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REVIEW

A review on anaerobic microorganisms isolated from oil reservoirs

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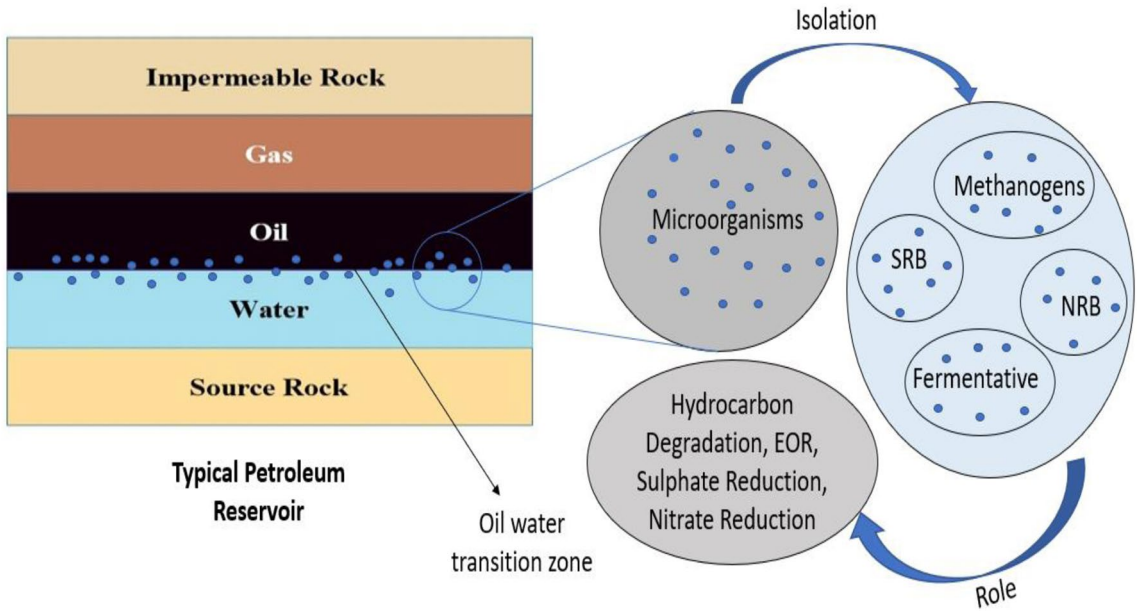
Abstract

The Role of microorganisms in the petroleum industry is wide-ranging. To understand the role of microorganisms in hydrocarbon transformation, identification of such microorganisms is vital, especially the ones capable of in situ degradation. Microorganisms play a pivotal role in the degradation of hydrocarbons and remediation of heavy metals. Anaerobic microorganisms such as Sulphate Reducing Bacteria (SRB), responsible for the production of hydrogen sulphide (H_2S) within the reservoir, reduces the oil quality by causing reservoir souring and reduction in oil viscosity. This paper reviews the diversity of SRB, methanogens, Nitrogen Reducing Bacteria (NRB), and fermentative bacteria present in oil reservoirs. It also reviews the extensive diversity of these microorganisms, their applications in petroleum industries, characteristics and adaptability to survive in different conditions, the potential to alter the petroleum hydrocarbons properties, the propensity to petroleum hydrocarbon degradation, and remediation of metals.

Graphic abstract



Keywords Anaerobic · Sulphate-reducing bacteria · Enhanced oil recovery · Hydrocarbon degradation

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Introduction

An oil reservoir contains thousands of complex mixtures of petroleum hydrocarbons and other organic compounds (Cooney et al. 1985). Petroleum is a heterogeneous mixture

of hydrocarbons, including aliphatic (n-alkanes), alicyclic and complex hydrocarbons which vary in compositional and physical properties according to the reservoir depth and geological locations (Peixoto et al. 2011; Li et al. 2020). Complex hydrocarbon such as monocyclic aromatic compounds like Benzene, Toluene, Ethylbenzene and Xylene (BTEX), and Polycyclic Aromatic Hydrocarbons (PAHs) are the most often encountered surface and subsurface contaminants (Holliger et al. 1997). PAHs are predominantly mutagenic, cytotoxic, teratogenic, and carcinogenic hydrocarbons (Peixoto et al. 2011; Qian et al. 2021). Degradation of petroleum hydrocarbon and change in crude oil quality is mostly caused by anaerobic microorganisms which are present in oil reservoirs. Oil reservoirs contain rich species of indigenous microbes and species of active surfactants production, methanogenesis, and hydrocarbon degradation functions (Lin et al. 2014). Ecologically, hydrocarbon-metabolizing microorganisms are widely distributed in an oil reservoir (Van Hamme et al. 2003). The anaerobic microorganisms can either degrade or produce hydrocarbons depending on the presence of certain metabolic pathways and environmental conditions (Peixoto et al. 2011). Numerous anaerobic microorganisms such as SRB, methanogens, NRB, and fermentative bacteria can exist in an oil reservoir (Youssef et al. 2009). Few microorganisms found are *Archaeoglobus fulgidus*, *Desulfacinum infernum*, *Desulfovibrio longus*, *Desulfovibrio gobonensis*, *Methanobacterium bryantii*, *Methanobacterium ivanovii*, *Methanobacterium thermoaggregans*, *Methanobacterium thermoautrophicum*, *Thauera phenylacetica*, *Pseudomonas stutzeri*, *Geobacillus subterraneus, Geobacillus uzenensis*, *Geotoga petraea*, *Anaerobaculum thermoterranum*, *Acetoanaerobium romashkovii*, *Geotoga subterranean* (Magot et al. 2000; Sierra-Garcia and de Oliveira 2013). These microorganisms have several roles in petroleum exploration and production activities. Bass (1999), studied the importance of microorganism in the petroleum industry and stated that petroleum microbiology can be divided into six categories, starting with the diagenesis of organic component in sediments and subsequent oleogenesis, degradation of hydrocarbons, and remediation of metals, Enhanced Oil Recovery (EOR) from oil reservoir, modification of hydrocarbon products either in the formation or past production, mitigation of its effect of organisms during production and bioremediation of escaped products either crude or processed (Bass 1999). Anaerobic microorganisms are injected into depleted oil reservoirs for EOR, removal of sulphur by bio desulphurization methods without degradation of associated carbon moieties. Microorganisms are also used for the removal of nitrogen (N) from crude oil leading to a reduction of emissions of nitric oxide (NO). Recently bacterial biosensors have also been used to analyze petroleum-contaminated environments (Van Hamme et al. 2003). Several microbial products, hydrocarbon metabolism, biosurfactants, biopolymers, solvents, acids, gases and emulsifiers are used for various applications in petroleum industries. A few such applications are removal of paraffin deposits, oil degradation, oil emulsification, Interfacial Tension (IFT) reduction, viscosity reduction and wettability alteration.

