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# Defense on surface: macroalgae and their surface-associated microbiome

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## Abstract

Macroalgae surfaces are considered as a potentially suitable substratum present underwater for the dynamic epibiotic microbiome. They secrete various organic substances as nutrients for the multiplication of bacteria and the formation of microbial biofilms. The microbial biofilm itself acts as a biological defense mechanism to prevent the establishment of pathogenic microbes as well as to protect the surface of the seaweed from the macrofoulers. In most cases, the presence and diversity of these organisms are host-specific. The macroalgal host and their associated microbiont are often referred to as a 'Holobiont'. The surface-associated microbiome of macroalgae plays a crucial role in the growth, morphogenesis and defense in the normal favorable environmental conditions of the macroalgae (Symbiotism). Whereas, when there is a change i.e. reversed, unfavorable conditions, the microbiome reverses its symbiotic nature and affects growth and degrades the macroalgae by causing different diseases in different species (Parasitism). In parallel, marine macroalgae employ different defense mechanisms, a physical defense such as continuous shedding of the outer layer of cells, and the mucilaginous covering and chemical defense such as the production of secondary metabolites. The following chapter focuses on the macroalgal surface-associated microbiome and its defense system with a certain number of relevant examples from related literature on this subject.



## 1. INTRODUCTION

Macroalgae, being important habitat formers and primary producers in the marine ecosystem, provide potential settling substrate and protective environments for the early life and development of many invertebrates. Attached to their substrate, marine seaweeds are linked to their environment and confronted with various abiotic and biotic stresses. They are affected by wave action, light radiation, desiccation, and variations in salinity, temperature, nutrient supply, herbivore predation, epibiosis, microfouling and human activity. In the marine environment, competition for space and nutrients is intense. Each species lives in this complex environment according to its own physiological parameters, and its ability to resist changes in the state of the environment, particularly, during low tides or in reduced space. Due to the extraordinary complexity of the marine environment, seaweeds establish close associations with other species to ensure their survival and competitiveness for space.

Macroalgal surfaces represent a major physiological and highly functional interface with the environment. Such an interface is always threatened by fouling, and thus macroalgae need to develop many defense strategies to protect their surface from a vast number of conse-

quences (Wahl, Goecke, Labes, Dobretsov, & Weinberger, 2012). *Biofilms on solid surfaces* are omnipresent and therefore macroalgae are of no exception to this. Biofilm formation is an interactive process affected by local hydrodynamics of the fluid environment, physicochemical properties of the surface and behavioral response of bacterial colonizers (Geesey, 2001). In biofilms, the self-produced matrix is mainly composed of polysaccharides, proteins and eDNA synthesized by the associated bacteria, diatoms, fungi, and other microorganisms (Garg, Jain, & Bhosle, 2009).

*Host-microbe interactions* play a crucial role in marine ecosystems, in a symbiotic community where the largest partner, based on its size, is considered as a host, e.g. macroalgae (Dittami et al., 2019). The host and all of its associated microbiota, which can be acknowledged as all the microorganisms which are present or associated in a particular environment is now considered as a *Holobiont* (da Gama, Plouguerné, & Pereira, 2014; Duarte et al., 2018; Egan et al., 2013; Hollants, Leliaert, De Clerck, & Willems, 2013; ; Wahl et al., 2012). The term 'holobiont' was coined by Lynn Margulis which referred to *symbiotic associations* that last for a significant part of an organism's lifetime (Cavalier-Smith, 1992). As it includes all the associated microbiota, their interactions may be harmful, beneficial or of no consequence, which may be coevolved or opportunistic, competitive or cooperative (Skillings, 2016). The combined genetic information of the associated microbiota is known as a microbiome (Dittami et al., 2019; Skillings, 2016) These microbiomes are functionally connected with their eukaryotic hosts and they are highly diverse. Specific functional genes of the associated microbiome are now regarded as secondary genomes (Singh & Reddy, 2016). *Any disturbances to the microbiome* or even *uncontrolled microbial colonization* could be *associated with stress and disease of the host organism* (Beattie, Lachnit, Dinsdale, Thomas, & Steinberg, 2018; Lachnit, Blümel, Imhoff, & Wahl, 2009; Morris et al., 2016; Rohde, Hiebenthal, Wahl, Karez, & Bischof, 2008).

Lacking a cell-based adaptive immune response, macroalgae have two different defense capabilities: constitutive defense under normal circumstances, such as the *production of metabolites by macroalgae* or its *bacterial symbionts* and *induced defense activated by any tissue damage* (Egan, Fernandes, Kumar, Gardiner, & Thomas, 2014; Weinberger, 2007). Surface-associated microbiome proved a wide range of bioactive compounds with a broad spectrum of activities, such as antibacterial, an-

tifungal, antiviral, antiplasmodial, nematicidal, anti-inflammatory, anti-cancer and antiangiogenic activities (Singh, Baghel, Reddy, & Jha, 2015). Here we consider the defense provided by the macroalgae themselves through the production of secondary metabolites as 'Chemical Defense' and the defense provided by the associated microbiota as 'Microbial/Biological Defense', however, it is now known that many of the bioactive compounds previously attributed to seaweeds were in fact produced or metabolized by their associated microbiota, the microbiome (da Gama et al., 2014; Egan et al., 2013; Hollants et al., 2013; Wahl et al., 2012). In this association, a highly and dynamic complex set of chemical, physical and biological interactions regulates the relationships between the *basibiont and its epibionts* (Singh, Kumari, & Reddy, 2014).



