**MICROBIAL MATS ECOSYSTEM**

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**ABSTRACT**

Microbial mats are a dynamic community visible to the naked eye. They are classified based on the nature of their environment as hypersaline mats, coastal mats, acids microbial mats and microbial mats in oligotrophic environment. In microbial mats, different groups of microorganisms are found and are involved in different biological processes and interaction such as symbiosis, neutralism, commensalism, competition and parasitism. Most of these organisms in microbial mats are involved in different biological processes such as sulfate reduction, methanogenesis, nitrogen fixation, metal reduction, denitrogenation and photosynthesis. In microbial mats, photosynthesis is the major main source of nutrients and energy. It has shown to play many important roles in modifying the atmospheric composition yielding H2, O2, as wel as CH4. Microbial mats have found many biotechnological applications such as cancer treatment, bioremediation, bioenergy, aquaculture and molecular biology. Thus, microbial mat being a unique ecosystem where processes as microbial diversity, evolutionary trend and their adaption to extreme conditions of the environment can be studied makes it a natural laboratory.

**Keywords**: Microbial mat, biofilm, autoinducers, biological processes, biotechnological applications, ecosystem, functional diversity, signaling system

**INTRODUCTION**

Microorganisms do not exist in isolation. They are found in active interaction with both biotic and abiotic factors of their environment**.** The interaction between these microorganisms may often result in the creation of microbial communities with special structures capable of attaching to solid material forming an intricate ecological entity in various environments across the world (Davey and O’Toole, 2000). Adherence to a surface is an adaptive mechanism developed by microbes several million years ago. This ability gave them a better chance at survival and evolution in communities while allowing them to withstand severe climatic and environmental factors. Microbial interactions include a simple biofilm nonspecific in nature composed of a single species of microorganism and an intricate microbial mats which comprise vast array of microorganisms (Bonilla *et al*., 2012).

According to Ruvindy *et al*. (2016), communities of microorganisms arising from different species attach to the surface of solid materials, which aid the formation of complex ecological entity in various environments around the world. The technique adopted by microorganisms for over a million years is the attachment to a solid surface, which aid survival and evolution of organisms in various communities and also enhances their adaptation to the abiotic factors surrounding them, although some conditions may impose stress on them. Bolhuis *et al*. (2014) and Wong *et al*. (2016) reported that microbial mats are commonly found on the seafloor occurring in different vertical layers each with distinct communities that are usually formed at the boundary between the solid and liquid components of various environments. Unlike what is obtainable in biofilms, a microbial mat consists of several million species of microorganisms. (Ruvindy *et al*., 2016) reported that all microorganisms in a microbial mat are in constant interaction and signal exchange, and to ensure swifter flow of resources and energy to enable continuous survival of the community, they are surrounded by a matrix of exopolysaccharide and nutrients. There are limitations to the type of interactions commonly encountered in microbial mats, with symbiosis being the most prominent, thus, giving them relatively selective advantage (Al-Thani *et al*., 2014).

Furthermore, according to Batman *et al*. (2016), microbial mats comprise diverse species amounting to several millions of microorganisms, which are in continuous interaction and signal relay lodged in a matrix of exopolysaccharide and nutrients to aid increase in resources and energy transmission for the community of different microorganisms to survival the adverse conditions in the environment. According to Nutman *et al*. (2016), the existence of microbial mats on earth dates back to the paleolithic era, with the most ancient being found in some classes of sedimentary rocks, 3.7 GA west of Australia and 3.4 GA South Africa from the Archean era. Although, proterozoic has shown to contain the highest abundance of microbial mats (2.5-0.57 GA) and it's found in different regions of the world. The detailed study of the fossils proposes that there is stability and flexibility in the different communities found in microbial mats in adapting to the constantly changing conditions of the environment (Revsbech *et al*., 2016).

Persistence of these communities is commonly observed in hypersaline ponds, hot springs, sulfur springs amongst other extreme environments where growth and proliferation of some multicellular organisms and eukaryotes are limited and restricted by some environmental conditions (Revsbech *et al*.,2016). Microbial mats have been shown to play many important roles in different environment ranging such as modifying atmospheric composition, producing hydrogen, oxygen as well as methane through the process of photosynthesis and other anaerobic degradation processes, and also represent the earliest ecosystem along with stromatolites (Bolhuis *et al*., 2014). Microbial mat is a unique ecosystem where processes as microbial diversity (structure and patterns of the community), evolutionary trend and their adaption to extreme conditions of the environment can be studied making it a natural laboratory (Inskeep *et al*., 2013).