Anaerobic microorganisms can be isolated from both non-water flooded and water flooded oil reservoirs. Microorganisms species such as *Desulfotomaculum halophilim*, *Desulfotomaculum thermocisternum* and *Desulfovibrio longus* have been isolated from non-water flooded oil reservoirs (Magot et al. 2000; Sierra-Garcia and de Oliveira 2013). These microorganisms can belong to the indigenous microbial communities. Many novel species of microorganisms such as *Desulfacinum subterraneum*, *Desulfobacter vibrioformis*, *Desulfobacterium cetonicum*, *Desulfobulbus rhabdoformis*, *Desulfovibrio gabonensis*, *Desulfovibrio vietnamensis*, and *Thermodesulfobacterium norvegicus* were isolated from the water flooded oil reservoirs like (Lien et al. 1998; Magot et al. 2000; Rozanova et al. 2001; Sierra-Garcia and de Oliveira 2013). Hence, it cannot be concluded that these species are indigenous microbial communities to the oil reservoir. Rather these microorganisms are considered to be growing in the upper parts of the well or originating from injection waters. A sketch of a typical petroleum reservoir with various microbial inhabitants is shown in Fig. 1. Most of the microorganisms are found in the oil-water transition zone and microbial degradation in oil reservoirs is believed to be taken place in this zone (Pannekens et al. 2020).

The survival and activities of anaerobic microorganisms depend on several environmental factors. The existence and survival of various microorganisms in oil reservoirs were studied by Pannekens et al. (2019), which was performed in the different environmental conditions of high toxicity, temperature, pressure, salinity, hydrophobicity, and low water activity (Pannekens et al. 2019). This study revealed that the survival conditions of various microorganisms differ from each other. Temperature is considered the most influential factor for the growth of microorganisms. The microorganisms can survive up to 80–90°C inside an oil reservoir. The other influenced factors are pH, the activity of water, salinity, oxygen availability, nutrient availability, permeability (Al-Hawash et al. 2018; Rajbongshi and Gogoi 2020).

Significance of the study

Anaerobic microorganisms have become prominent in the petroleum exploration and production industry because of their diversity and their wide applications in the petroleum industry. Many anaerobic microorganisms have been isolated from different kinds of petroleum reservoirs of varying depths and geographic locations of varying temperatures

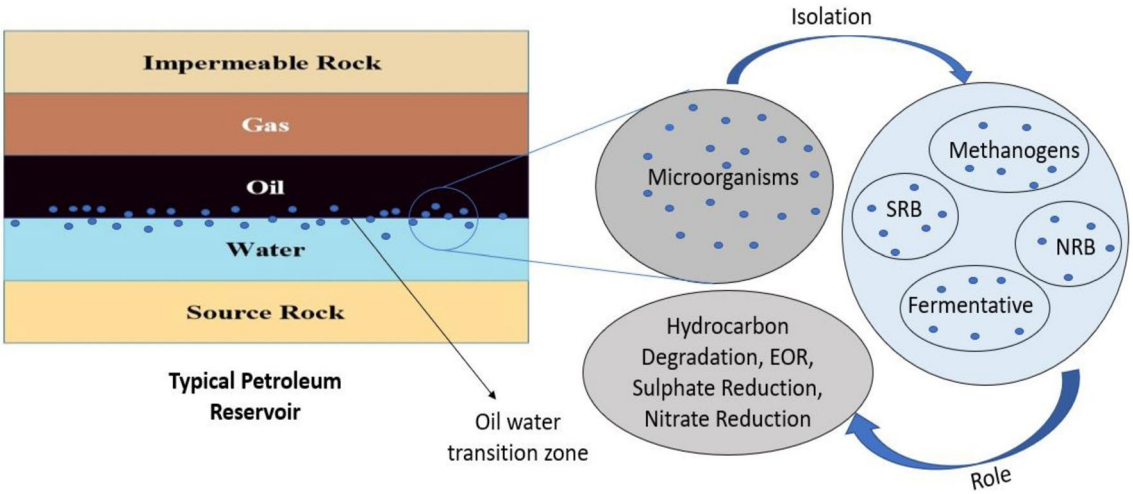

Fig. 1 A sketch of a typical petroleum reservoir showing various microorganisms inhabitant

and pressures. Several studies have been performed on these microorganisms, but still knowledge on these microorganisms is limited. Therefore, extensive and collective reviews are required to understand the diversity of these microorganisms, their applications in the petroleum industry, their characteristics and adaptability to survive in different conditions, their potential to alter the petroleum hydrocarbons properties, the propensity to petroleum hydrocarbon degradation as well as remediation of metals. This review intends to compile information on the diversity of various anaerobic microorganisms and their applications in the petroleum industry.

Anaerobic microorganisms in oil reservoirs

Sulphate reducing bacteria

SRB grow on environmental contaminants of petroleum hydrocarbon constituents such as BTEX, PAHs, and alkanes (Novelli 1944; Ensley and Suflita 1995). SRB are responsible for the production of H_2S within the reservoir as shown in reaction no (1), which can reduce the oil quality by causing reservoir souring, reduction of oil viscosity, degradation of hydrocarbons (both aliphatic and aromatic), corrosion of steel, reduction of the injectivity of water injection wells by precipitation of amorphous iron sulphide (FeS), reduction of permeability of oil-bearing rock pore spaces (plugging). SRB can lead to inefficient secondary oil recovery and can affect workers' health due to its high toxicity (Castro et al. 1997; Bass et al. 1998; Magot et al. 2000; Barton and Fauque 2009; Al-Sulaimani et al. 2011; Song et al. 2014). SRB are extensively studied microorganisms in oilfields because of their reservoir souring problems. It uses sulphate (SO_4^{2-}) as a final electron acceptor instead of oxygen (O_2) for respiration (Al Zuhair et al. 2008). The troublesome and most common SRB belong to the genus *Desulfovibrio* and these species have been isolated from the deep subsurface Formation Water (FW) of oil reservoirs (Basso et al. 2005). They get energy from the organic compounds available in the well as in reaction (1).

$$4H_2 + SO_4^{2-} + 2H^+ \rightarrow 4H_2O + H_2S + \text{Energy} \quad (1)$$

Bastin et al. (1926), has reported the presence of SRB in oil reservoirs and stated that these microorganisms can belong to the indigenous microbial communities to the subsurface oil reservoirs (Bastin et al. 1926). SRB have been isolated from a variety of environments such as fresh to saline and hyper saline waters or FW (Risatti et al. 1994; Nilsen et al. 1996a; Nilsen et al. 1996b; Bahr et al. 2005), either from surface or subsurface habitats (Kovacik Jr et al. 2006), marine or lake sediments (Sass et al. 1998; Ravenschlag et al. 2000; Mußmann et al. 2005; Webster et al. 2006), hydrothermal vents (Jeanthon et al. 2002), hydrocarbon seeps and mud volcanoes (Knittel et al. 2003; Stadnitskaia et al. 2005; Kniemeyer et al. 2007), rhizosphere of plants (Hines et al. 1999).

