} \quad (1)$$

Modified Gompertz =
$$y=A\exp\left\{-\exp\left[\frac{\mu_m e}{A}(\lambda-t)+1\right]\right\} \quad (2)$$

Modified Richards =
$$y=A\left\{1+v\exp(1+v)\exp\left[\frac{\mu_m}{A}(1+v)\left(1+\frac{1}{v}\right)(\lambda-t)\right]\right\}^{\left(\frac{-1}{v}\right)} \quad (3)$$

Modified Schnute =
$$y=\left(\mu_m\frac{(1-\beta)}{\alpha}\right)\left[\frac{1-\beta\exp(\alpha\lambda+1-\beta-\alpha t)}{1-\beta}\right]^{\frac{1}{\beta}} \quad (4)$$

Baranyi-Roberts =
$$y=A+\mu_m x+\frac{1}{\mu_m}\ln\left(e^{-\mu_m x}+e^{-h_0}-e^{-\mu_m x-h_0}\right) \text{ or } -\ln\left(1+\frac{e^{\mu_m x+\frac{1}{\mu_m}\ln\left(e^{-\mu_m x}+e^{-h_0}-e^{-\mu_m x-h_0}\right)}-1}{e^{(y_{max}-A)}}\right) \quad (5)$$

Von Bertalanffy =
$$y=K\left[1-\left[1-\left(\frac{A}{K}\right)^3\right]\exp^{-\left(\mu_m x/3K^{\frac{1}{3}}\right)}\right]^3 \text{ or } y=A+y_{max}-\ln\left(e^A+\left(e^{Y_{max}}-e^A\right)e^{-\mu_m B(x)}\right) \quad (6)$$

Huang = $$B(x) = x + \frac{1}{\alpha}\ln\frac{1+e^{-\alpha(x-\lambda)}}{1+e^{\alpha\lambda}}$$ *(7)*

Buchanan = y = A, if x < lag

y=A + k(x–λ), if λ ≤ x ≥ x_{max} *(8)*

Where

A isthe microbial growth lower asymptote
μ_m is the maximum specific bacterial growth rate
v is the effect near which asymptote maximum bacterial growth occurs
λ is the period involved in the microbial lag phase
y_{max} is themicrobial growth upper asymptote
e is the exponent (2.718281828)
tis the sampling time
α,ß, k are the curve fitting parameters
$h_0$is the dimensionless parameter quantifying the initial state of the degradation.

Kinetics modeling will enhance specific microbial growth rate as theoretical maximum growth is achievable whether the lag period changes or not. Likewise, modeling results can highlightinhibitory properties, if any, of growth at high concentrations, as was demonstrated by several workers (Al-Darbi *et al.,* 2005; Campo *et al.,*2007). Then, it is possibleto model specific growth rates at various initial concentrations of the substrate using different secondary models (Equations 9 to 15). Such are the specific secondary model equations used during biodegradation of organic pollutants.Secondary modeling can also reveal whether the substrate is not inhibitory to reduction rate (Monod) or if it is inhibitory to the rates (Haldane, Teissier, Aiba, Yano and Luong). Multiple researches had been conducted on modeling microbial growth on lipid rich substrates using the classical Monod kinetics (Nweke*et al.*,2014; Nkeiruka and Tagbo, 2014).The utilization ofthose models in thereduction kineticis the best evidenced that substrates are toxic or inhibitory to the microbes (Mercurio *et al.*,2004; Saifuddin and Chua 2006). The Haldane models has been utilized in modeling hydrocarbon degradation and this is understandable as hydrocarbons are toxic(Ahmad *et al.*,2014).