**Structure of Microbial Mats**

Microbial mats can be seen with unaided eyes, unlike biofilms. Biofilms are mainly composed of single species that form a mass on electrode surfaces whereas, microbial mats exhibit a high diversity of species with different levels of metabolism taking place simultaneously. Biofilms are observed actively covering solid surfaces while microbial mats are seen covering sediments. Few cell layers to a few millimeters in thickness but ranges from <1 mm to several centimeter depending on the communities involved as seen in Figure 1. Microbial mats are often formed *via* the combination of several biofilms of organisms, which are embedded in a matrix of exopolysaccharides (Bolhuis and Stal, 2011). The energy flow in biofilm is strictly heterotrophic and rely on the provision of substrate whereas microbial mat can exist in different forms ranging from photoautotrophic to chemoautotrophic levels. These organisms serve as the primary producers in the first few millimeters of the mats.

Mats exist in vertical fashions due to the physical gradients, which forms the major factor of biological biodiversity in the mats. The biological processes and physical gradients observed in microbial mats make available the needed microenvironment and explicate the functional roles of the microorganisms in the microbial mat ecosystem (Gemerden, 1993). The organisms found in microbial mats are usually bacterial species with some Archaea, and Eukarya. Studying microbial mats requires a combination of chemical and physical parameters with a sound knowledge of biological interactions. Chemical parameters like saline concentration, redox potential, pH, and presence of oxygen, electron donor and electron acceptor and the availability of various chemical species are tantamount to studying microbial mats. Physical parameters such as pressure, temperature and light must be closely monitored. It is pertinent to note that processes like metal reduction, nitrogen fixation, photosynthesis, denitrification, reduction in sulfate compounds and methanogenesis amongst other processes are key in describing the microbial mat performance (Woebken *et al*., 2015).

**Microbial Communities found in Microbial Mats**

The biological communities commonly found in microbial mats include the cyanobacteria, proteobacteria (purple bacteria), Green sulfur bacteria (Chorobi), anoxygenic photosynthetic bacteria, aerobic and anaerobic heterotrophs, methanogenic archaea, sulfur oxidizing and sulfate-reducing bacteria (SRB) as shown in Figure 2 (Klatt *et al*., 2016).

Microbial mats consist of many microbial groups that are closely compacted into mat of various biological activities and processes such as sulfate reduction, photosynthesis, metal reduction, nitrogen fixation, methanogenesis and denitrification. Because of myriads of microbial communities in microbial mats, several ecological relationships exist within the microbial communities. Interactions in microbial mats could be beneficial or detrimental to all participating species or they could be neutral with species neither benefitted nor harmed. Mutualism, commensalism and proto-cooperation are the various forms of beneficial interaction occurring among the participating species while ammensalism, antagonism, predation, parasitism and competition are the detrimental associations among the various species in a microbial mat. Some photosynthetic activities of the photosynthetic group, mainly cyanobacteria, may create an anoxic environment especially in the upper layer. This may create an excellent environment for the anaerobes such as the SRBs at the lower layer (Rich and Maier, 2015).

**Energy Transfer in Microbial Mats**

Although there are possible cases where non-photosynthetic mats exist, photosynthesis is the major source of energy in microbial mats. The primary producers or cyanobacteria perform the photosynthetic activity. Various biogeochemical cycles coupled with biochemical processes are associated with all microbial mats which function as a consortium. The immediate interaction among different species in the microbial mat enables the utilization of the metabolic product of one group by other groups of microorganisms (Severin *et al*., 2010). The filamentous cyanobacteria communities found in microbial mats carry out the process of nitrogen fixation. However, SRBs also play vital roles in the biological process. The flow of nutrients in a microbial mat is summarized in Figure 3.

Ecological succession brings about the formation of complex communities in a mat, with cyanobacteria serving as the colonizers and modifiers of microenvironment for the later colonization by specialized bacteria with greater and more specific environmental requirements (Boomer *et al*. 2009). Microbial mat also serve as a dynamic community allowing change in position of motile organisms in the mat to achieve a stable and favorable environmental conditions like redox potential and luminous intensity (Cohen *et al*., 1994).