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## **2. SEAWEED SURFACE-MICROBE INTERACTIONS – BIOFILM DEVELOPMENT**

Biofilms, a consortia of surface-attached microbial cells dispersed in a self-secreted extracellular polymeric matrix, constitute the principal form of microbial growth and a widespread survival strategy among microorganisms (Costerton, Geesey, & Cheng, 1978; Donlan, 2002). In the marine environment, surfaces are rapidly colonized by marine organisms in a process known as biofouling (Callow & Callow, 2002). The adsorption of dissolved macromolecules by the substratum is a preliminary step before bacterial colonization. The *algal cell wall structure* is a selective factor in the settlement of macromolecules and microorganisms. Bacteria are typically the primary colonizers of submerged surfaces. Marine macroalgae are known to produce secondary metabolites to defend themselves from the colonization of their exposed surfaces. In fact, *these metabolites and pioneering bacterial species* contribute to the chemical and physicochemical conditions responsible for a secondary recruitment of other microorganisms, but also sponges, macroalgae and invertebrates (Dang & Lovell, 2000). In addition, multi-layered Extracellular Polymeric Substances (EPSs), which include polysaccharides and also proteins, nucleic acids and lipids, form a base of biofilm structural organization (Brian-Jaisson et al., 2016; Lage & Graça, 2016).

## **2.1. Seaweed surface: as a substratum**

A highly specific association exists between bacterial communities and marine macroalgae. The physiological and biochemical properties of the macroalgae surface predetermine the composition of the adhering microbial communities (Goecke, Labes, Wiese, & Imhoff, 2010). Macroalgae surfaces provide a rich habitat and release large amounts of organic carbon and oxygen into the surrounding environment, providing nutrients for microorganisms, triggering chemotactic behavior of bacteria or inducing microbial colonization and reproduction (Goecke et al., 2010; Steinberg, De Nys, & Kjelleberg, 2002).

### **2.1.1. Cell wall structure**

The cell wall structure of macroalgae is mainly composed of mannans, xylans, cellulose, hemicellulose and sulfated or/and anionic polysaccharides. The cell wall polysaccharides are specific: Chlorophyta (green seaweeds) contain sulfated xyloarabinogalactans, glucuronoxylorhamnans, glucuronoxylorhamnogalactans and ulvans. Phaeophyceae (brown seaweeds) produce alginate and fucose-containing sulfated polysaccharides, whereas Rhodophyta (red seaweeds) contain neutral and sulfated polysaccharides such as agars and carrageenans (Guedes, Amaro, Sousa-Pinto, & Malcata, 2019; Percival, 1979). Within the algal lineages, these polysaccharides are highly diversified in terms of their degree of sulfation, esterification, molecular weight and conformation of sugar residue (Kloareg & Quatrano, 1988; Mabeau & Kloareg, 1987; Popper et al., 2011). Apart from the above mentioned structural polysaccharides, the red, green and brown macroalgae also contain storage polysaccharides such as floridean starch, and, laminarin and mannitol, respectively (Stiger-Pouvreau, Bourgougnon, & Deslandes, 2016).

### **2.1.2. Surface topographical features**

The composition and function of surface consortia are significantly influenced by the chemically mediated interactions and communication between the associated microorganisms and the hosts (Egan, Thomas, & Kjelleberg, 2008). The surface topographical features include a mucilage and sheath demonstrating a gelatinous covering of the macroalgae (Chapman et al., 2014) and it influences the overall epibiosis (Sullivan & Regan, 2011). The microtopography of the interface is a selective fac-

tor in the settlement of macromolecules and microorganisms. (Chapman et al., 2014; Sullivan & Regan, 2011). Therefore, the physical and chemical properties of the substratum play a key role in the attachment and establishment of the initial bacterial colonization. Surface roughness is often speculated to have a deterring role either in attaching or promoting the easy release of fouling organisms (Callow & Callow, 2011). In a study on 'bioinspired synthetic macroalgae' the surface topography of the brown algae, *Saccharina latissima* and *Fucus guiryi*, was replicated on synthetic elastomer and evaluated for its antifouling nature. Together with the chemical defense, the surface topography efficiently reduced the fouling by 40%, where it has been proved that the topography and chemistry work synergistically (Chapman et al., 2014).

## 2.2. Macroalgae defense

Macroalgae control epiphytic microbial colonization by several processes.

### 2.2.1. Removal of surface layers

Under pressure from epibionts, some algal thalli can decompose, generating a kind of desquamation of tissues on the surface. This phenomenon has been observed in several species of brown algae *Ascophyllum nodosum*, *Sargassum muticum*, some Corallinaceae and *Dilsea carnosa*. In the summer where light intensity and temperature are at extremes, physical processes involve regular shedding of biofilm surface cell layers. For example, the Gigartinales *Chondracanthus chamissoi* whitens and decomposes. During this period, many epiphytes and herbivores were observed. Over time, the alga, which is more vulnerable, produces defense molecules.

