

Marine bacteria: potential candidates for enhanced bioremediation

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Abstract Bacteria are widespread in nature as they can adapt to any extreme environmental conditions and perform various physiological activities. Marine environments are one of the most adverse environments owing to their varying nature of temperature, pH, salinity, sea surface temperature, currents, precipitation regimes and wind patterns. Due to the constant variation of environmental conditions, the microorganisms present in that environment are more suitably adapted to the adverse conditions, hence, possessing complex characteristic features of adaptation. Therefore, the bacteria isolated from the marine environments are supposed to be better utilized in bioremediation of heavy metals, hydrocarbon and many other recalcitrant compounds and xenobiotics through biofilm formation and production of extracellular polymeric substances. Many marine bacteria have been reported to have bioremediation potential. The advantage of using marine bacteria for bioremediation in situ is the direct use of organisms in any adverse conditions without any genetic manipulation. This review emphasizes the utilization of marine bacteria in the field of bioremediation and understanding the mechanism behind acquiring the characteristic feature of adaptive responses.

Keywords Marine bacteria · Adaptation · Stress response · Diversity · Bioremediation

Introduction

Microorganisms play an important role in the maintenance and sustainability of any ecosystem as they are more capable of rapid adjustment towards environmental changes and deterioration. They are present everywhere, be it in the volcanic eruptions or Antarctic glacier or mars conditions; hence, marine environments are not far apart. Ninety-seven percent of the earth's water is saline in nature and it accounts for approximately 71 % of the earth's surface which generates 32 % of world's net primary production (Alexander 1999). Oceans are the source of wealth, opportunity, and abundance as they provide us food, energy, and water and are helpful in sustaining the livelihoods of hundreds of millions of people. Besides, oceans are also the main highway of the international trade and are the main stabilizer of the world's climate. As per the report of the United Nations Environment Programme on Global Biodiversity Assessment, marine organisms include 178,000 species which fall in 34 phyla (UEPA 2006).

Due to various factors like pressure from economic development on local and global scale as well as modifications of river flows to the coasts which carry pollutants from the land, pollution level is increasing gradually in the marine environments (Crossland et al. 2005). In spite of the presence of many adverse conditions in the marine environment, varieties of organisms are found to be present in the marine ecosystem from the tiny microbes to the large mammals. Pulse field gel electrophoresis and shot-gun sequencing results showed the presence of vast varieties of viruses which are extraordinarily diverse in nature (Rohwer and Thurber 2009). Both autotrophic and heterotrophic bacteria are present in abundant numbers in the marine environment, like chemosynthetic heterotrophic bacteria and euryhaline organisms (Stanley 2005). The marine environment is also found to be a good reservoir for many human pathogenic bacteria, e.g.

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Actinomyces, *Bacillus anthracis*, *Mycobacterium tuberculosis*, *Vibrio parahaemolyticus*, *Vibrio alginolyticus*, and many more (Oberbeckmann et al. 2012). Most of the marine bacteria are well known for their association with the wide variety of functions like antibiotics and enzyme production (Okami 1986), marine light absorption (Stramski and Kiefer 1998), heavy metal bioremediation (Rainbow 1995), biosurfactant production (Maneerat and Phetrong 2007), biodegradation and bioremediation of hydrocarbons (Margesin and Schinner 2001), oil biodegradation (Nweke and Okpokwasili 2003), bioremediation of diesel-contaminated soils (Gallego et al. 2001), degradation of metatoluic acid (Prakash et al. 2008), agar degradation (Vijayaraghavan and Rajendran 2011), polyphosphate accumulation (Ohtake et al. 1985), degradation of plastic debris (Derraik 2002), and antibiofilm activity (Jiang et al. 2011), to mention a few.

Bioremediation technology utilizes the metabolic potential of microorganisms to clean the contaminated environments. It is the metabolic ability of the microorganisms to mineralize or transform organic contaminants into less harmful substances which can be integrated into natural biogeochemical cycles. Bioremediation is an attempt to accelerate naturally occurring degradation by optimizing the limiting conditions which is nondestructive, treatment-, and cost-effective as well as with a logistically favorable clean-up technology (Margesin and Schinner 2001). However, the sole obstacle in bioremediation in situ is the unfavorable conditions of the environments. Most of the environments are characterized by elevated or low temperature, alkaline or acidic pH, high pressure, or high salt concentration. Marine bacteria are such a group of bacteria which get exposure to such unfavorable conditions naturally. Hence, any marine bacteria having the potential for bioremediation can become the ideal candidates for the biological treatment of polluted extreme habitats.