Since the discovery of mats, geologists and microbiologist have continued to explore the best ways to understand the physiology of mats. It was quite impossible to investigate microbial processes taking place in mats due to their sizes (about 1 millimeter thick). This narrative changed when the applications of microelectrodes and microlight sensors became widespread. These instruments allow researchers to measure microbial activity at tens-of-micrometer scales thus revealing a detailed high resolution spatial and temporal information on photosynthesis, redox, pH, sulfide, oxygen and light levels in the mats. Even with this technological advancement, the activities of microorganisms in mats are difficult to measure or observe. It was the application of genetic techniques that led to exploring the information of organisms found in mats. The cultivation and microscopy of communities in mats show that they exhibit a high level of diversity with different metabolic pathways depending on the energy need of the organisms. Since organisms existing in mats depend on each other for survival, the waste product of one organism usually serve as the energy source of the next and the chain continues. (Stal, 2012).

T**YPES OF MICROBIAL MATS**

According to Drewniak *et al*. (2016), microbial mats are commonly found in the biosphere although they thrive and prosper in extreme environments. Microbial mats exhibit high diversity of species, described in the following sections are the various microbial diversity that characterize the different microbial mats, which are mostly phototrophic with a significant photosynthetic components making them light dependent.

**Hypersaline Mats**

Hypersaline mats are commonly found in areas of saline lakes (Figure 4). These mats are characterized by extreme conditions such as high salt content (salinity), high temperature, high radiation energy. These factors impede the formation of complex microbial communities (Charlesworth and Burns, 2016). Various molecular techniques have been studied extensively to provide adequate information for the description of the community in mats, common among the techniques include microbial culture, amplification, cloning and sequencing of 16S rRNA and metagenomics. Bacteria are the dominant organism in this community with an approximate 90% bacteria, 9% archaea and 1% eukaryotes (Tripathi *et al*., 2016). The distribution of bacterial species in hypersaline mats is determined by the presence of light, oxygen, H2S (hydrogen sulphide) and the formation of spatiotemporal chemical gradients (Kunin *et al.,* 2008). The distribution of the different groups of bacteria into vertical sections is a function of the presence of oxygen, light and hydrogen sulfide, and the structure of the microbial community is strongly affected by the formation of spatiotemporal chemical gradient (Feller, 2013).

**Coastal Mats**

The two most biologically diverse microbial mats with extensive coastal distribution are the coastal and hypersaline mats. These mats are commonly found in irregular flood, in intertidal coastal zones with fluctuations in high salt content and intense temperature. Cyanobacteria are the most commonly encountered species inhabiting the mats with other bacterial groups like Bacteriodetes and Proteobacteria (Bolhuis and Stal, 2011). According to Mahajan and Balachandran (2017), Schiermonnikoog Island off the coast of the Netherlands measuring 300 m in width and 5 Km in length has a green bench with a massive strip of microbial mats. The dominant bacteria divisions were identified using sequence analysis of the 16S rRNA gene and were shown to be cyanobacteria, proteobacteria of the order rhodobacteriales and sphingomonadales, chromatiales and S-proteobacteria of the order desulfobacteriales and desulfovibrionales, and actinobacteria. important archean elements as euryarchaeota (particularly methanogens) are crenarchaeota are also scarcely present (Feller, 2013).

Mahajan and Balachandran (2017), reported that the most abundant divisions in the great Sippewisset swamp (Massachusetts, USA) are the cyanobacteria, proteobacteria and chloroflexi, with traces of spirochetes, verrucomicrobia, acidobacteria, caldithirix, and actinobacteria. Vast majority of microbial mats have shown similar trend in organizational levels and structural complexity, although large number of eukaryotes have been discovered in the coastal mats, mainly diatoms of the genera *Navicula* sp., *Amphora* sp, *Diploneis* sp, and *Cylindrotheca*, and the algae of the genera *Chlorophyta* and *Enteromorpha*.

**Microbial Mats in Oligotrophic Environment**

Al-Thani *et al.* (2014) reported the detailed study of the features of the oligotrophic mats of Cuatro Cienegas present in the Coahuila desert, to the North of Mexico. These mats are extremely low in concentration of phosphorus. Phosphorus in form of phosphate is one of the major constituents of the DNA, proteins and other energy molecules making it an essential limiting factor upon which all life forms depend (Thiel *et al*., 2017). The diversity of community largely depends on the degree of exposure and disturbance, mats with little exposure to constant disturbances has high diversity of community with no dominant groups, with most diverse groups as proteobacteria, cyanobacteria and bacteriodetes alongside 16 other divisions and 28 bacterial orders (Bolhuis and Stal, 2011).