Diversity of sulphate reducing bacteria

SRB have been determined by the use of 16 S rRNA or dsrAB (dissimilatory sulfite reductase) gene molecular techniques (Dar et al. 2007). For the rapid determination of SRB diversity in different environments, the dsrAB gene fingerprinting methods t-RFLP, DGGE, and gel-retardation analyses have been widely used in the last few decades. Microbial communities can also be characterized by SEM-EDS (Daghio et al. 2018). The 16 S rRNA gene sequence

can be aligned with the related sequences from GenBank and EzBioCloud databases and the phylogenetic tree can be constructed using MEGA software (Wang et al. 2020). More than 220 SRB species of 60 genera have been described till now (Barton and Fauque 2009). Varieties of SRB have been isolated from oilfields around the world like Canada, France, USA, North Sea, Vietnam, Congo, Paris, California. Many researchers isolated SRB from FW of different oilfields such as *Desulfotomaculum nigrificans* (Nazina and Rozanova 1978), *Desulfotomaculum kuznetsovii* (Nazina et al. 1988), *Desulfacinum subterraneum* (Rozanova et al. 2001), *Desulfobacter cetonicum* (Galushko and Rozanova 1991), *Desulfovibrio gracillis* and *Desulfovibrio longus* (Magot et al. 1992, 2004), *Thermodesulforhabdus norvegicus* and *Archaeoglobus fulgidus* (Beeder et al. 1994, 1995), *Thermodesulfobacterium commune* (l'Haridon et al. 1995), *Desulfacinum infernum* (Rees et al. 1995), *Desulfovibrio vietnamensis* (Dang et al. 1996), *Desulfotomaculum thermocisternum* (Nilsen et al. 1996b), *Desulfovibrio gobonensis* and *Desulfotomaculum halophilum* (Tardy-Jacquenod et al. 1996b, 1998), *Desulfobacter vibrioformis* (Lien and Beeder 1997), *Desulfobulbus rhabdoformis* (Lien et al. 1998), *Desulfovibrio alaskensis* (Feio et al. 2004), *Desulfovermiculus halophilus* (Belyakova et al. 2006), *Desulfotignum toluenicum* (Ommedal and Torsvik 2007), *Desulfonauticus autotrophicus* (Mayilraj et al. 2009). The most frequently isolated SRB from FW belong to deltaproteobacteria. They comprise of mesophilic members of the genera *Desulfovibrio*, *Desulfobulbus*, *Desulfobacterium*, *Desulfobacter* and thermophilic members of the genera *Thermodesulforhabdus* and *Desulfacinum*. *Desulfovibrio* sp. are the most frequently isolated microorganisms (Tardy-Jacquenod et al. 1996a). *Desulfomicrobium* and *Desulfovibrio* species have been found in high-temperature oil-bearing formations (Orphan et al. 2000; Watanabe et al. 2002). Many microbiological and molecular studies revealed the presence of *Desulfotomaculum* species of Gram-positive group in oil reservoir (Rozanova and Nazina 1979; Rosnes et al. 1991; Christensen et al. 1992; Nilsen et al. 1996b; Watanabe et al. 2002). The *Desulfotomaculum* species were also isolated from a high-temperature North Sea oil well and a continental high-temperature oil reservoir in Western Siberia, Russia (Nilsen et al. 1996a; Bonch-Osmolovskaya et al. 2003). *Thermodesulfobacterium* species are generally considered as the most thermophilic sulphate-reducing microorganisms of the domain bacteria, with an upper limit temperature around 80 °C for growth (Christensen et al. 1992; l'Haridon et al. 1995). These species are considered as indigenous community of deep subsurface ecosystem of an oil reservoir (Bonch-Osmolovskaya et al. 2003). Thermophilic and mesophilic species like *Thermodesulfobacterium thermophilum*, *Thermodesulforhabdus norvegicus*, *Archaeoglobus fulgidus*, *Desulfacinum infernum*, *Desulfotomaculum*, *Desulfobulbus rhabdoformis* and *Desulfomicrobium* from North Sea reservoir were isolated by many researchers (Rosnes et al. 1991; Christensen et al. 1992; Beeder et al. 1995; Rees et al. 1995; Lien et al. 1998; Leu et al. 1999). *Desulfotomaculum halophilum*, *Desulfovibrio longus*, *Desulfovibrio putealis*, *Archaeoglobus fulgidus* and *Thermotoga elfii* were isolated from oilfields of Paris basin while, *Desulfovibrio vietnamensis*, *Desulfacinum subterraneum* were isolated from Vietnam oilfields (Magot et al. 1992; Dang et al. 1996; Tardy-Jacquenod et al. 1998; Rozanova et al. 2001; Basso et al. 2005; Fardeau et al. 2009). Some SRB that were isolated from various oil reservoirs are given in Table 1.

Role of sulphate-reducing bacteria in the enhanced oil recovery process

Microbial Enhanced Oil Recovery (MEOR) processes use microbial technology to improve the recovery of crude oil from oil reservoirs (Sen 2008). MEOR technology is used to harness the indigenous microorganism resources present in the reservoirs. MEOR is considered to be a cost-effective and environment-friendly EOR process (Lin et al. 2014). MEOR technologies have been approved universally as cost-effective and eco-friendly to improve oil production because their products are biodegradable and have low toxicity (Sarkar et al. 1989; Lazar et al. 2007; Suthar et al. 2008; Banat et al. 2010; Al-Bahry et al. 2013). MEOR depends on an adequate understanding of the relationship between the microbial community structure and oil reservoir conditions (Lin et al. 2014). Therefore, several studies on the microorganisms in oil reservoirs have been performed (Basso et al. 2005; Grabowski et al. 2005; Nazina et al. 2005; Li et al. 2007; Song et al. 2010; Xiu et al. 2010). Several books on MEOR have been published (Zajic et al. 1983; Yen 1986; Donaldson et al. 1989). The diversity of SRB is widely distributed in global oil reservoirs. Therefore, special emphasis has been given on SRB for EOR by researchers and reviewers (Champagne et al. 1996; Callbeck et al. 2013; Song et al. 2014). Metabolites of SRB can reduce both Surface Tension (ST) and IFT between gas/liquid and oil/liquid respectively and form a stable emulsion system with crude oil in an oil reservoir (Song et al. 2014). Many studies reported that metabolites produced by a variety of microbes can act as biosurfactants to reduce IFT between oil and water (Singer and Finnerty 1988; Banat 1993; Singh et al. 2007). Oil viscosity plays an important role in EOR and SRB metabolite/oil emulsion and biodegradation has contributed partially to the reduction of oil viscosity (Al-Sulaimani et al. 2011; Ghosh and Al Shalabi 2011; Homayuni et al. 2011; Song et al. 2014). The degradation of hydrocarbons by microorganisms is important for MEOR because of its role in increasing the mobility of crude oil (Li et al. 2020). Zobell (1946), has used the method of injection of microorganisms

Table 1 Some SRBs with their taxonomical group isolated from various oil reservoirs

Organism	Taxonomical group	Metabolism	Origin	References
Thermodesulforhabdus norvegicus	Deltaproteobacteria	Sulphate-reducer	Oil reservoir, Norway	(Sierra-Garcia and de Oliveira 2013)
Desulfacinum infernum			Oil reservoir, North Sea, Scotland	
Desulfomicrobium norvegicum			Oil reservoir, Canada	
Desulfovibrio sp.				
Dethiosulfovibrio peptidovorans	Bacteria, Synergistetes		Emeraude oilfield, Congo, Central Africa	
Deferribacter sp.	Bacteria, Deferribacteres		Oil reservoir, California	
Archaeoglobus fulgidus	Archaea, Euryarchaeota		Oil reservoir, North Sea	(Magot et al. 2000)
Desulfacinum infernum	Deltaproteobacteria			
Desulfobacter vibrioformis				
Desulfobacterium cetonicum			–	
Desulfomicrobium apsheronum			Oil reservoir, Apsheron Peninsula	
Desulfotomaculum kuznetsovii	Bacteria, Firmicutes		Oil reservoir, Paris Basin	
Desulfotomaculum nigrificans			Oil reservoir, Western Siberia	
Desulfotomaculum thermocisternum			Oil reservoir, North Sea	
Desulfovibrio gabonensis	Deltaproteobacteria		–	
Desulfovibrio longus			Oil reservoir, Paris Basin, France	
Desulfovibrio vietnamensis			Vietnamese oilfields	
Thermodesulforhabdus norvegicus			Oil reservoir, North Sea	
Thermodesulfobacterium mobile	–			
Desulfacinum subterraneum	Deltaproteobacteria		White Tiger oilfield	(Rozanova et al. 2001)
Desulfovibrio gracillis			Emeraude Oilfield, Congo	(Magot et al. 2004)
Desulfovibrio bastinii				
Desulfovibrio alaskensis			Oil reservoir, Purdu Bay, Alaska	(Feio et al. 2004)
Desulfobulbus rhabdoformis			North Sea oil reservoirs	(Lien et al. 1998)
Desulfotignum toluenicum			–	(Ommedal and Torsvik 2007)
Desulfonauticus autotrophicus			Oil reservoir, Northern Germany, Hamburg	(Mayilraj et al. 2009)
Desulfovibrio gracilis			Emeraude Oilfield, Congo	(Magot et al. 2004)
Desulfovermiculus halophilus			–	(Belyakova et al. 2006)
Archaeoglobus fulgidus	Archaea, Euryarchaeota		Oil reservoir, North Sea	(Beeder et al. 1994)