### 2.2.2. Production of reactive oxygen species

Many seaweed species are known to produce bioactive compounds through their specialized metabolism. The production of ROS or oxidative burst forms an important component of the stress produced in marine organisms. This production is triggered by the contact of the cells with products resulting from the degradation of the algae wall - oligosaccharides (for example oligoguluronates in *Laminaria*; oligo-agars in *Gracilaria*) (da Gama et al., 2014). When a macroalga is colonized by bacteria or herbivores, it receives a signal that will enable it to activate

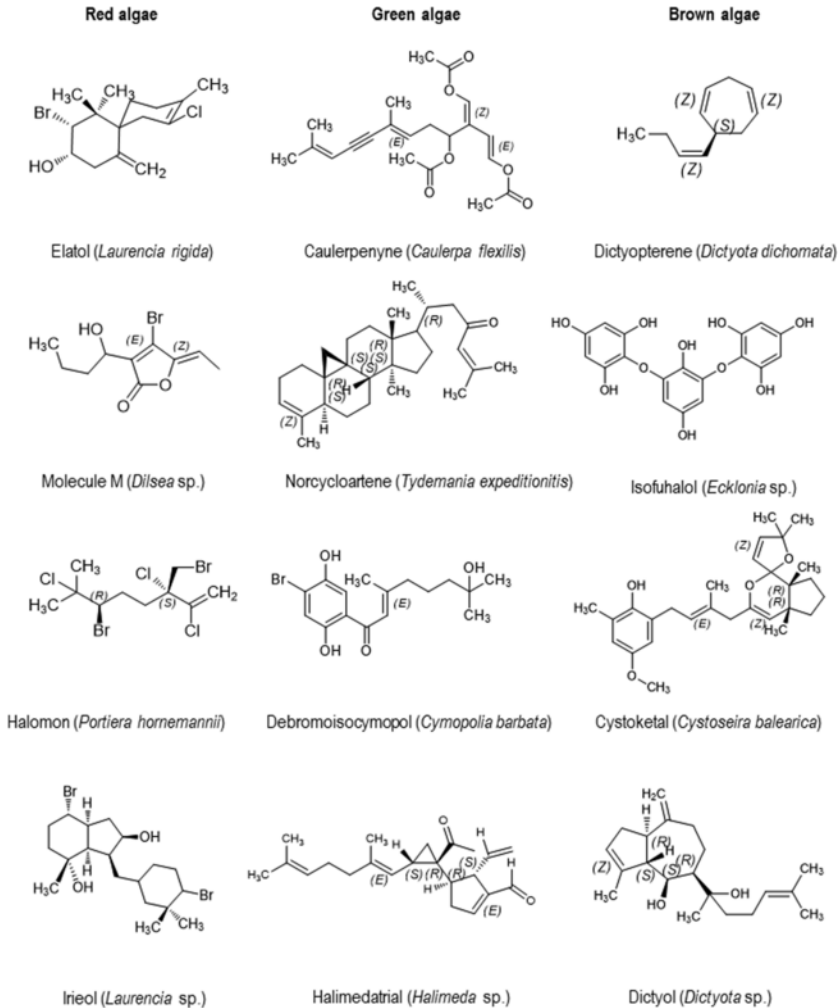
its defense systems. These signals of aggression or Elicitors are defined as chemical compounds that can induce physiological changes in the target organism. In marine macroalgae, they are most often oligosaccharides resulting from the degradation of the algae walls. The presence of Polysaccharides (xyloglucan, laminarin), peptides or proteins or lipid derivatives have also been reported (Potin, Bouarab, Salaün, Pohnert, & Kloareg, 2002).

### 2.2.3. Antimicrobial compounds

Exuded algal bioactive compounds on the surface have antimicrobial properties, which protect the seaweed's surface from grazers, fouling organisms and bacterial pathogens. In different macroalgae species, the defense molecules rise to the surface as an antifouling. They can also be stored in different types of specialized structures, for example, gland cells of *Delisea pulchra*, 'corps en cerise' in *Laurencia* species. Physodes in brown seaweeds present in the thallus cortex are known for their antifouling compound delivery systems (Dahms & Dobretsov, 2017; Dworjanyn, Wright, Paul, de Nys, & Steinberg, 2006; Harizani, Ioannou, & Roussis, 2016). In green algae, the identified compounds mainly belong to di- and sesquiterpenes. They have been relatively little studied (Fig. 1). The diversity and richness of Rhodophyte in terms of secondary metabolites are the most important of all macroalgae with more than 1600 compounds identified. Red macroalgae mainly produce terpenoids and nonterpenoids such as acetogenins. Acetogenins are fatty acid derivatives and are usually halogenated, particularly C-15 acetogenins (Bawakid et al., 2017). Red algae are also characterized by the production of halogenated compounds containing bromine and chlorine. For example, the red alga *D. pulchra* produces an analogous molecule of bacterial N-acyl-homoserine lactones (AHLs) known to inhibit the signal pathways in the Gram-positive and Gram-negative bacteria *Bacillus subtilis* (Ren, Sims, & Wood, 2002), *Escherichia coli* (Ren, Sims, & Wood, 2001) and *Pseudomonas aeruginosa* (Hentzer et al., 2002) these lead to selective colonization of bacteria on thalli (Steinberg & de Nys, 2002).