**Acid Microbial Mats**

Vast majority of microbial mats form primarily at alkaline pH, with few being developed in an acidic environment. A number of microbial mats lack photosynthetic microbial groups and as such the predominant metabolism in the communities being oxidation of iron and sulfur compounds. Baker and Banfield (2003) observed that pyrite, chalcopyrite, arsenopyrite, FeS2, FeAsS, CuFeS2 amongst other sulfur minerals are present in acid mine drainage which is strongly acidic with pH values between 0.77 and 1.21, characterized by high concentration of toxic metals. The rate of propagation of microbial diversity of a mat is usually very minimal due to the effects of environmental conditions, Archaea and Bacteria being the predominant organisms with oxidation and reduction of iron sulfate reduction as the metabolism. Firmicutes, S-proteobacteria, actinobacteria, nitrospirae are the various phyla in acidic microbial mats. Others being *Ferromicrobium acidophilus, Leptospirillum, Acidomicrobium* and Thermoplasmales (Baker and Banfield, 2003).

The pH value of acidic springs ranges between 3-3.5, and the mats from  Yellowstone National Park are the most studied mats. Metabolism of iron and sulfur compounds are crucial for a dynamic community in acid mines. *Hydrogenobacculum* sp, *Metallosphaera yellowstonensis*, heterotrophic archaea and members of a new Geoarchaeota archaea division are present in springs on hundreds of springs plain and Beowulf (Beam *et al*., 2016).

**Psychrophile Microbial Mats**

Psychrophilie microbial mats is shown in Figure 5. According to Drewniak *et al*. (2016), vast array of cold environments occupies the largest proportion of earth with low temperature of less than 5°C found in oceans, caves, polar regions and Alpine areas. Polar region mats in Antarctica and Arctic shelter serve as hot spot of ecological diversity and primary production (Brito *et al*., 2014). These environments include alpine areas, caves, oceans and polar regions. Locations like Artic shelter and Antarctica represent the best locations for studying the various ecological diversity and primary production in extremely cold mat. The photosynthetic mats in cold regions are dominated by filamentous cyanobacteria, various species of diatoms, algae, nematodes, protozoans (ciliates and flagellates), rotifers and microinvertebrates (Siddiqui and Cavicchioli, 2006). Filamentous cyanobacteria of the order Dichothrix, Nostocales-Tolypothrix, and Oscillatoriales-Tychonema dominate the photosynthetic mats of these poles, they help in producing wide variety of polysaccharides matrix that afford protection to other organisms such as ciliates, diatoms, rotifers, algae, flagellates and microinvertebrates with lower tolerance that make up the community (Drewniak *et al*., 2016).

Charlesworth and Burns (2016), reported various growth limiting factors as low temperature, drought, selective pressure, high solar radiation, prolonged winter darkness, nutrients deficiency, freezing, as well as thawing cycle are imposed by the psychrophilic conditions. Heterotrophic bacteria play vital role in nutrients cycling in Antarctica with major bacterial phyla as Proteobacteria, Actinobacteria, Firmicutes, Bacteroides and Deinococcus-Thermus (Charlesworth and Burns, 2016). The dominant group of the photosynthetic bacteria in the mat are the Cyanobacteria with the orders Nostocales and Oscillatoriale which are filamentous in nature being the most abundant. Chloroflexi and Chorobi amongst other photosynthetic groups are also present in trace amount (Brito *et al*., 2014).

**Hot Spring Microbial Mats**

Hot spring microbial mats is shown in Figure 6. They are associated with high temperatures extreme environments such as hot springs and geysers. The limiting factors that affect the development of life and diversity of community are temperature, sulfur concentration and pH, with temperature serving as the most essential factor for the distinctive modeling of the communities (Cardoso *et al*., 2017). Within phototrophs, hot spring microbial mats have the lowest diversity, however, the study of the most ancient communities on earth are best understood using these mats (Klatt *et al*., 2016).

Thermophilic communities maybe associated with water columns, sediments, streams and microbial mats (Wong *et al*., 2015). The vital role of metabolic dynamics of the community in microbial mats are carried by photosynthetic organisms. There are two major problems associated with photosynthesis in heated water; high temperature decreases the concentration of dissolved gases such as CO2 and O2 and it also denatures the proteins and their biomolecules, as a result high temperature limits the activity and proliferation of photosynthetic bacteria which is normal 75°C, as chlorophyll degrade at that temperature (Cardoso *et al*., 2017).