into the depleted oil reservoir to enhance the oil recovery rate (Zobell 1946). Bass (1999), mentioned that Zobell in 1970, isolated a strain of *Desulfovibrio* that can grow on salt solution which tolerated relatively high temperature. These microorganisms can enhance the oil production from a depleted oil reservoir by producing biosurfactants. The direct action of biosurfactant on petroleum hydrocarbon may increase hydrocarbon production by reducing the IFT of unsaturated hydrocarbons such as long-chain hydrocarbon and shorter chain hydrocarbon which strongly hold on rock surface (Bass 1999). Song et al. (2014), reported that the oil recovery rate of SRB from a saturated oil reservoir was 39.2 % (Song et al. 2014). A field-wide test was done in the Mink Unit of Delaware-Childers field in Nowata County, Oklahoma to measure the production rate in a mature waterflood field by MEOR process and it was found that the production was increased by 13 % in that year while water/oil ratios at the producing wells dropped to nearly 35 % (Bryant et al. 1990). The efficacy of some biosurfactants used in the MEOR process is given in Table 2.

Table 2 Efficacy of biosurfactants used in MEOR (Li and McInerney 2017; Arora et al. 2019)

Biosurfactant	Microorganism	Lowest ST (mN/m)	Lowest IFT (mN/m)	Critical micelle concentration (mg/L)	Additional oil recovery (%)	Yield (gm/L)
Surfactin	*Bacillus subtilis, B. mojavensis*	28–30	0.006-0.3	10–35	40–80	0.5-1
Lichenysins	*Bacillus licheniformis*	28	0.3–0.5	10–19	37	1.1
Lipopeptide	*Acinetobacter baylyi*	35	15	90	28	–
Rhamnolipid	*Pseudomonas aeruginosa*	25–27	0.2-2	11–120	10–27	0.7–50
Glycolipids	*Rhodococcus sp.*	27–30	1	57	65–86	0.5–12.9
Glycolipids	*Enterobacter cloacae and E. hormaechei*	31	0.6–3.2	–	27–48	1.5–1.7
Lipopolysacharide	*Alcaligenes faecalis*	20	< 1	–	9	1.2 ± 0.05
Sucrose lipid	*Serratia marcescens*	–	–	–	90	–
Sophorolipid	*Candida bombicola*	33 ± 0.05	1.6 ± 0.3	–	27	–
Glycoprotein	*Clostridium sp.* N-4	32 ± 0.04	–	100	36.92	1.0

The action of indigenous microorganisms during the MEOR process in an oil reservoir is shown in Fig. 2. In the first phase, the microorganisms utilize oil as a nutrient (carbon source) and produce natural surfactant (biosurfactant), and oil is released from the trapped rock pores. In the second phase, the microorganisms multiply and after some time, blocks the usual water flow paths. This opens a new path for water that pushes the oil out and allows the microorganisms to reach the trapped oil. In the third phase, once the trapped oil is released, the microbes disperse because there is no carbon source (nutrient) for the microbes. For this reason, the blocked water pathways reopen. Bryant reviewed the MEOR field tests in the US and reported that the oil production increased by 20 to 200 %, depending on a variety of factors including initial oil saturation, temperature, salinity, permeability, microorganism, nutrients employed, and injection procedures (Bryant 1987; Bryant and Douglas 1987). Some applications of microbial products in petroleum exploration and production industries are given in Table 3.

Role of sulphate-reducing bacteria in biodegradation of petroleum hydrocarbon

Biodegradation of crude oil in subsurface oil reservoirs is an important alteration process with major economic consequences. Biodegradation of crude oil in subsurface oil reservoirs has adversely affected the majority of the world's oil, making recovery and refining of the oil more costly (Meyer 1987). Anaerobic hydrocarbon degradation is a common process in biodegraded subsurface oil reservoirs which dominate subsurface sedimentary environments (Head et al. 2003; Aitken et al. 2004). The hydrocarbon-degrading microorganisms produce biosurfactants of diverse chemical nature and molecular size. These surface-active materials increase the surface area of hydrophobic water-insoluble substrates and increase their bioavailability, thereby enhancing the growth of microorganisms and the rate of bioremediation (Ron and Rosenberg 2002). At water flooded oilfield, the most active microbial processes of oil degradation occur near the bottom zone of an injection well

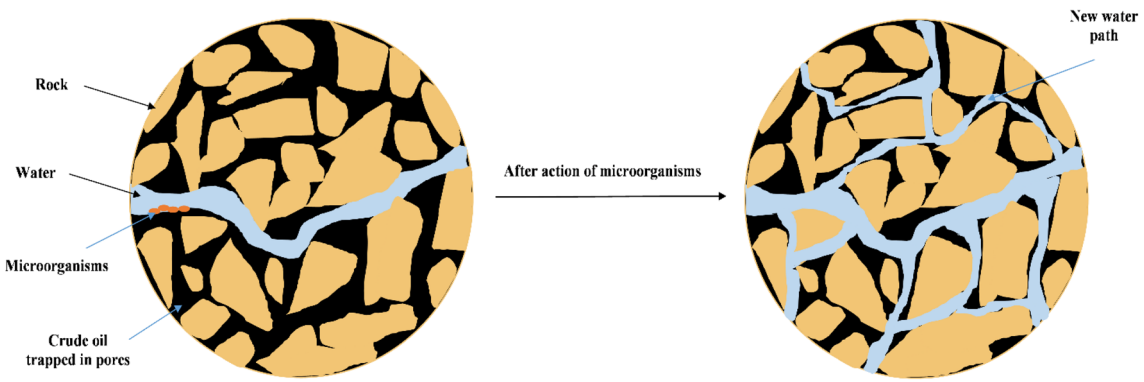

Fig. 2 Action of microorganisms during recovering of trapped crude oil

Table 3 Application of microbial products in petroleum exploration and production industry (Youssef et al. 2009; Putra and Hakiki 2019; Nikolova and Gutierrez 2020)