This review summarizes the recent discoveries regarding the exclusive characteristics of marine bacteria, their physiologic and genetic adaptation in the dynamic environmental condition, biogeography and diversity, and the role of marine bacteria in various remediation aspects to establish that marine bacteria can be utilized in enhanced bioremediation.

Characteristic features of marine bacteria

Marine environment is the largest habitat on the earth which accounts for more than 90 % of total biosphere volume and the microorganisms present in that are responsible for more than 50 % of the global primary production and nutrient cycling (Lauro et al. 2009). These marine bacteria can be isolated from the marine water, sediments, and mangroves associated with the marine habitats, normal flora of the marine organisms, and deep sea hydrothermal vents. They

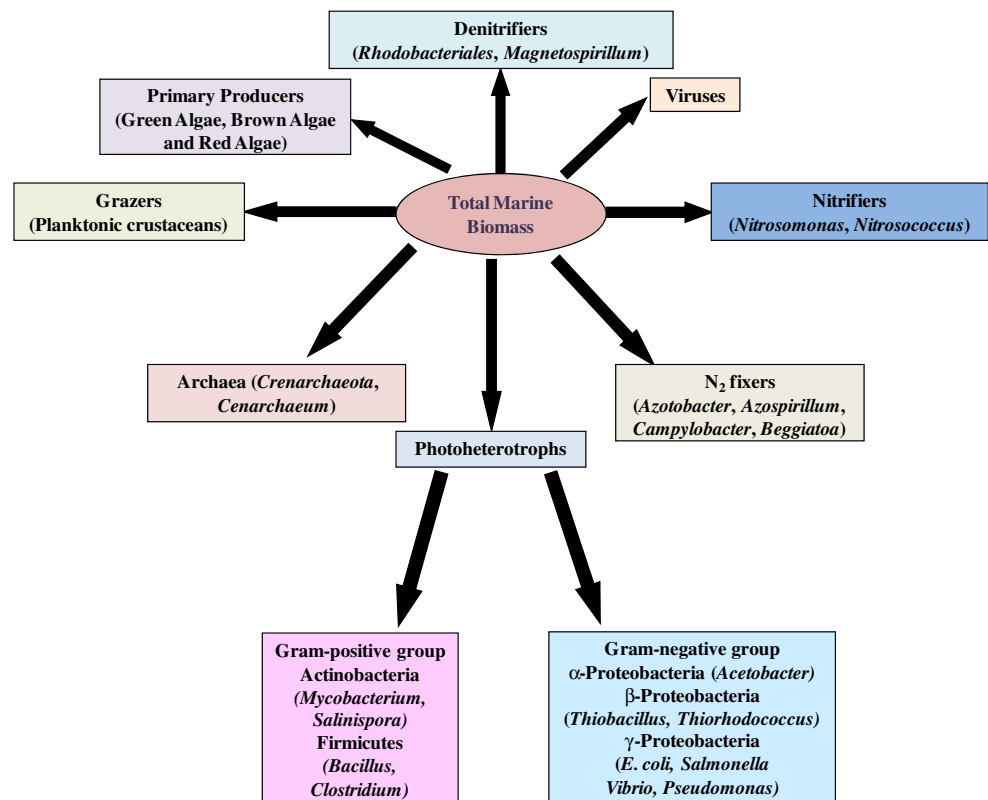
usually require sodium and potassium ions for their growth and to maintain osmotic balance of their cytoplasm (MacLeod and Onofrey 1957). This requirement for Na^+ ion is an exclusive feature of the marine bacteria which is attributed to the production of indole from tryptophan (Pratt and Happold 1960), oxidation of L-arabinose, mannitol, and lactose (Rhodes and Payne 1962) as well as transport of substrates into the cell (Hase et al. 2001). Other physical characters imputed to marine bacteria include facultative psychrophilicity (Bedford 1933), higher tolerance to pressure than their terrestrial counterparts (Zobell and Morita 1957), capacity to survive in seawater, mostly Gram-negative rods (Buck 1982), and motile spore formers (Buerger et al. 2012) which distinguishes them from the terrestrial bacteria. β -aminoglutaric acid or β -glutamate which is rare in nature is present in higher amounts in marine sediments and is utilized by the marine bacteria as osmolytes (Robertson et al. 1990). Some of the thermophilic marine bacteria isolated from the deep sea hydrothermal vents are also capable of nitrogen fixation (Ruby and Jannasch 1982).