Cyanobacteria are major and one of the most abundant groups in these mats. Cyanobacteria function as nitrogen and carbon fixers in the community. *Synechococcus* amongst other unicellular cyanobacteria are commonly associated with springs with thermal water temperature exceeding 55°C (Woebken *et al.*, 2015). Various thermophilic microbial mats have been discovered in different regions of the world with the Yellowstone National Park in the USA being the most studied, others include Thailand Tibet, Romania, Patagonia, the Philippines, the geothermal zones determine the geographical distribution of the mats (Thiel *et al*., 2017).

**Quorum Sensing in Biofilm - Mat Production**

A cell to cell communication process in bacteria involving the detection of signal, generation of response to extracellular signaling or messenger molecules called Autoinducers (AIs) is termed as quorum sensing. Increase in the bacterial population density results in accumulation of the autoinducers, and bacteria detect changes in their cell number thereby collectively altering the gene expression by monitoring the information. A compound is detected when a certain threshold concentration of the signal is attained translating into activation or repression of the target gene. N-acyl-homoserine lactones (AHL) are the most studied bacterial autoinducers and they are synthesized by LuxI-type proteins (Boyer and Wisniewski-Dye, 2009). Certain genes that regulate the beneficial activities of group of bacteria acting in synchrony are controlled by quorum sensing. Antibiotics production, plant-microbe interaction, bioluminescence, biofilm formation, virulence factor secretion are the various processes controlled by quorum sensing (Williams and Camara, 2009).

Biofilms are multicellular sessile communities formed by bacteria in which the cells of a community are surrounded by matrix of secreted extracellular polymeric substances. Quorum sensing and the formation of biofilms are fundamental and mostly the interrelated features that characterize bacterial social life (Li and Tian, 2012). The development of various microbial community in a mat is described as biofilm formation while the various checkpoints of different phases in biofilm progress is referred to as quorum sensing (Irie and Parsek, 2008). It may be difficult to ascertain the differences between the primary quorum sensing system responsible in biofilm-related phenotype, however, quorum sensing related mechanisms are found to regulate many steps in biofilm development. Involvement of quorum regulatory units is observed in the formation and maturation of biofilms, this was revealed by studies on different quorum sensing mutant strains (Kjelleberg and Molin, 2002).

Biofilms are assemblage of small group of microorganisms that are attached to one another and fastened to a surface, and are embedded in a matrix secreted by the organisms themselves. Vast majority (99.9%) of microorganisms have the capability to form a biofilm. Various benefits bacteria derive from forming biofilms include, protection against antibiotics and other disinfectants, bacterial tolerance to harsh environmental conditions are enhanced and it prevents the washing away of bacteria by water flow and blood stream. Also, bacterial motility is retarded by the formation of biofilm and it also increases the cell density thereby providing a suitable environment for easy transfer of plasmid among organisms in a community through the process of conjugation. Antibiotics resistance gene may be carried in some of these plasmids to enable them withstand various environmental stresses. Quorum sensing is a unique chemical communication technique used be bacteria in a biofilm to relay information among themselves.

The formation of biofilm takes place in the following stages (i) The organisms are accumulated or adsorbed on the surface of aggregator, i.e. substrate, this is known as deposition; (ii) Formation of polymer bridges upon desegregation of the layer between the organisms and the aggregator; (iii) Multiplication or proliferation of the organisms on the surface of the aggregator; (iv) Formation and maturation of biofilm; and (v) Dispersal or detachment. High cell concentration in biofilm is characterized by the involvement of a cascade of cell signaling mechanisms. Gene expression is triggered by the autoinducers or signaling molecules such as homoserine lactones and small peptides through enzymatic process for the formation and maturation of the biofilm (Subramani and Jayaprakashvel, 2019).