Another mechanism involved in red algae defense reactions against pathogen attack is the oxidation (enzymatic or non-enzymatic) of fatty acids that results in the production of oxylipins. Sugars (floridoside) from photosynthesis are involved in the defense mechanisms. In brown algae, more than 1200 molecules have been characterized, including ter-





**Fig. 1.** Bioactive compounds produced by the red, green and brown macroalgae.

penes, galactoglycerolipids, fatty acids, phlorotannins and small C11 acetogenins. For example, in *Dictyota ciliolata*, pachydictyol A, dictyol B acetate, dictyodial, and sterols were shown to be present in higher concentrations in older, less palatable tissues than in apical meristem (Cronin & Hay, 1996). Therefore, the different allocation and concentration of the chemical compounds may lead to different microbial communities at the different parts of macroalgae. There is little data about the authenticity and ecological significance of algal chemical defense compounds hav-

ing verified their production, presence and/or release at ecologically realistic concentrations (Kubaneck et al., 2003; Lane et al., 2009; Maximilien et al., 1998; Nyadong et al., 2009; Nylund et al., 2010). In 2010 Lachnit et al. demonstrated that available surface chemical compounds on *Fucus vesiculosus* have different main effects on bacterial colonizers; one group of compounds reduced the overall abundance of epiphytic bacteria non-discriminatively, whereas the other displayed selective and attractant features for bacteria. Consequently, the community patterns and overall densities of epiphytic bacteria are likely to have resulted from some sort of equilibrium between these opposite effects. These authors propose that the effect size will vary over the course of the year due to environmental changes, thus resulting in algal-specific but temporally variable patterns of epibiosis in accordance with previous observations. The results of this study suggest that unidentified compounds and fucoxanthin may be significant drivers of the interaction between the alga and colonizing bacteria. Dimethylsulphopropionate (DMSP) and proline from the surface of *F. vesiculosus* are active against the attachment of five different bacterial strains isolated from the algae (Saha et al., 2012). Further dynamics downstream of the initial colonization by bacteria, such as microorganism–microorganism interactions are expected to add another effective layer that results in spatial heterogeneity of epiphytic bacterial biofilms.



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## 3. MICROBIOME ON THE SURFACE

### 3.1. Bacteria

Descriptive studies of bacteria isolated from the surface of macroalgae were reported as early as 1875 (Johansen, Nielsen, & Sjöholm, 1999). The interest in bacterial populations living in association with macroalgae has increased during recent decades (Goecke et al., 2010). In 2010, Goecke et al. found 107 studies on bacterial communities associated to a total of 148 macroalgae (36 Chlorophyta, 46 Phaeophyceae, 55 Rhodophyta, 12 undetermined algae) within the last 40 years. Bacteria often have a protective role through the production of compounds into the water that prevents the installation of biofilm on the surface. The primary biofilm of bacteria serves as cues for the further settlement of unicellular and multicellular eukaryotes. These cues can be either positive or negative (Rao et al., 2007). The presence of both attractants and antibac-

terial molecules will determine the promoter or inhibitory effect on biofilm establishment, predation deterrence, and germination of an epiphyte spore or metamorphosis of an epibiont invertebrate.

Earlier studies have mainly focused on elucidation of the roles of the epiphytic bacterial communities in the ecophysiology of the host macroalga. However, mutualistic interactions have become a topic of current interest. It is evident from recent studies that a fraction of epiphytic bacterial communities can be categorized as “core microbial species”, suggesting an obligate association. However, the precise composition of microbiomes and their functional partnership with hosts are not fully understood (Singh & Reddy, 2016). Bacterial communities associated with marine macroalgae differ strongly from those of their surrounding seawater, sediment or substrate (Aires, Serrão, & Engelen, 2016; Bengtsson, Sjøtun, & Øvreås, 2010; Bengtsson & Øvreås, 2010). For example, the surface microbiome of *F. vesiculosus* was analyzed comparatively by amplicon sequencing, using seawater as reference, and it was found that the majority of microbial OTUs (relative abundances) were assigned to *Alphaproteobacteria* (64%–68%) and their share in the seawater bacterial community was even higher (84%) (Parrot et al., 2019). Bacterial communities associated to marine macroalgae are not fixed and can change temporally and spatially across seasons, lifespans, life stages and tissue types by biotic and abiotic factors (Aires et al., 2016; Mancuso, D’Hondt, Willems, Airoidi, & De Clerck, 2016; Michelou, Caporaso, Knight, & Palumbi, 2013; Staufenberg, Thiel, Wiese, & Imhoff, 2008). For example, the epibacterial diversity of *Laminaria hyperborea* (*Phaeophyta*) increases with the age/successive colonization of the kelp surface (Bengtsson, Sjøtun, Lanzén, & Øvreås, 2012). Bacterial density and community composition follow the brown seaweed seasonal growth cycle. As most of the biofilm seems to consist of bacteria utilizing carbon produced by the host (Bengtsson & Øvreås, 2010), microbiome dynamics are probably strongly linked to seasonal changes in the kelp metabolome and seawater temperature (Bengtsson et al., 2010). Table 1 illustrates the list of bacteria isolated from the major ‘3’ phyla, red, green and brown, of macroalgae.