The most unique feature of a photosynthetic marine bacterial genome is the presence of rhodopsin which contains 2,197 genes, far lower than any other genes (Newton et al. 2010). In addition to that, marine cyanobacteria also harbor a similar pattern of gene contents which are correlated with their isolation sources (Martiny et al. 2009). The sole cause behind the diverse genetic level in marine microbes is due to the acquisition of alternative mechanism for obtaining carbon and energy. Copiotrophs from marine habitats have higher genetic potential to sense, undergo transduction, and integrate extracellular stimuli. These characteristics are likely to be crucial for their ability to fine-tune and rapidly respond to the changing environmental conditions like sudden nutrient influx or depletion (Lauro et al. 2009).

Global diversity of marine bacteria

Most of the bacteria in seawater fall under viable but unculturable group (Eliers et al. 2000). To overcome this problem and to study the diversity pattern of the marine bacterial species, many advanced techniques like metagenomics, 16S rRNA gene amplification, denaturing gradient gel electrophoresis (Diez et al. 2001), cloning, and restriction fragment length polymorphism (Liu et al. 1997) have been used. However, the major problem encountered during these processes is that, most of the isolates cannot be assigned to known species. Marine environment is a huge resource of marine organisms (Fig. 1), and the marine microorganisms are highly abundant in nature, i.e. 3.6×10^{29} bacterial cells (Sogin et al. 2006), 1.3×10^{28} archaeal cells (Karner et al. 2001), and 4×10^{30} viruses (Suttle 2005).

Fig. 1 Distribution of total marine biomass and their subgroups (following Gontang et al. (2007) and Stevens et al. (2007))



The systematic documentation of bacterial diversity in marine environment dated back to 1944 when ZoBell and Upham (1944) characterized 60 species. Marine bacteria have been isolated from mangrove and coral reef ecosystems, besides deep and inshore waters of all the oceans and seas (reviewed in Das et al. 2006). Biological productivity in the Indian Ocean basin was attributed to the higher level of benthic bacterial population which was reported in the range of $0.48\text{--}1.21 \times 10^5$ CFU/g (Loka Bharathi and Nair 2005). Most of the bacterial communities in the Indian Ocean were categorized under six major taxonomic groups, i.e., α , β , and γ proteobacteria, actinobacteria, bacilli, and flavobacteria (Piskorska et al. 2007). However, in the Pacific Ocean, dominant bacterial genera are *Desulfobacterium*, *Desulforhopalus*, *Desulfococcus*, *Desulfosarcina*, *Pelobacter*, and *Syntrophus* (Inagaki et al. 2006). The number and diversity of bacteria vary with the depth, as α - and γ -proteobacteria are abundant at all depths, whereas at 800–440-m depth, *Actinobacteria*, *Chloroflexi*, *Planctomycetaceae*, β -Proteobacteria, *Acidobacteria*, *Firmicutes*, and *Verrucomicrobia* are common (Brown et al. 2009). Liao et al. (2011) also reported γ -proteobacteria as the most common bacterial entity in the cobalt-rich crust deposit regions of the Pacific Ocean. Both photoautotrophic and photoheterotrophic prokaryotic population in the Arctic ocean decreases about threefold (Cottrell and Kirchman 2009) which may be due to the reported global warming, increased water column mixing (due to loss of ice cover), and changing current patterns (Lovejoy et al. 2006).

The environment of polar oceans also varies from that of the other oceans due to the various factors like limitation of light penetration to upper part of the ocean water. However, many groups of microbes including phytoplankton, algae, and bacteria which are collectively called as sea-ice microbial community have been isolated from these polar oceans (Hollibaugh et al. 2007). Additionally, psychrophilic bacteria like *Colwellia*, *Marinobacter*, *Planococcus*, and *Shewanella* inhabit in these regions (Bowman et al. 1997). By employing both cultivable and uncultivable techniques, the dominant taxonomic bacterial groups at both the poles were found to be α - and γ -proteobacteria and the cytophaga–flavobacterium group (Brinkmeyer et al. 2003).