The functioning of quorum sensing signal molecules in a biofilm and how often quorum sensing is activated in a biofilm remains largely unknown. Biofilm formation is promoted by some quorum sensing systems while others are involved in the dispersion of biofilms. Biofilm formation is seen as series of stages involving continuous attachment of microbial communities to aggregator surfaces, while quorum sensing is described as checkpoint for restarting the cycle by aiding dispersion or dissolution of a subpopulation of cells. In this case, the nutritional stress that accompanies inducing concentrations of quorum sensing signal is overcome by the dispersing cells. The population density of non-motile species in a biofilm is regulated using different mechanisms. The mechanistic pathway of biofilm development such as the production of exopolysaccharide and other secreted factors is altered as quorum sensing induce behaviors in the biofilm cells (as they transition from QS-uninduced state to QS-induced state) (Irie and Parsek, 2008; Li and Tian, 2012; Munir *et al*., 2020).

Group activities such as surface motility might be induced or repressed by quorum sensing, which could have a profound impact on the structure of biofilm. The production of vps exopolysaccharide in *Vibrio cholerae* is regulated by quorum sensing. Biofilm formation was observed to be promoted by the expression of vps (Silva and Benitez, 2016). Alem *et al*. (2006) reported that at the initial stages of biofilm development, hyphal formation is promoted or enhanced by the quorum sensing signal tyrosol, while in the later stages, dispersal of yeast cells from the biofilm is promoted by farnesol another quorum sensing signal. This implies that tyrosol and farnesol syntheses are differential throughout biofilm development, and as such the quorum sensing signal that accumulates at specific stages of biofilm development determines the cells response.

The role of the regulatory protein las quorum sensing is the formation of biofilm of *Pseudomonas aeruginosa*. Quorum sensing in the biofilm of this organism in very intricate and has two interconnected N-acyl homoserine lactone-dependent regulatory circuit, these are acted upon by regulators at translational and post-translational levels, thus modifying them. It was discovered that the lasI mutant, which lacks the capacity to produce autoinducer N-3-oxo-dodecanoyl-L-homoserine lactone (3-oxo-C12-HSL) formed biofilm cell clusters with thickness of 20% of the wild-type biofilm and they were found to be highly sensitive to detergent removal (Venturi, 2006). The lasI mutant was found to regain the ability to form structured biofilm when autoinducer 3-oxo-C12-HSL was added to the system. The study reveals the important role played by quorum sensing in biofilm development, and most significantly it establishes an inextricable link between quorum sensing and biofilm formation. *Staphylococcus aureus*, and wide variety of *Streptococcus* sp amongst other Gram positive bacteria make use of signal peptide-mediated system for quorum sensing (Rutherford and Bassler, 2012). The main causative agent of nosocomial infection worldwide is *S. aureus*, and it causes diseases ranging from mild skin infection to potentially fatal systemic disorders. Infections like endocarditis, osteomyelitis and foreign body related infections caused by *S. aureus* are caused by biofilms and not by a free-living cells. Various aspects of the biofilm phototype may be influenced by the agr phototype locus in *S. aureus* and pattern of expression from the accumulated evidence. These include cells attachment to surfaces, dispersal of biofilm, and to some extent the chronic nature of biofilm-associated infections (Tong *et al*. 2015)

Bacteria in liquid cultures are believed to be physiologically similar and thus the rate of signal molecules production is the same. However, complications might be encountered in quorum sensing and signal transduction in biofilms, these are attributed to the range of chemical, physical and nutritive factors influencing signal production, stability, distribution and efficiency to interact with their cognate receptors in the biofilm (Li and Tian, 2012). ALH are observed to have little problem to reach their target receptors through free diffusion in the biofilm matrix, this is due to the free diffusion of these molecules across the cell membrane. However, the physical, chemical and biological factors within a biofilm likely influences the signaling peptides produced by Gram positive bacteria because of the interaction of the small peptides with the charged molecules. Presently, there is little knowledge of the chances of signal peptides being affected by the limit of diffusion or by non-specific binding to polysaccharides, proteins, DNA and the components of the cell wall within the biofilm (Horswill *et al.,* 2007, Roya *et al*., 2018).

The cost of producing an active signal peptide by Gram positive bacterium is very expensive process. The estimated cost for production of signal peptide in *S. aureus* by Keller and Surette is 184 ATP but for ALH in *P. aeruginosa* is only 8 ATP. Generally, in Gram positive bacteria the cost of producing a signal peptide is much more expensive. It is therefore necessary to assume that the signal peptide-mediated quorum sensing and activities in Gram positive biofilms are influenced by important factors as Nutrient and energy source. Theoretically, the concentration of a signal molecules affects the signal molecules which is used to estimate the population density. Signal molecules could also be affected by other factors as the limit of diffusion, accessibility to the receptor, degradation and synthesis of the same autoinducer such as AI-2 by third parties, intentionally or by chance. Since activation of quorum sensing depends on the diffusion of a signal molecule to and interact with the cognate receptor, quorum sensing could be regarded as diffusion sensing (DS) (Moghaddam *et al*., 2014, Radlinski *et al*., 2017, Hotterbeekx *et al.,*2017).