Products	Application
Hydrocarbon metabolism	Removal of paraffin deposits, oil mobilization
Biomass/polymer production	Selective biomass plugging, viscosity reduction, oil degradation, rock wettability alteration, pour point alteration, oil emulsification, and de-emulsification, oil desulphurization
Biosurfactants	Oil emulsification, interfacial tension reduction, viscosity reduction, wettability alteration
Biopolymers	Injectivity profile modification, mobility control, selective plugging
Solvents	Oil dissolution, viscosity reduction, wettability alteration, interfacial tension reduction, promotes emulsification
Acids	Permeability and porosity improvement, emulsification, dissolve carbonaceous minerals or deposits, CO_2 production
Gases (H_2, N_2, CH_4, CO_2)	Reservoir re-pressurization, oil swelling, interfacial tension reduction, viscosity reduction, permeability improvement, carbonate rocks solubilization by CO_2
Emulsifiers	Emulsify oil to form o/w emulsions or less commonly w/o emulsions

and in deep subsurface oil (Nazina et al. 2017). Oil degradation probably occurs via methanogenesis in the biodegraded reservoir and it is the dominant terminal process for hydrocarbon degradation driven by anaerobic biodegradation (Silva et al. 2013). The anaerobic microorganisms belonging to the microbial diversity of bacteria have the potential to metabolize hydrocarbon and inorganic compounds (Silva et al. 2013). Hydrocarbons such as toluene (Edwards et al. 1992; Langenhoff et al. 1997; Elshahed and McInerney 2001), alkylbenzenes including m-, o- and p-xylene and trimethylbenzenes (Ball and Reinhard 1996; Chen and Taylor 1997; Haner et al. 1997; Phelps and Young 1999), benzene (Kazumi et al. 1997; Burland and Edwards 1999; Rooney-Varga et al. 1999), naphthalene and phenanthrene (Coates et al. 1996; Bedessem et al. 1997; Zhang and Young 1997; Meckenstock et al. 2000), methylnaphthalene and tetralin (Annweiler et al. 2000, 2002), n-alkanes (Caldwell et al. 1998; Anderson and Lovley 2000; Ehrenreich et al. 2000; So and Young 2001), branched alkanes (Bregnard et al. 1996, 1997), organic acids (Devereux et al. 1992; Ensley and Suflita 1995; Karr et al. 2005) and hydrocarbon mixtures (Grishchenkov et al. 2000) can be metabolized by bacteria under anaerobic conditions. All SRB genera preferentially degrade certain organic acids and cannot degrade others. Only a few SRB genera are known to readily degrade a wide range of organic acids. E.g., *Desulforhabdus amnigenus* can degrade lactate, acetate, butyrate, and propionate (Elferink et al. 1995). Recent research on SRB revealed that they can also degrade long-chain alkanes, alkenes, and short-chain alkanes (Davidova et al. 2006; Grossi et al. 2007; Kniemeyer et al. 2007; Fullerton et al. 2013; Kleindienst et al. 2014; Herath et al. 2016). Song et al. (2014), mentioned that SRB could be directly used for anaerobic biodegradation of oil components (C_{11}- C_{13} n-alkanes) (Song et al. 2014). Zhao et al. (2018), performed in situ bioremediation and reported more than 50 % of oil spilled pollutants n-alkanes (C_{12}-C_{27}) and PAHs were degraded within 70 days of bioremediation (Zhao et al. 2018). Ayangbenro et al. (2018), mentioned that complex organic compounds such as carboxylic acids (acetate, fumarate, butyrate, malate), amino acids (alanine, glycine, serine), alcohols, and aromatic compounds can be degraded by SRB in anaerobic condition (Ayangbenro et al. 2018). The biological technique of SRB generates H_2S under anaerobic conditions in a reaction between elemental sulphur (S) with an electron donor organic compound (acetic acid) as in reaction (2).

$$4S + CH_3COOH + 2H_2O \rightarrow 4H_2S + 2CO_2 \quad (2)$$

SRB are important regulators of various processes in wetland soils, including organic matter turnover, biodegradation of chlorinated aromatic pollutants in anaerobic soils, and sediment sand mercury methylation (Miller and Wakerley 1966; Plugge et al. 2011). SRB cannot degrade substrates like cellulose, fats, nucleic acids, proteins, starch, polymeric organic compounds directly but depends on other microorganisms to degrade these substrates (Muyzer and Stams 2008).

Role of sulphate-reducing bacteria in remediation of metals

Heavy metal pollution caused by exploration and production activities of the oil & gas industry and other mining industries has induced an adverse impact on the environment. Heavy metal causes pollution because of its high toxicity and non-biodegradability. This has threatened the health of human beings and the stability of the ecological system. The remediation and detoxification of active heavy metal ions in the natural environment can be achieved through microbial activities (Yin et al. 2019). SRB are good in the detoxification of active heavy metal ions which have been successfully applied on the industrial scale for the remediation of metals from various wastewater. SRB are the most studied

biosulfidogens which have immense potential of remediating metal-rich wastewater. They also can reduce SO_4^{2-}, thiosulphate ($S_2O_3^{2-}$), S and takes part in the breakdown process of sulphur-containing amino acids in proteins to produce sulphide (S^{2-}) (Hussain et al. 2016). The remediation of metals by SRB has proved to be effective in metal removal and also in controlling environmental pollution. This process is a very cost-effective technique in the elimination of heavy metals like arsenic (As), cadmium (Cd), cobalt (Co), chromium (Cr), copper (Cu), mercury (Hg), manganese (Mn), molybdenum (Mo), nickel (Ni), lead (Pb), selenium (Se) and zinc (Zn) (Ayangbenro et al. 2018; Yin et al. 2019). Many researchers have declared that chemical treatment methods are environmentally non-compatible, has low treatment efficiency, high operational cost, complicated in operation with a possible generation of secondary pollutant (Rocha et al. 2009; Abbas et al. 2016).

The most recent approach for remediation of metallic waste is the precipitation of metal ions in the form of their respective sulphides. A fruitful way to know the efficiency of a microorganism in the remediation of heavy metals is the study of the adsorption isotherm model. Mathematical isotherm models help to verify their suitability for describing biosorption of heavy metals by microorganisms as well as to understand the sorption isotherm phenomenon between the biomass surface and the metal molecules (Brouers and Al-Musawi 2015). Yin et al. (2019), reviewed the adsorption isotherm model for microorganisms like *Pesudomonas aeruginosa*, *Bacillus* sp., *Arthrobacter viscosus*, *Eichhornia* sp., *Brevibacterium* sp., *Rhodobacter capsulatus*, *Ochrobactrum* sp. during removal of heavy metal ions like Hg (II), Pb (II), Cr (VI), Cu (II), Zn (II), Cd (II) where the best-fitted isotherm model was Langmuir isotherm (Yin et al. 2019).