Adaptation of marine bacteria to changing environmental patterns

The vast diversity of marine microorganisms is significant to the functional role they play in the marine environment. They respond very quickly to changing environmental patterns which makes them ideal for potential bioremediation and bioindicator purposes. There are various changes that occur periodically in the marine environment which include sea surface temperature, pH of the surrounding environment, changing pattern of light and UV light, sea level rise, tropical storms, and terrestrial inputs. Microorganisms get continuous exposure to changes of oceanic temperature;

however, the level of exposure varies in different microbial niches. Some groups of microorganisms overcome this problem by shifting their physical locations beneath sediments or by symbiosis with other organisms which is mostly found in pathogenic microorganisms (Jannasch and Wirsén 1984). Other reported mechanisms of adaptation towards elevated temperature in seawater are chemotaxis and adhesion to a β -galactoside receptor in the coral mucus (Banin et al. 2001a), penetration into epidermal cells, differentiation into a viable-but-not-culturable state, intracellular multiplication, production of toxins that inhibit photosynthesis (Banin et al. 2001b), and production of superoxide dismutase to protect the pathogen from oxidative stress (Banin et al. 2003).

Ocean acidification is mainly caused by accumulation of CO₂ gas in the marine environments, but the lowering of pH is not below 6.0. Bacteria are more adapted to this variation of pH conditions in some unknown mechanisms. However, Takeuchi et al. (1997) showed that the oceanic pH will very soon go below 6.0 and may reach 5.5 which will create a serious problem. Though the adaptive capacity of microbial system to pH is quite low, this study showed that marine bacteria are better adapted to pH variations than other terrestrial and aquatic microorganisms. However, the projected decline of 0.4–0.5 in oceanic pH by 2100 will have some significant consequences on the marine ecosystem functions having a direct impact on nitrogen cycle and microbial loop.

Ultraviolet light is a powerful mutagen which interferes with accurate DNA replication and induces the incorporation of wrong bases during that process of DNA repair. Hence, the changes in ultraviolet light pattern in marine environment have the potential to change the biomass and species composition in that community (Davidson and Belbin 2002). However, the microorganisms exposed to those conditions get adapted to that situation by genetic changes and causing shifts in community compositions, thus increasing UV-tolerant species and declining UV-sensitive species.

Sea level rise facilitates the introduction of new microbes from terrestrial sources to marine ecosystems which may include pathogenic strains. Furthermore, rainfall and river flood add pollutants and xenobiotics into the seawater, having the potential to alter the microbial community structure and function. However, bacteria adapt to such situations by changing their pattern of growth rates, gene expression, physiological or enzymatic activities, and changes in intimate or symbiotic associations with other organisms. Some group of marine bacteria have also been reported to develop many unique mechanisms like synthesis of bioactive compounds (Carvalho and Fernandes 2010), biofilm formation in marine environment (Poli et al. 2010), and production of biosurfactants (Safary et al. 2010) when they are exposed to extreme conditions like pressure, temperature, salinity, and

depletion of micronutrients. By adopting metagenomic approach, environmental adaptation of marine bacteria was quantified and the change in energy conversion strategies, variation in amino acid pathways, variation in methionine-dependent pathways, modulation of lipid, and glycan metabolism were also assessed when marine bacteria were exposed to various environmental conditions (Gianoulis et al. 2009).

α -Proteobacteria is the major group among the microorganisms distributed in the marine environment, and this may be due to their greater adaptation capability in the dynamic marine environments. Many studies have been conducted to deduce the molecular mechanism of adaptation in this group of bacteria; however, no strong conclusion has been drawn so far. Thus, α -proteobacteria are the most diverse bacterial subdivisions in terms of their lifestyle, geographical distribution, and genome size (Ettema and Anderson 2009). Recently, the discovery of 61 signature proteins (Fig. 2) in the genome of this group of organisms provided a ray of hope to solve the problem in understanding the mechanism of their adaptation (Kainth and Gupta 2005).