Macroalgal growth and morphogenesis are particularly shown to depend on the associated bacterial communities which produce plant growth-promoting substances, quorum sensing signal molecules and several bioactive compounds (Singh & Reddy, 2014). Bacterial biofilms

**TABLE 1** List of bacteria isolated from the '3' major phyla of macroalgae.

Macroalgae	Bacteria isolated	References
<b>Red</b>		
<i>Polysiphonia stricta</i>	<i>Pseudoalteromonas arctica</i> <i>Shewanella basaltis</i>	(Nasrolahi et al., 2012)
<i>Gracilariopsis heteroclada</i>	<i>Vibrio parahaemolyticus</i> ; <i>V. alginolyticus</i>	(Martinez & Padilla, 2016)
<i>Gracilaria blodgettii</i>	<i>Agarilytica rhodophyticola</i>	(Ling, Xia, Liu, Chen, & Du, 2017)
<i>Laurenciae papillosa</i>	<i>Bacillus amyloliquefaciens</i>	(Chakraborty et al., 2017b)
<i>Ahnfeltia tobuchiensis</i>	<i>Polaribacter staleyi</i>	(Nedashkovskaya et al., 2018a)
<i>Tichocarpus crinitus</i>	<i>Aquimarina algiphila</i>	(Nedashkovskaya et al., 2018b)
<i>Iridaea cordata</i>	<i>Streptomyces pratensis</i>	(Alvarado, Huang, Wang, Garrido, & Leiva, 2018)
<i>Gracilaria corticate</i>	<i>Bacillus</i> sp.; <i>Pseudomonas stutzeri</i> ; <i>Vibrio owensii</i>	(Karthick & Mohanraju, 2018)
<i>Mastophora rosea</i>	<i>Vibrio</i> sp.	(Karthick & Mohanraju, 2018)
<i>Gracilaria edulis</i>	<i>Corynebacterium</i> sp. <i>Bacillus megaterium</i> <i>Klebsiella oxytoca</i> <i>Bacillus pasteurii</i> <i>Bacillus cereus</i> <i>Aeromonas</i> sp. <i>Lysinibacillus xylanilyticus</i> <i>Lactobacillus casei</i> <i>Aeromonas hydrophila</i>	(Suvega & Arunkumar, 2019)
Undetermined	<i>Alteromonas macleodii</i>	(Naval & Chandra, 2019)
<i>Kappaphycus alvarezii</i>	<i>Bacillus</i> sp., <i>Vibrio</i> sp.	(Mohammed Riyaz et al. 2019)
<b>Green</b>		
<i>Ulva australis</i>	<i>Pseudoalteromonas tunicate</i> <i>Phaeobacter</i> sp.	(Rao et al. 2007)

TABLE 1 (Continued)

Macroalgae	Bacteria isolated	References
<i>Ulva</i> sp.	<i>Kordia ulvae</i>	(Qi, Huang, Lai, Li, & Shao, 2016)
<i>Ulva fenestrata</i>	<i>Olleya algicola</i>	(Nedashkovskaya, Kim, Zhukova, & Mikhailov, 2017)
<i>Ulva lactuca</i>	<i>Bacillus</i> sp. <i>Shewanella oneidensis</i> <i>Shewanella</i> sp. <i>Pseudoalteromonas</i> sp. <i>Pseudoalteromonas rubra</i> <i>Vibrio</i> sp. <i>Bacillus cereus</i> <i>Pseudomonas pseudoalcaligenes</i> <i>Alcanivorax dieselolei</i>	(Ramya et al., 2017) (Karthick & Mohanraju, 2018)
<i>Monostroma hartioides</i>	<i>S. pratensis</i> ; <i>S. brevispora</i> ; <i>Pseudonocardia adelaidensis</i> ; <i>Agrococcus baldri</i>	(Alvarado et al. 2018)
<b>Brown</b>		
<i>Fucus vesiculosus</i>	<i>Pseudoalteromonas mariniglutinosa</i> <i>Pseudoalteromonas tunicata</i> <i>Shewanella baltica</i> <i>Bacillus foraminis</i>	(Nasrolahi et al. 2012)
<i>Fucus serratus</i>	<i>Ulvibacter litoralis</i> , <i>Photobacterium halotolerans</i>	(Nasrolahi et al. 2012)
<i>Ascophyllum nodosum</i>	<i>Zobellia</i> sp.; <i>Maribacter thermophilus</i> ; <i>Maribacter forsetii</i> ; <i>Cellulophaga baltica</i> ; <i>Cellulophaga geojensis</i> ; <i>Algibacter miyuki</i> ; <i>Vibrio</i> sp.; <i>Shewanella</i> sp.; <i>Paraglaciecola</i> sp.; <i>Colwellia</i> sp.; <i>Pseudoalteromonas</i> sp.; <i>Marinomonas</i> sp.; <i>Cobetia</i> sp.;	(Martin et al. 2015)
<i>Padina tetrastratica</i>	<i>Halolactibacillus alkaliphilus</i>	(Suresh, Renugadevi, Brammavidhya, Iyapparaj, & Anantharaman, 2015)

TABLE 1 (Continued)