Methanogens

Methanogens are a unique group of anaerobic archaea that are more metabolically diverse. Methanogenic archaea are an important group of microorganisms present in oil reservoirs (Magot et al. 2000). Methanogens can generate only methane (CH_4) by coupling the oxidation of products formed by fermentative bacteria with the reduction of carbon dioxide (CO_2) (Holmes and Smith 2016). The activity of the methanogenic archaea is affected by physical and chemical factors such as temperature, salt content, and pH (Parthipan et al. 2017). Many methanogens thrive in neutral pH, low salinity, and temperate environments. Most methanogens are mesophilic, some are extremophiles e.g. *Methanopyrus kandleri* and *Methanococcus vulcanicus* which survive at temperatures of 110°C (Kurr et al. 1991). Several thermophilic species having the ability to oxidize hydrogen have been identified and reported from various onshore and offshore reservoirs. Examples of such species are *Methanothermococcus* and *Methanothermobacter*. Anaerobic methanogenic archaea can also be isolated from a saline environment (Elias et al. 1999). Methanogenic microorganisms isolated from oil reservoirs belong to species of *Methanosarcinales*, *Methanomicrobiales*, *Methanobacteriales*, and *Methanococcales* (Parthipan et al. 2017). An incumbent process occurring in oil reservoirs and also the contaminated aquifers is methanogenic biodegradation of crude. Biodegradation of fuel components by the anaerobic electron-accepting process has also been reported in various hydrocarbon-impacted subsurface environments (Widdel et al. 2010). However, when available electron acceptors are depleted in such environments, hydrocarbon biodegradation has to proceed via methanogenesis (Berdugo-Clavijo and Gieg 2014). The biodegradation of hydrocarbons under methanogenic conditions have been widely investigated for crude oil and its components such as *n*-alkanes, benzene, toluene and polycyclic aromatic hydrocarbons (Grbić-Galić and Vogel 1987; Godsy et al. 1992; Edwards and Grbić-Galić 1994; Zengler et al. 1999; Anderson and Lovley 2000; Townsend et al. 2003; Ulrich and Edwards 2003; Chang et al. 2006; Jones et al. 2008; Gieg et al. 2010; Berdugo-Clavijo et al. 2012; Zhang et al. 2012). An iron corroding methanogen, *Methanococcus maripaludis* strain KA1, isolated from a crude-oil storage tank produces CH_4. This strain can oxidize iron much faster than *Methanococcus maripaludis*, strain JJ^T (Uchiyama et al. 2010). Dinh et al. (2004), isolated a methanogen (strain IM1) that produces CH_4 more rapidly than *Methanococcus maripaludis* (Dinh et al. 2004). Methanogen can be used in biogas production. *Methanobacterium* which is found in anaerobic sludge can be used as an anaerobic bacteria feed on cellulose which generates large amounts of CH_4 along with CO_2 and H_2. Some anaerobic methanogens that were isolated from various oil reservoirs are given in Table 4.

Nitrate reducing bacteria

Nitrate reducing microorganisms isolated from oil reservoirs is currently the need of the hour due to in situ use of nitrate by oil companies to decrease S^{2-} concentration in oilfields (Davidova et al. 2001). In most surface or subsurface environments N and phosphorus (P) are often the main limiting nutrients. Nitrate is reduced to ammonium. Dissimilatory Nitrate Reduction to Ammonium (DNRA) can proceed through chemoautrophy or a fermentative pathway as in reaction (3) and (4) (Tobias and Neubauer 2019).

Table 4 Some methanogens with their taxonomical group isolated from various oil reservoirs

Organism	Taxonomical group	Metabolism	Origin	References
Methanococcus	Archaea, Euryarchaeota	Methanogen	California oilfields, North central Louisiana oilfield, USA	(Orphan et al. 2000; Shelton et al. 2016)
Methanococcus thermolithotrophicus			Oil reservoir, North Sea, Norway	(Nilsen and Torsvik 1996)
Methanoculleus			California oilfields	(Orphan et al. 2000)
Methanobacterium			California oilfields; Alsaka oil reservoir	(Orphan et al. 2000; Pham et al. 2009; Mayumi et al. 2011)
Methanolobulus			Alsaka oil reservoir; Bokor oilfield, Malaysia; North central Louisiana oilfield, USA	(Dinh et al. 2004; Pham et al. 2009; Li et al. 2012)
Methanosaeta			Enermark oilfield, Canada	(Kryachko et al. 2012)
Methanothermococcus			North central Louisiana oilfield, USA	(Li et al. 2012)
Methanohalophilus			North central Louisiana oilfield, USA	
Methanomethylovorans			Oilfields of China	(Wang et al. 2012)
Methanothermobacter				
Methanoculleus				
Methanobacteria				
Methanocalculus				
Methanolinea				
Methanobacterium bryantii			Mykhpai oilfield (Western Siberia)	(Magot et al. 2000)
Methanobacterium ivanovii			Bondyuzhskoe oilfield, Tatarstan	
Methanobacterium thermoaggregans			San Miguelito oilfield	
Methanobacterium thermoalcaliphilum			Mykhpai oilfield (Western Siberia)	
Methanococcus thermolithotrophicus			Oil reservoir, North Sea	
Methanohalophilus euhalobius			-	
Methanoplanus petrolearius			oilfield of the Gulf of Guinea, West Africa	
Methanosarcina mazei			Bondyuzhskoe oilfield, Tatarstan	
Methanosarcina siciliae			Gulf of Mexico	
Methanocalculus halotolerans			Alsacian oilfield (France)	

Autotropic DNRA

$$HS^- + NO_3^- + H^+ \rightarrow SO_4^{2-} + NH_4^+ \quad (3)$$

Fermentative DNRA

$$CH_2O + 0.5NO_3^- + 5H_2O \rightarrow NH_4^+ + HCO_3^- \quad (4)$$

However, if N is limited in the reservoirs, the abundant ammonium ions (NH_4^+) present there can be used as the primary N source for in situ bacterial activity (Head et al. 2003). In oilfields, N is also available as dinitrogen (N_2) gas or as heterocyclic aromatic nitrogen compounds in petroleum. Researchers have revealed that nitrate-reducing bacteria may inhabit oilfield reservoir ecosystems (Greene et al. 1997; Ollivier and Cayol 2005). A thermophilic heterotrophic bacterium, *Garciella nitratireducens* which reduces nitrate to ammonium was isolated from an oil well located in the Gulf of Mexico (Miranda-Tello et al. 2003). The activities of NRB can remove existing S^{2-} from oilfield FW and also inhibit the production of S^{2-} (Davidova et al. 2001). Nitrate serves as an electron acceptor for the reoxidation

of S^{2-} to SO_4^{2-} or S by sulfur-oxidizing chemolithotrophic bacteria as shown in reaction (5) (Sublette et al. 1994; Telang et al. 1999). Nitrite produced by NRB can react with dissolved sulphide to produce S as shown in reaction (6) (Jenneman et al. 1996).

$$5HS^- + 2NO_3^- + 7H^+ \rightarrow 5S + N_2 + 6H_2O \quad (5)$$

$$3HS^- + 2NO_2^- + 5H^+ \rightarrow 3S + N_2 + 3H_2O \quad (6)$$

A chemoautotroph, *Thiobacillus denitrificans* can convert S to SO_4^{2-} as in reaction (7) (Doelle 2014). The production of SO_4^{2-} from nitrite is shown in the reaction (8) (Zhang et al. 2019).

$$5S + 6NO_3^- + 2N_2O \rightarrow 5SO_4^{2-} + 3N_2 + 4H^+ \quad (7)$$

$$S + 2NO_2^- \rightarrow N_2 + SO_4^{2-} \quad (8)$$

Some anaerobic NRB that were isolated from various oil reservoirs are given in Table 5.