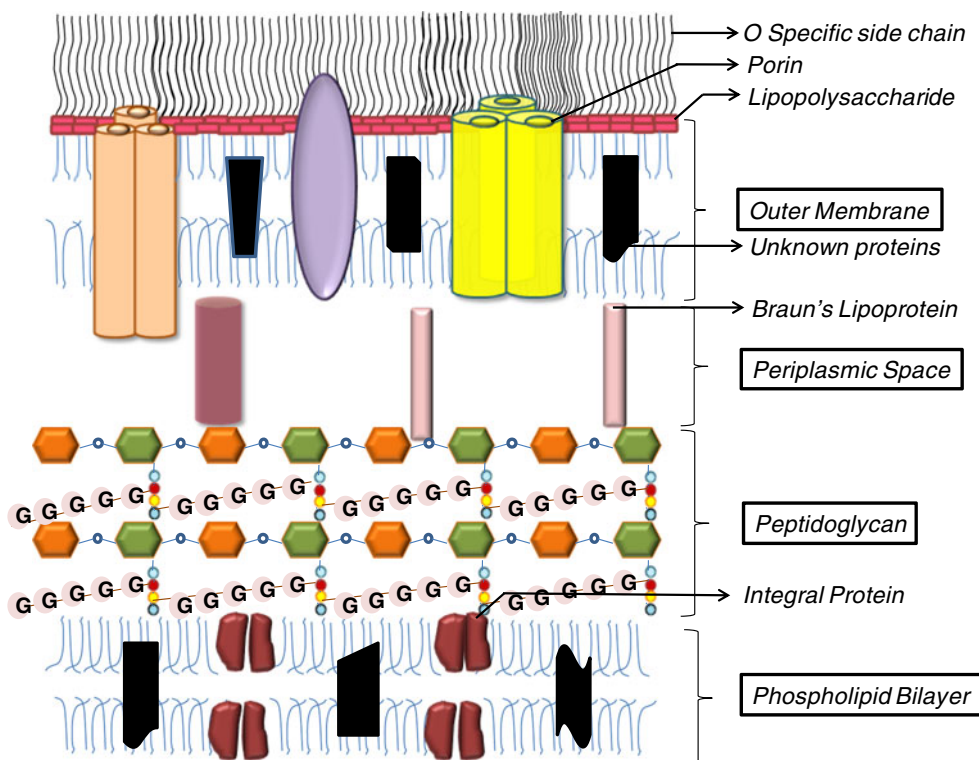
Application of marine bacteria in bioremediation

The use of marine bacteria for biodegradation of various natural and synthetic substances and thereby reducing the level of hazardous compounds is increasingly drawing attention because of the huge potential of these isolates for environmental restoration. Marine bacteria possess a wide variety of bioremediation potentials which are beneficial from both environmental and economic point of view (Amidei 1997). The bioremediation and biotransformation methods have been employed to tap the naturally occurring metabolic ability of marine microorganisms to degrade, transform, or accumulate toxic compounds including hydrocarbons, heterocyclic compounds, pharmaceutical substances, radionuclides, and toxic metals (Karigar and Rao 2011).

Removal of heavy metals

Heavy metal pollution is one of the most important environmental concerns due to various natural and anthropogenic activities. Though various physical and chemical methods have been proposed to remove such hazardous metals from the environment, they are of least success in terms of cost-effectiveness, limitations, and generation of harmful substances (Wuana and Okieimen 2011). Marine microorganisms solve these problems as they do not produce any by-products, and they are highly efficient even at low metal concentrations (De et al. 2008). *Vibrio harveyi*, a normal inhabitant of the marine environment is reported to possess

Fig. 2 Hypothetical schematic presentation of the structure of cell wall of a typical α -proteobacteria in marine environment. The proposed cell wall structure showing the unknown signature proteins (a total of 61) in addition to the normal components which were supposed to have the function related to the adaptation in the dynamic marine conditions



the potential for bioaccumulation of cadmium up to 23.3 mg Cd^{2+} /g of dry cells (Abd-Elnaby et al. 2011). In line with that, Canstein et al. (2002) reported a consortium of marine bacteria to efficiently remove mercury in a bioreactor in disturbance-independent mechanism. A new combination of genetic systems in marine bacteria for the potential degradation of phenol and heavy metals was also described (EI-Deeb 2009). Marine bacteria also possess the properties of chelation of heavy metals, thus removing them from the contaminated environment by the secretion of exopolysaccharides which have been evident from the reports of *Enterobacter cloacae*, a marine bacterium. This bacterium have been reported to chelate up to 65 % of cadmium, 20 % copper, and 8 % cobalt at 100 mg/L of metal concentration (Iyer et al. 2005). In line with that certain purple nonsulfur marine bacterial isolates, e.g., *Rhodobium marinum* and *Rhodobacter sphaeroides* have also been found to possess the potential of removing heavy metals like copper, zinc, cadmium, and lead from the contaminated environments either by biosorption or biotransformation (Panwichian et al. 2011). Thus, the marine bacteria have been designated for assessing marine pollution through tolerance (Das et al. 2007) and biosorption of heavy metals (Das et al. 2009).