Macroalgae	Bacteria isolated	References
<i>Splachnidium rugosum</i>	<i>Vibrio cyclitrophicus</i> ; <i>Vibrio splendidus</i> ; <i>Vibrio comitans</i> ; <i>Vibrio celticus</i> ; <i>Pseudoalteromonas carrageenovora</i> ; <i>Pseudoalteromonas espejiana</i> ; <i>Alteromonas stellipolaris</i> ; <i>Psychromonas arctica</i> ; <i>Pseudomonas poae</i> ; <i>Pseudomonas fluorescens</i> ; <i>Neptumonas naphthovorans</i> ; <i>Cobetia amphilecti</i> ; <i>Shewanella</i> sp.; <i>Sphingomonas</i> sp.; <i>Sulfitobacter</i> sp.; <i>Polaribacter</i> sp.; <i>Bacillus</i> sp.; <i>Staphylococcus saprophyticus</i> .	(Albakosh, Naidoo, Kirby, & Bauer, 2016)
<i>Padina pavonica</i>	<i>Paracoccus</i> sp.; <i>Devosia</i> sp.; <i>Vibrio</i> sp.; <i>Pseudomonas</i> sp.; <i>Pseudomonas putida</i> ; <i>Brevibacterium iodinum</i> ; <i>Staphylococcus</i> sp.; <i>Bacillus pumilus</i> ; <i>Pseudoalteromonas</i> sp.; <i>Acinetobacter</i> sp.; <i>Planomicrobium glaciei</i> ; <i>Erwinia bilingiae</i> .	(Ismail et al. 2016)
<i>Anthophycus longifolius</i>	<i>Bacillus subtilis</i>	(Chakraborty et al., 2017a)
<i>Sargassum myriocystum</i>	<i>Bacillus subtilis</i>	(Chakraborty et al. 2017a)
<i>S. polycystum</i>		(Susilowati, Sabdono, &
<i>S. duplicatum</i>		Widowati, 2015)
<i>S. echinocarpum</i>		
<i>Ecklonia cava</i>	<i>Flavivirga eckloniae</i> ; <i>F. aquimarina</i>	(Lee, Kang, Choe, & Seong, 2017a)
<i>Sargassum fulvellum</i>	<i>Winogradskyella flava</i> <i>Dokdonia lutea</i>	(Lee, Kang, Shin, & Seong, 2017b) (Choi, Kang, Lee, & Seong, 2017)
<i>Adenocystis utricularis</i>	<i>Arthrobacter flavus</i> ; <i>Staphylococcus haemolyticus</i> ; <i>Micrococcus luteus</i> ; <i>Tessaracoccus flavescens</i> ; <i>Pseudarthrobacter oxydans</i>	(Alvarado et al. 2018)

TABLE 1 (Continued)

Macroalgae	Bacteria isolated	References
<i>Fucus serratus</i> L.	<i>Cellulophaga baltica</i> sp. <i>Cellulophaga fucicola</i> sp.	(Johansen, Nielsen, & Sjraholm, 2018)
<i>Turbinaria</i> <i>ornate</i>	<i>Exiguobacterium profundum</i>	(Karthick & Mohanraju, 2018)
<i>Pelvitia</i> <i>canaliculata</i>	<i>Kocuria marina</i>	(Uzair et al. 2018)
<i>Laminaria</i> <i>japonica</i>	<i>Algibacter alginolytica</i> ; <i>Alginococcus</i> <i>marinus</i>	Sun et al., 2016 (Ying et al., 2019)
Undertermined	<i>Gilvimarinus polysaccharolyticus</i>	(Cheng et al. 2015)
Undertermined	<i>Marinirhabdus citrea</i>	(Yang, Oh, Seo, Lee, & Kwon, 2018)

can have a repellent effect, for example, nonviable bacteria tended to repel cyprids when compared to the surfaces without a biofilm, which ultimately prevent heavy fouling on the surface (Nasrolahi, Stratil, Jacob, & Wahl, 2012). Bacterial communities belonging to the phyla *Proteobacteria* and *Firmicutes* are generally the most abundant epiphytic bacteria associated with macroalgal host (Singh & Reddy, 2016). The '71' heterotrophic bacteria isolated from the green alga *Ulva rigida* belong to the four phyla *Proteobacteria*, *Bacteroidetes*, *Firmicutes* and *Actinobacteria* (Ismail et al., 2018). *Marinomonas* sp. and *Bacillus* spp. were observed to have the morphogenesis-inducing ability toward its host macroalgae *Ulva fasciata* (Singh et al., 2011). An in-depth study on the 16s rRNA gene libraries of the bacterial community on the surface of *Ulva australis* and the surrounding water determines the uniqueness of the association. Both the surface and seawater libraries were dominated by *Alphaproteobacteria* and *Bacteroidetes* families, but they were observed to be clearly distinct from each other through clustering into operational taxonomical units (OTUs) (Burke, Thomas, Lewis, Steinberg, & Kjelleberg, 2011). *Pseudoalteromonas tunicata* and *Phaeobacter* sp. in association with the green alga *U. australis* inhibits the common fouling organisms by producing extracellular compounds even at low densities,  $10^2$ – $10^3$  cells  $\text{cm}^{-2}$  and  $10^3$ – $10^4$  cells  $\text{cm}^{-2}$ , respectively (Rao et al., 2007).