Fermentative bacteria

Besides SRB, methanogens, NRB, fermentative microorganisms have also been frequently isolated from the FW of the oilfields. Stetter et al. (1993), first provided evidence of the presence of *Thermotoga* strains in oilfields FW (Stetter et al. 1993). Fermentative microorganisms isolated from various oilfield environments have been reviewed by Ollivier and Cayol (2005), (Ollivier and Cayol 2005). A wide range of mesophilic and thermophilic fermentative bacteria have been identified from oil reservoirs. Most of them belong to the domain bacteria (*Halanaerobium* and *Thermotoga*), however, only a few hyperthermophiles belong to the domain Archaea (*Thermococcus* sp. and *Pyrococcus* sp.) (Ollivier and Cayol 2005). Researchers have also isolated fermentative microorganisms from oilfield environments like *Thermotoga elfii*, *Thermotoga subterranean*, *Thermotoga hypogeal*, *Thermotoga petrophila*, *Thermotoga naphthophila*, *Thermosipho geolei*, *Petrotoga sibiria, Petrotoga olearia*, *Geotoga petraea, Geotoga subterranean*, *Petrotoga miotherma*, *Petrotoga mexicana*, *Thermotoga brockii*, *Caldanaerobacter subterraneus*, *Anaerobaculum thermoterranum* at different temperature and salinity (Davey et al. 1993; Cayol et al. 1995; Jeanthon et al. 1995; Ravot et al. 1995; Fardeau et al. 1997, 2004; Rees et al. 1997; Haridon et al. 2001; Takahata et al. 2001; l'Haridon et al. 2002; Miranda-Tello et al. 2003). Some fermentative bacteria which were isolated from various oil reservoirs are given in Table 6.

Environmental impact on anaerobic bacteria

The activities of anaerobic microorganisms can be affected by several environmental factors such as temperature, pH, the activity of water, salinity, oxygen availability, nutrient availability, the permeability of the reservoir (Al-Hawash et al. 2018; Rajbongshi and Gogoi 2020). The optimal growth condition of temperature, pH, salinity, and nutrients for some anaerobic microorganisms are given in Table 7.

Temperature

The possibility of living organisms surviving in oilfield environments depends on the physical characteristics and chemical composition of the ecosystem. Temperature is the most influenced factor that affects the rate of degradation of crude oil in oil reservoirs and microbial community structures (Chen et al. 2010). The largest microbial diversity occurs at moderate temperatures up to 55 °C, where higher metabolic activity increases the abundance of genes involved in carbon cycling and the degradation of aromatic and other organic compounds. Approximately above 80 °C, oil reservoirs are considered to be sterile (Pannekens et al. 2019). In situ oil degradation was never observed in reservoirs where the temperature exceeded 82°C and maximum biodegradation occurred below 80 °C (Philippi 1977; Barth

Table 5 Some NRB with their taxonomical group isolated from various oil reservoirs

Organism	Taxonomical group	Metabolism	Origin	References
Thauera phenylacetica	Betaproteobacteria	Nitrate reducer	Oil reservoir, Canada	(Sierra-Garcia and de Oliveira 2013)
Pseudomonas stutzeri	Gammaproteobacteria			
Garciella nitratireducens	Bacteria, Firmicutes		Oilfield in Tabasco, Gulf of Mexico	
Geobacillus subterraneus, Geobacillus uzenensis	Bacteria, Firmicutes		Oil reservoir, China	
Denitrovibrio acetiphilus	Bacteria, Deferribacteres		Statfjord oilfield, North Sea	(Myhr and Torsvik 2000)

Table 6 Some fermentative bacteria with their taxonomical group isolated from various oil reservoirs

Organism	Taxonomical group	Metabolism	Origin	References
Lactosphaera pasteurii	Bacteria, Firmicutes	Fermentative	Oil reservoir, Canada	(Sierra-Garcia and de Oliveira 2013)
Propionicimonas paludicola				
Anaerobaculum	Bacteria, Synergistetes		California oilfields	
Thermococcus sp.	Archaea, Euryarchaeota			
Thermococcus sibericus	Archaea, Euryarchaeota		Oil reservoir, Western Siberia	
Petrotoga sp.	Bacteria, Thermotogae		California oil fields	
Thermotoga sp.	Bacteria, Thermotogae		California oil fields	
Petrotoga olearia; P. siberica	Bacteria, Thermotogae		Oil reservoir, Western Siberia	
Thermoanaerobacter	Bacteria, Firmicutes		California oilfields	
Thermosipho geolei	Bacteria, Thermotogae		Oil reservoir, Western Siberia	
Anaerobaculum thermoterrenum	Bacteria, Synergistetes		Oil reservoir, Utah	
Fusibacter paucivorans	Bacteria, Firmicutes		Oil reservoir, Emeraude Oilfield Congo, Central Africa	
Thermovirga lienii	Bacteria, Synergistetes		Oil reservoir, North Sea	
Lactosphaera pasteurii	Bacteria, Firmicutes		Oil reservoir, Canada	
Propionicimonas paludicola	Bacteria, Firmicutes			
Anaerobaculum	Bacteria, Synergistetes		California oil fields	
Thermococcus sp.	Archaea, Euryarchaeota			
Acetoanaerobium romashkovii	-		Bondyuzhskoe oil field	(Magot et al. 2000)
Anaerobaculum thermoterrenum	Bacteria, Synergistetes		Redwash oilfield, Utah	
Dethiosulfovibrio peptidovorans	Bacteria, Firmicutes		Emeraude oilfield	
Geotoga petraea	Bacteria, Thermotogae		Oklahoma and Texas oilfield	
Geotoga subterranea				
Haloanaerobium acetoethylicum	Bacteria, Firmicutes		Gulf of Mexico	
Haloanaerobium congolense			Emeraude offshore oilfield, Congo	
Haloanaerobium salsugo			Oil reservoir, Okla	
Petrotoga miotherma	Bacteria, Thermotogae		Oklahoma and Texas oilfield	
Spirochaeta smaragdinae	Bacteria, Spirochaetes		Emeraude oilfields, Congo	
Thermoanaerobacter brockii	Bacteria, Firmicutes		African oilfields	
Thermotoga elfii	Bacteria, Thermotogae			
Thermotoga hypogea				
Thermotoga subterranea			Oil reservoir, East Paris Basin, France	

1991). Since, temperature increases with depth at a mean rate of 3 °C per 100 m (but regional geothermal gradients may be significantly different), deep oil reservoirs which attain in situ temperature exceeding 130–150°C cannot sustain bacterial growth (Magot et al. 2000). This temperature range is considered the highest theoretical limit for growth due to the thermal instability of biological molecules (Stetter et al. 1993). In a microbiological study, hyperthermophilic bacteria could not be isolated from 100 oilfield water samples whose reservoir temperature was higher than 82 °C (Bernard et al. 1992). Researchers have also stated that the presence of indigenous bacteria in oil reservoirs are limited to a threshold temperature between 80–90 °C. But hyperthermophilic microorganisms, growing at temperatures as high as 103 °C, have been isolated from some reservoirs (Stetter et al. 1993).

pH

Change in pH affects the growth of microorganisms and biodegradation of hydrocarbons as different microorganisms have different pH range for optimal functioning. Microorganisms that grow optimally at a pH less than 5 are called acidophiles, within pH 5–8 are neutrophiles and above pH 8 are called alkaliphiles (Jin and Kirk 2018; Keenleyside 2019). The highest microbial growth and biodegradation rates are generally observed at neutral pH. Extreme pH affects the structure of all macromolecules. It also affects the thermodynamics and kinetics of microbial

Table 7 Some anaerobic microorganisms with their optimal growth conditions and nutrition