Degradation of PAHs and other recalcitrants

Polyaromatic hydrocarbons (PAHs) are ubiquitous in nature and are of great environmental concern due to their persistence, toxicity, mutagenicity, and carcinogenicity in nature

(Cerniglia 1992). However, many marine bacteria have been reported to have the potential for bioremediation of the same in the process of metabolism to produce CO_2 and metabolic intermediates, thus gaining energy and carbon for cell growth. The bioremediation potential in these marine bacteria can be increased, which has been successfully experimented by Latha and Lalithakumari (2001) when they transferred a catabolic plasmid of *Pseudomonas putida* containing hydrocarbon degradation genotype in a marine bacterium which increases its efficiency. Some novel marine bacterial species like *Cycloclasticus spirillensus*, *Lutibacterium anuloederans*, and *Neptunomonas naphthovorans* have also been utilized in enhanced biodegradation of PAHs in marine environment (Hedlund et al. 1999; Chung and King 2001). Similarly, *Achromobacter denitrificans*, *Bacillus cereus*, *Corynebacterium renale*, *Cyclotrophicus* sp., *Moraxella* sp., *Mycobacterium* sp., *Burkholderia cepacia*, *Pseudomonas fluorescens*, *Pseudomonas paucimobilis*, *P. putida*, *Brevundimonas vesicularis*, *Comamonas testosteroni*, *Rhodococcus* sp., *Streptomyces* sp., and *Vibrio* sp. have been isolated from marine sources and were capable of degrading naphthalene, one of the greatest entity of PAHs by the process of mineralization (Samanta et al. 2002). However, bacteria belonging to genus *Cycloclasticus* play the major role in biodegradation of hydrocarbons (Teramoto et al. 2009). Bacterial isolates like *Sphingomonas paucimobilis* EPA505 have been found to utilize fluoranthene as their sole carbon source (Kanally and Harayama 2000).

Petroleum and diesel biodegradation

Crude oil is the most important organic pollutant in the marine environment as $1.7\text{--}8.8 \times 10^6$ tonnes of petroleum hydrocarbons has been estimated to be released to the marine and estuarine environments annually (McKew et al. 2007). These organic pollutants can be degraded by the oil-eating microbes present in the marine environment which are used for their carbon and energy source. Some of the important genera of marine bacteria that are capable of degrading oil include *Acinetobacter*, *Marinococcus*, *Methylobacterium*, *Micrococcus*, *Nocardia*, *Planococcus*, and *Rhodococcus* (Sakalle and Rajkumar 2009). In commercial basis, a consortium has been developed by Deppe et al. (2005) by using arctic bacteria like *Agreia*, *Marinobacter*, *Pseudoalteromonas*, *Pseudomonas*, *Psychrobacter*, and *Shewanella* for significant degradation of crude oil and its components. In addition to that, a more potent bacterium has been isolated from the Arabian Sea sediments capable of degrading oil by 39 % in 8 days in laboratory conditions (Mukherji et al. 2004). Recently, bioaugmented and biostimulated products of marine bacteria have been reported to be used for oil remediation in marine environments (Nwadinigwe and Onyeidu 2012).

Biofilm formation

Biofilms are matrix-enclosed community of microbes attached to surface and are predominate in diverse range of ecosystem as well as highly structured and dynamic in nature (Mangwani et al. 2012). These structures are very common in marine environments which are often formed by multiple bacterial species. In marine environment, biofilms cover many subtidal and intertidal unyielding surfaces such as rock, ships, loops, etc. These biofilm structures develop in nature as a protective microenvironment for bacteria which is resistant to a variety of environmental stresses of marine environments like UV radiation, pH shifts, osmotic shock, and desiccation (Mayer et al. 1999). Hence, marine bacteria capable of forming biofilms

become a potential candidate to be utilized in the process of bioremediation. Marine bacterial biofilms have been proved to be an efficient technology for remediation of a variety of organic and inorganic pollutants which can also help to eliminate petroleum oil from contaminated oceans or marine systems (Vu et al. 2009). However, advanced research and development of more advanced technology is required at genetic level of marine bacteria for better understanding of the biofilm-forming processes and their better utilization in the field of bioremediation.