The *Roseobacter* species from the surface of a green alga *Ulva mutabilis* exhibits a specific chemotactic affinity to the alga and chemically communicates with the alga as well as with another associated bacterium *Cytophaga* sp. forming a symbiotic tripartite community (Spoerner, Wichard, Bachhuber, Stratmann, & Oertel, 2012). Additionally, some bacterial species produce regulatory compounds resembling cytokinin (from *Roseobacter*, *Sulfitobacter*, and *Halomonas*) and auxin (from *Cytophaga*) that assist in the differentiation of *U. mutabilis* (Spoerner et al., 2012). The epibiotic bacteria associated with the brown alga *F. vesiculosus* tended to repel the cyprids benefitting the host by preventing heavy fouling on its surface (Nasrolahi et al., 2012). Specific functionally active bacterial species (FABS) will serve to improve the health and performance of the associated host by suppressing the growth of pathogens (Singh & Reddy, 2016). Bondoso et al. (2017) hypothesized that specific association of *Planctomycetes* and their macroalgal hosts, such as the brown alga *Fucus spiralis*, the green alga *Ulva* sp. and the red alga *Chondrus crispus*, is likely to be determined by the nutrients provided by the host and the set of sulfatases inherent to the associated *Planctomycetes* species.

In red alga, *Asparagopsis armata*-associated bacteria exhibited a potential antitumor and antibacterial activity. The extract of *Shewanella* sp. ASP 26 showed increased antimicrobial activity against *Bacillus subtilis* and *Staphylococcus aureus* (Horta et al., 2019). Ma, Liu, Yu, Li, and Cao (2009) isolated 192 bacterial strains from the surfaces of seaweeds, of which '63' isolates were shown to inhibit the settlement of algal spores and '62' isolates inhibited larval settlement under laboratory conditions. About '25' heterotrophic algae-associated bacteria from the surfaces of *U. rigida* show antibacterial activity whereas the free-living bacteria from the surrounding seawater did not show such activity (Ismail et al., 2018). Sixty of the '180' strains isolated from different marine macroalgae exhibited antibiotic activity contrary to a series of fouling bacteria and therefore have the potential to control the microbial population on the seaweed's surface either by inhibiting their growth or by influencing the tactic behavior of potentially competing bacteria (Boyd, Adams, & Burgess, 1999).

A broad range of antibacterial activity contra important food pathogens such as *Vibrio parahaemolyticus*, *Vibrio vulnificus* and *Aeromonas hydrophilia* was observed in *Bacillus subtilis* associated