Monod = $$\mu_{\max}\frac{S}{K_s + S}$$ *(9)*

Haldane = $$\mu_{\max}\frac{S}{S + K_s + \frac{S^2}{K_i}}$$ *(10)*

Teissier = $$\mu_{\max}\left(1-\exp\left(-\frac{S}{K_i}\right)-\exp\left(\frac{S}{K_s}\right)\right)$$ *(11)*

Aiba = $$\mu_{\max}\frac{S}{K_s + S}\exp\left(-K_p P\right)$$ *(12)*

Yano and Koga = $$\frac{\mu_{\max} S}{S + K_s + \left(\frac{S^2}{K_1}\right)\left(1+\frac{S}{K}\right)}$$ *(13)*

Han and Levenspiel = $$\mu_{\max}\left[1-\left(\frac{S}{S_m}\right)\right]^n\left[\frac{78}{\frac{S}{S+K_s\left(1-\frac{S}{S_m}\right)^m}}\right]$$ *(14)*

Luong

$$= \mu_{\max} \frac{S}{S + K_s} \left[1 - \left(\frac{S}{S_m} \right)^n \right] \quad (15)$$

Where

μ_{max} is the maximal growth rate (h^{-1})
K_s is the half saturation constant for maximal reduction
S_m is the maximal concentration of substrate tolerated
m, n, K are the curve parameters
*S*is the substrate concentration
P is the end product concentration

Assessment of the best models, for both primary and secondary modeling can be achieved using the statistical tests involving root-mean-square error, adjusted coefficient of determination (R^2), bias factor, accuracy factor and corrected Akaike Information Criterion (Halmi *et al.*,2014). Increasingorganic substrates concentrations without optimization cells population as the experiment progresses signified the accumulation of toxicants to the microbial cells (AbdEl-Mongy *et al.*,2015). Such toxicants might include aromatic and halogenated hydrocarbons, phenolics, pesticides, and dyes which forces the microbial growth to be severely retarded at higher concentrations. Glucose is apparently a harmless substrate, but studies indicated that higher concentrations greater than 105 w/v can inhibit its oxidation in aerobic batch microbial culture (Misenheimer*et al.*,1965). Monod model can be less effectivedue to substrate-inhibition to microbial cells. Therefore, microbial growth inhibition due to substrate higher concentrationis a derivative ofMonod kinetics model. This can beimprovedthrough the Ki constant as the unstructured models are strongly recommended to describe the hyperbolic curve of microbial growth under substrate inhibition. Hence,Haldane-Andrews (Haldane), Teissier-Edwards (Teissier), Aiba, Yano and Koga, Han and Levenspiel and Luong models are the best to handle experiments ofmore than two parameters.

Equations 9 to 15 were developed from the theory of enzyme inhibition as the equation 10was the first to be applied during kinetics of microbial inhibition(Knowles *et al.,* 1965). In these equations, enzyme inhibition is explained by more than two substrate moleculesthat formed inactive complex. Excess nitrite inhibition to *Nitrobacter winogradskyi* growth was successfully explained by model of the equation 10(Kornegay and Andrews, 1968). The equation is modified to assume the existence of two different inactive forms of substrate-enzyme complexes.

Another classic model used in microbial population growth is the Gompertz function (Quintas *et al.,* 2007). Initially, this model was used in actuarial science for appropriate human death data, but as time goes, it was applied to model organ growth, deterministically(Okpokwasili and Nweke, 2006). Improvements in the Gompertz function have allowed designing models that candescribe the influences of inherent elements such as temperature and availability of oxygen on microbial growth factors. This model thrives on the exponential relationship between specific growth rate and population density, and had been used quite recentlyto model bacterial growth on hardy substrates(Haji *et al.,* 2011;Salam *et al.*,2012).