**Ecology and Functional Diversity of Microbial Mat**

In microbial mats, different communities of microorganisms are found and these organisms carryout different biological processes. The microenvironment required by the organisms and the functional roles of microorganisms with specific needs are provided by the biological processes and physical gradients (Sauder *et al*., 2017). The communities that make up these microbial mats are mostly bacteria, although, other less abundant domains such as Archaea and Eukarya with low diversity are found in microbial mats. Chemical parameters such as pH, presence of Oxygen, redox potential, presence of electron donor and acceptor compounds, saline concentration, as well as diversity of chemical species are considered for studying microbial mats, while light, temperature, and pressure are important physical factors also to be considered (Adessi *et al*., 2017).

The biological interaction that exist in this microbial mats include symbiotic, neutralism, and ammensalism while essential processes for efficient performance of microbial mats include nitrogen fixation, photosynthesis, metal reduction, iron and sulfate reduction, denitrogenation, and methanogenesis (Langille *et al*., 2013). The basic functional groups of microbial mats are Cyanobacteria, green sulfate bacteria (Chorobi), Proteobacteria (purple bacteria), anoxygenic photosynthetic bacteria (known as non-sulfur green bacteria of the Chloroflexi division), aerobic and anaerobic heterotrophs, sulfate-reducing bacteria (SRBs), sulfur oxidizing bacteria and methanogenic archaea (Nelson *et al*., 2015).

Photosynthesis is the primary source of energy and nutrition in microbial mats, although non-photosynthetic mats exist (Nelson *et al*., 2015). Photosynthesis is the first step for survival of this tropical network in typical mats, it is a process in which the primary producers Cyanobacteria transform the inorganic carbon (CO2) to organic carbon ((CH2O)n) using light energy with the release of oxygen (Tripathi *et al*., 2016). According to Lun-Wong *et al.* (2015), the close interaction between the biogeochemical cycle and various biological processes in the consortium enables the utilization of the product of metabolism of one group by other microorganisms. Filamentous cyanobacteria, and unicellular organisms carry out nitrogen fixation while SRBs are those group of organisms that have the ability to reduce sulfates to sulfur, and also oxidized organic matter as well in the process obtained energy (Sauder *et al*., 2017).

Vital processes such as calcium precipitation and lithification of mats are carried out by the sulfate-reducing bacteria (SRBs), therefore they are responsible for the preservation of mats in fossil records (Sauder *et al*., 2017). Complex communities are formed by a process of ecological succession where Cyanobacteria serve as colonizers and modifiers of microenvironment for subsequent colonization by more specialized bacteria with higher and more specific environmental requirements (Langille *et al*., 2013).

**Signaling system in Microbial Mat**

The high microbial diversity exhibited by mats is an indication that several signals may exist in them. The organisms present in mats exhibit diversity with different functional groups, enclosed in a matrix of extracellular polymeric substances. The laminated sedimentary biofilms can provide a perfect system for examining the environmental effects of quorum sensing. This is largely because wide range of extractable quorum sensing signals are produced by mats, they possess an extensive small-scale horizontal gradient of physicochemical conditions that may vary dramatically over a diel cycle (Jorgensen, 1983).

Chemical signals between microbes in a mat can operate within short range (usually tens of micrometer). This is sponsored by the diffusion constraints. Moving chemical signals over long distances may take too long. The chemical signals exchanged by microbes in a mat can be utilized as extracellular sensor, providing information to cells about the properties of their proximal environment such as local diffusivity. The process is known as "efficiency sensing". For instance, the potential benefits of contributing to extracellular processes can be assessed using important determinants such as gauging the relative diffusivity of molecules released by cells into the environment.

Thus, microbial mats have shown to play many important roles from modification of atmospheric compositions, producing H2, O2, as well CH4. Microbial mats along with stromatolites also represent the first ecosystem. In addition, vital processes such as microbial diversity, evolutionary trend and their adaptation to extreme environments can be efficiently studied making microbial mat a natural laboratory.

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