Microorganism	Optimal growth conditions	Nutrition	References
Methanobacterinum strain CB12	56 °C, pH 7.4	H_2+CO_2, formate	(Zhao et al. 1986)
Methanococcus strain AG86	85 °C, pH 6.5, 1.8% NaCl	H_2+CO_2	(Zhao et al. 1988)
Methanococcus igneus	88 °C, pH 5.7, 3 % NaCl	H_2+CO_2	(Burggraf et al. 1990a)
Methanococcus jannaschii	85 °C, pH 6.0, 2–3 % NaCl	H_2+CO_2	(Jones et al. 1983)
Archaeoglobus profundus	82 °C, pH 6.0, 1.8 % NaCl	H_2, acetate, lactate, pyruvate, yeast extract, SO_4^{2-}	(Burggraf et al. 1990b)
Caldococcus litoralis	88 °C, pH 6.4, 2.5 % NaCl	Peptides	(SVETLICHNYJ et al. 1987)
Pyrococcus woesei	100–103 °C, pH 6.0–6.5, 2 % NaCl	H_2+CO_2	(Zillig et al. 1987)
Pyrodictium abyssi	97 °C, pH 5.5, 2 % NaCl	Isovalerate, isobutyrate, butanol formate, CO_2, H_2S	(Pley et al. 1991)
Pyrodictium brockii	105 °C, pH 5.5, 1.5 % NaCl	H_2+CO_2+S	(Stetter et al. 1983)
Pyrodictium occultum	105 °C, pH 5.5, 1.5 % NaCl	H_2+CO_2+S	
Staphylothernus marinus	92 °C, pH 6.5, 1.5 % NaCl	Complex organic substrates, S	(Fiala et al. 1986)
Themococcus celer	88 °C, pH 5.8, 3.8 % NaCl	Peptides, protein, S	(Zillig et al. 1983)
Thermotoga maritima	80 °C, pH 6.5, 2.7 % NaCl	Starch, glycogen, glucose, S	(Huber et al. 1986)
Thermosiphon africanus	75 °C, pH 7.2, 0.11–3.6 % NaCl	Yeast extract, peptone, tryptone, CO_2, cysteine, S	(Huber et al. 1989)
Thermotoga thermarum	70 °C, pH 7.0, 0.11–0.35 % NaCl	Carbohydrates	(Windberger et al. 1989)
Themococcus litoralis	88 °C, pH 6.0, 6.5 % NaCl	Yeast extract, peptone, tryptone, meat extract, casein, S	(Neuner et al. 1990)
Thermococcus stetteri	73–77 °C, pH 6.5, 2.5 % NaCl	Peptone, starch, pectin, S	(Miroshnichenko et al. 1989)
Themodiscus maritimus	88 °C, pH 5.0, 2 % NaCl	Yeast extract, H_2+S	(Fischer et al. 1983)

respiration, which then helps to shape the composition and function of microbial communities. It controls the energy yields of common redox reactions in anoxic environments, such as syntrophic oxidation, iron reduction, sulphate reduction, and methanogenesis (Jin and Kirk 2018).

Activity of water

Availability of water directly affects the movement and growth of microorganisms (Rajbongshi and Gogoi 2020). The biodegradation rates of hydrocarbons in terrestrial ecosystems may be reduced because of the water available for the metabolism and growth of microbes.

Salinity

Salinity is one of the important factors which influence the activities of bioremediation and biodegradation as well as microbial growth and diversity. A higher concentration of salt inhibits microbial degradation. Hydrocarbon degradation in saline environments also depends upon the types of microorganisms (Rajbongshi and Gogoi 2020). Ward and Brock (1978), reported a decline in microbial metabolic rates with an increase in salinity level (Ward and Brock 1978). In high saline reservoirs, anaerobic and denitrifying bacteria are not the predominant species. Lin et al. (2014), mentioned that the content of halophilic bacteria was 30 % in an oil reservoir with salinity up to 10,000 mg/L (Lin et al. 2014). *Achromobacter* bacteria is one of the halophilic bacteria which can be found in high salinity oil reservoirs (Lin et al. 2014).

Oxygen availability

Aerobic treatment in the subsurface is difficult due to the limited availability of oxygen where its low solubility restricts not only the respiration process but also the degradation (Holliger et al. 1997). It is an important parameter for aerobic bacteria to activate and cleave the aromatic ring by the action of oxygenases but anaerobes cannot grow in the presence of oxygen. It is toxic for them and they must therefore depend on other substances such as electron acceptors (Hentges 2011). Wilkinson (1983), studied the prevention of growth rate of SRB in water and oil by aeration method. Eventually, this method reduced the growth rate of SRB in water but unfortunately, he found no way to prevent the formation of H_2S in the oil storage system (Wilkinson 1983).

Nutrient availability

Nutrients play a vital role in successful biodegradation, including N, iron (Fe), and P in some cases which enhance the degradation process (Rajbongshi and Gogoi 2020). Other nutrients such as potassium (K), S, Cu, Zn, aluminum (Al), Co, and Ni are also necessary for the activities of the microorganisms (Mathir 2013). Carbon source is another factor that affects the growth of anaerobic microorganisms. The hydrocarbon compounds in the oil reservoirs can satisfy this nutrient requirement for biodegradation to CH_4 and CO_2. Whereas, dissolved CO_2 is the carbon source for autotrophic methanogens (Mathir 2013). The addition of surplus nutrients can stimulate bacterial activities and increase the metabolism of products (Zhou et al. 2015). Atlas (1985), reported that the excess concentration of nutrients can inhibit the activity of biodegradation (Atlas 1985). Adequate contact time between microbial consortia and the substrate plays an important role in the biodegradation of hydrocarbons (Mathir 2013). SRB is generally recognized as a hazard in the production process of oilfields (Castro et al. 1997). It is responsible for H_2S production and the ability of H_2S to precipitate FeS that could plug the reservoir rock pores is of utmost concern. A study on SRB was carried out by Wilkinson (1983), where he observed that the growth rate of SRB in stagnant seawater and the production rate of H_2S was 10 times greater when oil was added as a carbon source (Wilkinson 1983).

Permeability

Permeability plays an important role in the activity of microorganisms. High permeability viscous oil reservoirs after a long period of water injection resulted in a significant increase of microbial diversity by doubling the species and genera number of microorganisms (Lin et al. 2014).

Conclusions

Anaerobic microorganisms such as SRB, methanogens, NRB, and fermentative bacteria are widely distributed in oil reservoirs. They have become prominent in petroleum industries for their wide applications during exploration and production activities. Their major functions are oil degradation, viscosity alteration, reduction of IFT, wettability alteration, and remediation of toxic heavy metals. The review attributes to the diversity of these microorganisms in oil reservoirs, their applications in petroleum exploration and production activities, and growth in different environments. The study on SRB revealed their association with reservoir souring that causes reservoir plugging and corrosion of associated equipment. While the diversity of SRB showed that most of these belong to the taxonomical group of deltaproteobacteria, methanogens belonged to archaea and euryarchaeota. It is notable that with the MEOR process, the oil recovery rate could be as high as 90% while that from primary and secondary processes is only 10 % and 15–60 % respectively. The metabolites or biosurfactants produced from these microorganisms can reduce both ST and IFT between oil/gas or gas/liquid that will aid in the EOR process by increasing the oil mobility. NRB can remove sulphide existing from oilfield FW and also inhibit its production. The review gives a deep insight into the role of microorganisms in petroleum industries which would help researchers with in-depth knowledge on the role of microorganisms in oil field applications.

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Data Availability The datasets used and/or analyzed during the current study are available from the corresponding author on reasonable request.

Declarations

Conflict of interest The authors declare that they have no competing interests.

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