Similarly, Kim *et al.* (2005)used the product inhibition model to model the kinetics of various substrate inhibition through the introduction of another dimensionless constant (K). However, values of the dimensionless constant (K) are very large, thus, the first two equations are thought not suitable for modeling. Furthermore, Edwards' and Haldane-Andrew's equations are said to be statistically indistinguishable from each other, and, a comparison of the fit to the growth data of various organisms how no significant differences between the models (Tseng and Wayman, 1975). Nonetheless,as regards the Monod and Andrews functions, it is possible to consider the circumstances in which utilization of these models might cause inaccurate outcomes, even though the models suitablyexplain the consequences of substrate concentration on the growth of microorganisms. This is often true when the substrates are toxic xenobiotic,leading to inhibition of growth (Kulkarni and Chaudhari, 2006). Tackling this issue birthed the development of a number of inhibition models, including the Teissier, Luong and Han and Levenspiel models that directly ascribing the abovementioned characteristic (Schröder *et al.,* 1997). The Teissier/Tessier Model studies the effects of substrate diffusion on bacterial growth kinetics through the bacterial outer membrane (Şeker *et al.*,1997). Contrastingly, the Monod model studies the single rate-limiting effect and saturation

kinetics of substrate transport through the cytoplasmic membrane (Monod, 1949).

A similarity exists between the Tessier equation and the Edward model. The Edward model combines the mechanism of diffusion-controlled substrate supply of the Tessier model with a shielding diffusional control of high concentrations. Sabullah *et al.* (2016) successfully used the Tessier model in modeling bacterial reduction of molybdenum, likewise Tavassoli *et al.,* (2012) used it to model bacterial growth on asphaletes. Further studies were done on biopolymers, phenol, and other substrates using the same model (Agarry *et al.*, 2009). Other models such as the discontinuous models of, are tripartite, including exponential, stationary, and decay phases (Tseng and Wayman, 1975). In this model, growth inhibition doesn't exist below a threshold substrate concentration, like other models; as such, when a substrate concentration exceeds a particular level, the microbial growth level decreases in proportion to the concentration difference. Tseng and Wayman (1975) used this model to successfully model the kinetic data of two bacteria growing on butanol and methanol, which are *Pseudomonas methanica* and *Arthrobacter* AK19. The model applied in describing toluene degradation (Choi *et al.,* 2008).

The models of Luong and Han and Levenspiel are understood to be more effective than that of Tseng and Wayman models (Mulchandani and Luong, 1989). However, the integration of an exponential delay function in the Han and Levenspiel model, leads to the matching of the inflection point on the growth curve to a particular product concentration (Mulchandani and Luong, 1989). The Han and Levenspiel model has been readily applied, and it had been successful in modeling the growth of microorganisms on the congo red, solid waste, phenol, and m-cresol (Poggi-Varaldo *et al.*, 1997; Saravanan *et al.,* 2008; Bajaj *et al.,* 2009; Gopinath *et al.,* 2011). This had successfully modeled bio-hydrogen production and had accurately modeled microbial growth at high salt concentrations(Wang and Wan, 2008).

Luong developed a continuous version of the Han and Levenspiel model through the adaptation of the nonlinear product inhibition (Mulchandani and Luong, 1989). The proposed model is capable of describing both limiting effect of substrate to growth at low concentration, which is a Monod model, and the inhibiting effect of substrate to growth at high substrate concentrations. The model moreover introduced a parameter for the maximum substrate concentration, and the growth completely ceases above this constant value (Mulchandani and Luong, 1989). The model had been employed suitably in the growth of microorganisms on phenol, caffeine, ammonia, monochlorobenzene and 1,2-dichloroethane (DCE), 2-fluorophenol,dichloromethane, formaldehyde, m-cresol, 4-fluorocinnamic acid and methyl iso-butyl ketone (Saravanan *et al.,* 2008; Raghuvanshi *et al.,* 2012).

CONCLUSION

The use of microbial consortia is the best approach for biodegradation, as groups of microorganisms possess greater enzymatic capabilities than single strains. A variety of primary and secondary models exist that described microbial growth during biodegradation and its inhibition. Understanding these concepts will enable us in critically appreciating what contributions have been made in the past, learning what is currently being done and anticipating what needs to be done in the future. This will appreciate the current scientific effort and anticipates safer environmental future for the entire humanity.

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