Degradation of plastic

Several broad classes of plastic used in marine environments for fishing, packing, etc. which ultimately pollutes the environment include polyethylene, polypropylene, polystyrene, polyethylene terephthalate, and polyvinyl chloride. However, microorganisms can develop the mechanism to degrade the plastic to nontoxic forms. Recent finding showed that *Rhodococcus ruber* degrades 8 % of dry weight of plastic in 30 days in concentrated liquid culture in vitro (Andrady 2011). Similarly, bacterial isolates belonging to genera *Shewanella*, *Moritella*, *Psychrobacter*, and *Pseudomonas* isolated from deep seas of Japan possess the potential of degrading ϵ -caprolactone in an efficient manner (Sekiguchi et al. 2010). Some mangrove-associated bacterial species like *Micrococcus*, *Moraxella*, *Pseudomonas*, *Streptococcus*, and *Staphylococcus* were also found to degrade 20 % of plastic in 1 month (Kathiresan 2003).

Besides bioremediation function, marine bacteria have also been reported for biosurfactant production from *Acinetobacter anitratus*, *Bacillus pumilus*, *Bacillus subtilis*, *Myroides* sp, *Micrococcus luteus*, and *V. parahaemolyticus* which may be utilized in the process of enhanced bioremediation (Maneerat and Phetrong 2007). However, the genetic mechanisms of bioremediation towards toxic metals have been reduced for a fewer number of marine bacteria (Table 1).

Table 1 Catabolic genes reported in marine bacteria involved in bioremediation

Potential marine bacteria	Target substance	Catabolic genes	References
<i>Pseudomonas aeruginosa</i>	Inorganic mercury	<i>merA</i> , <i>merB</i>	De et al. (2008); Dash and Das (2012)
<i>Cycloclasticus</i> sp.	PAH	<i>phnA1</i> , <i>phnA2</i> , <i>phnA3</i> , and <i>phnA4</i>	Kasai et al. (2002)
<i>Pseudomonas</i> sp.	Phenol	<i>dmpN</i>	Selvaratnam et al. (1997)
<i>Staphylococcus aureus</i>	Chromate	<i>chrB</i>	Aguilar-Barajas et al. (2008)
<i>Bacillus subtilis</i> , <i>Bacillus cereus</i>	Cobalt–Zinc–Cadmium	<i>czcD</i>	Abdelatey et al. (2011)
<i>Pseudomonas</i> sp., <i>Bordetella</i> sp.	Nickel–Cobalt–Cadmium	<i>nccA</i>	Abou-Shanab et al. (2003)

Genetic manipulation in marine bacteria to enhance bioremediation efficiency

Microbial metabolic potential provides an effective mechanism for eliminating environmental pollutants. Anthropogenic pollution introduces some xenobiotic substances to which bacteria are not exposed before. Upon exposure, resistant bacteria slowly change their metabolic pathway to survive with the stress. However, in order to increase the bioremediation potential and/or metabolic activity of any bacteria, insertion of certain functional genes is necessary into their genome. This phenomenon can be achieved by insertion of new genes into the genomic complexion, insertion of new plasmid, alteration of metabolic pathways like transport and chemotaxis, and most importantly, adaption of features towards the environmental conditions (Pieper and Reineke 2000). Due to the significant development in the field of molecular microbiology and genetics, there is a success story for the development of genetically engineered microbes for bioremediation of toxic substances. However, limited reports are available to date for the genetic manipulation of marine bacteria to achieve a goal of enhanced bioremediation. Insertion of *bmtA* gene coding for metallothionein into suitable vector and its transformation into marine bacteria has been conducted and successfully employed in highly metal-contaminated environments (Chen et al. 1999). Similarly, *Pseudoalteromonas haloplanktis*, possessing a shuttle plasmid-encoding suppressor for amber mutation has been used for genetic manipulation for bioremediation (Kivela et al. 2008). Bacteria possessing plasmid with *merA* gene responsible for converting toxic form of mercury to nontoxic form may be transformed into marine bacteria for better application in field conditions of bioremediation of mercury (De Rore et al. 1994). *Deinococcus radiodurans*, the most radio-resistant organism, has been modified genetically to consume and digest toluene and ionic form of mercury from nuclear wastes (Brim et al. 2000). A list of bacteria possessing

genetic alteration in their genome to increase their bioremediation potential has been listed in Table 2.

Pros and cons of using marine bacteria in bioremediation

Marine bacteria are found in a wide range of environmental conditions from sea floor to fish stomachs and develop unique mechanism of resistance in adverse and diverse conditions. Thus, it gives ample opportunity to employ as potential bioremediating agents. When a bacterium utilizes the contaminant as its food source, its number increases rapidly in the contaminated environments and on subsequent decontamination, the number decreases to produce harmless biomass. The process is cost-effective in comparison to the chemical processes, and they can be carried out onsite. Utilization of marine bacteria in bioremediation is highly specific; hence, the chance of forming harmful by-products is less, which is the major advantage of utilizing these isolates.

However, there are some disadvantages in the process of using marine bacteria. In case of mixed contaminants, finding a suitable consortium becomes difficult. In the same case, the process is time-consuming, which may take years to finish. Though there are less chances of forming by-products, in some cases, lethal by products may form (Bamforth and Singleton 2005). After the process is over, the bacterial biomass is degraded, and the serious problem of biofouling may occur. Another problem associated with the use of recombinant strains is the instability of the cloned genes in the contaminated environment due to change of habitat (from saltwater to freshwater conditions) (Sanchez-Romero et al. 1998). These problems persist not only with the marine microorganisms but also with bacterial entity isolated from any environments. However, when the potential of the microorganisms is concerned in bioremediation, marine bacteria have been proved to be the valuable and efficient candidates.

Table 2 List of some engineered bacteria developed for enhanced bioremediation

Marine microorganisms	Modification	Application	References
<i>Vibrio harveyi</i>	Conjugation with <i>E. coli</i>	Detection of mutagens	Czyz et al. (2000)
<i>Staphylococcus aureus</i>	Fusion of <i>arsB</i> gene with <i>lux</i> genes	Antimonite and arsenite sensing	Ramanathan et al. (1997)
<i>Synechococcus</i> sp.	Insertion of <i>smtA</i> gene	Heavy metal tolerance	Sode et al. (1998)
SRB	Consortium with other SRB	Chromate reduction	Cheung and Gu (2003)
<i>Thalassospira lucentensis</i>	Change in culture medium	Hydrocarbon degradation	Sutiknowati (2007)
<i>Nocardia</i> sp.	NA	Remediation of oil contaminated soil	Balba et al. (1998)
<i>E. coli</i>	Change in Substrate specificity	PCB, benzene, toluene	Kumamaru et al. (1998)
<i>E. coli</i> FM5/pKY287	Regulation	TCE, toluene	Winter et al. (1989)

SRB sulfate-reducing bacteria

Conclusion and future prospects

The major problems that the twenty-first century is facing include the environmental pollution. This has gained a major attention to research communities. The global requirement for the solution to this problem includes various remediation aspects, but bioremediation is one step ahead of all these due to its many advantages over other modes of remediation protocols. Marine bacteria can adapt quickly to the rapidly changing, noxious environments which may be potentially utilized to solve the problem by remediating the toxic materials. Though many studies have been conducted and a large number of marine microbial entities have been discovered so far, still the microbial diversity from different marine habitats is yet to be explored. Who knows where some better potent strains are hiding inside? Hence, by combining the molecular aspects with the metabolic approaches, the microbial diversity of the oceanic environment should be explored. The treatment of environmental pollution by employing microorganisms is a promising technology; however, various genetic approaches to optimize enzyme production, metabolic pathways, and the growth conditions will be highly useful to meet the purpose. Though marine microorganisms are better adapted to rapidly changing environmental conditions, little has been known regarding the mechanism of resistance to the noxious environment. Hence, the research in this aspect will be helpful in understanding the genetic mechanism of the nature's wonder. Some modifications in their genetic system may provide useful, high-potential, and more efficient bacterial entity for enhanced bioremediation.

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