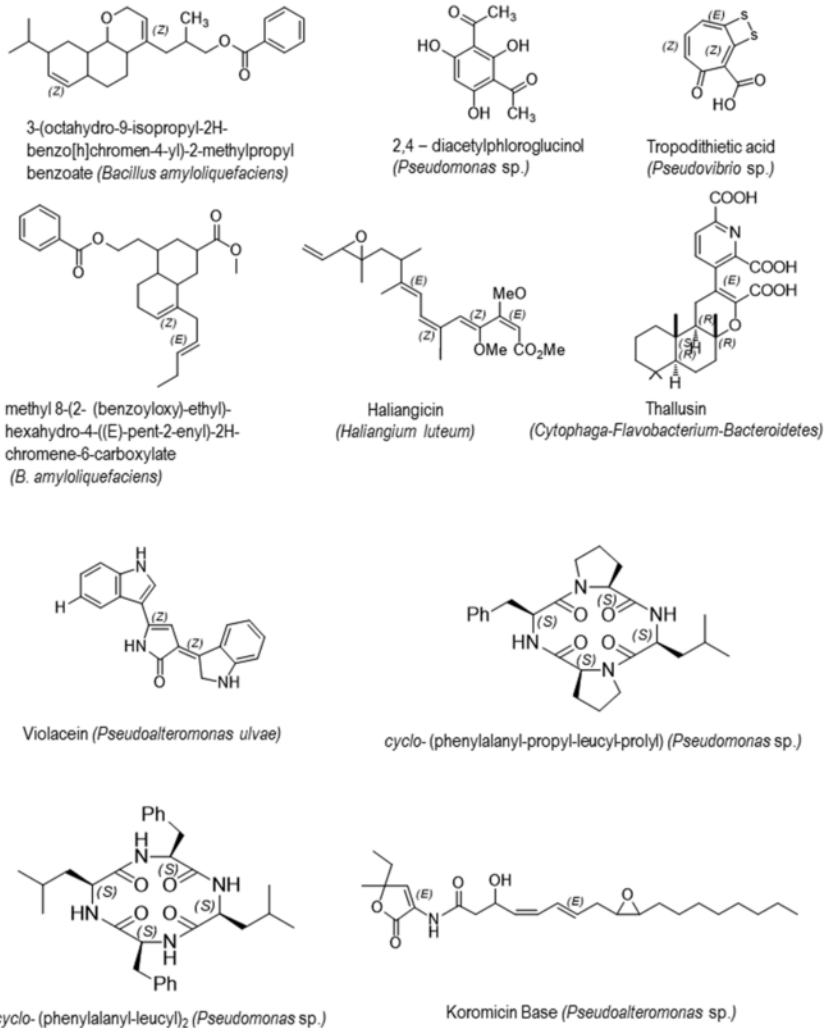


with the brown alga *Anthophycus longifolius* (Chakraborty, Thilakan, Raola, & Joy, 2017). Two polyketides from *Bacillus amyloliquefaciens*, a heterotrophic bacteria associated with the edible red alga, *Laurencia papillosa*, 3-(octahydro-9-isopropyl-2H-benzo[h]chromen-4-yl)-2-methylpropyl benzoate and methyl 8-(2-(benzoyloxy)-ethyl)-hexahydro-4-((E)-pent-2-enyl)-2H-chromene-6-carboxylate exhibits an activity contra to human opportunistic food pathogens (Chakraborty, Thilakan, & Raola, 2017b). Members of the genus *Pseudoalteromonas*, *Bacillus*, *Vibrio* and *Shewanella* isolated from the surface of the green alga, *Ulva lactuca*, showed an antidiatom activity on the pennate diatom, *Cylindrotheca fusiformis* (Kumar, Rao, Thomas, Kjelleberg, & Egan, 2011). Fig. 2 illustrates bioactive metabolites isolated from the macroalgal associated bacteria.

### 3.2. Fungi

The fungal population on the surface of seaweed mainly consists of parasites, saprobes or asymptomatic fungal endosymbionts where the ascomycetes and anamorphic fungi were dominant. Suryanarayanan et al. (2010) observed that among the different red, green and brown macroalgae studied, the brown algae supported a higher diversity of fungal endophytes whereas the green algae had a low diversity with dense colonization. In different seaweeds, members of genera *Acremonium*, *Alternaria*, *Arthrimum*, *Aspergillus*, *Cladosporium*, *Fusarium*, *Geomyces*, *Penicillium* and *Phoma* were the most common fungal endosymbionts (reviewed by Singh et al., 2014). More recently, fungi of the Eurotiomycetes class were visualized for the first time on the surface of the brown alga *F. vesiculosus*, by CARD-FISH imaging (Parrot et al., 2019).

*Aspergillus terreus* isolated from *Halimeda macroloba*, *Gracilaria edulis* and *U. lactuca* produced metabolites which were active against bacteria, algae and fungi (Suryanarayanan et al., 2010). However, in contrast to the well-studied bacteria-algae surface interactions, there is only a little evidence on fungi and their role on macroalgal surfaces (Egan et al., 2013). Most of the studies on macroalgal associated fungi dealt with the endophytic fungi and they are well detailed by Habbu, Warad, Shastri, Madagundi, and Kulkarni (2016) together with their antimicrobial activities. The filamentous fungal community associated with the healthy and the decaying brown alga, *Fucus serratus*, is observed to be different. Such a change in the community structure could be related



**Fig. 2.** Bioactive metabolites from the macroalgal associated bacteria.

to the release of nutrients resulting from tissue breakdown (Zuccaro et al., 2008). A total of '75' fungi were isolated from marine macroalgae of Antarctica and despite the fact that these fungi were isolated from living surfaces most of the isolates are probably saprobic decomposers, which may have an important role in the ecosystem for organic matter recycling (Loque et al., 2010). Table 2 illustrates the list of fungi isolated from the '3' major phyla of macroalgae, such as red, green and brown.

**TABLE 2** List of fungi isolated from the '3' major phyla of macroalgae.

<b>Macroalgae</b>	<b>Fungi isolated</b>	<b>References</b>
<b>Red</b>		
<i>Eucheuma</i> sp.	<i>Aspergillus flavus</i> , <i>A. niger</i>	(Vala, Anand, Bhatt, & Joshi, 2004)
<i>Palmaria decipiens</i>	<i>Metschnikowia australis</i> , <i>Cryptococcus carnescens</i>	(Loque et al. 2010)
<i>Grateloupia lithophila</i>	<i>Cladosporium</i> sp., <i>Chaetomium</i> sp., <i>Nigrospora</i> sp.,	(Murali, 2011)
<i>Halymenia</i> sp.	<i>Emericella nidulans</i> , <i>Chaetomium</i> sp., <i>Emericella nidulans</i> ,	(Murali, 2011)
<i>Portieria hornemonii</i>	<i>Cladosporium</i> sp., <i>Emericella nidulans</i> , <i>Phomopsis</i> sp.	(Murali, 2011)
<i>Jania adherens</i>	<i>Nigrospora</i> sp.	(Murali, 2011)
<i>Bostrychia radicans</i>	<i>Phomopsis longicolla</i>	(Erbert et al. 2012)
<b>Green</b>		
<i>Halimeda maculosa</i>	<i>Aspergillus</i> sp., <i>Aspergillus terreus</i> , <i>Penicillium</i> sp.	(Murali, 2011)
<i>Caulerpa racemosa</i>	<i>Aspergillus niger</i>	(Murali, 2011)
<i>Caulerpa scalpelliformis</i>	<i>Aspergillus niger</i> , <i>Aspergillus terreus</i> , <i>Paecilomyces</i> sp.	(Murali, 2011)
<i>Ulva lactuca</i>	<i>Aspergillus terreus</i> , <i>Chaetomium</i> sp., <i>Cladosporium</i> sp.,	(Murali, 2011)
<i>Chondrus ocellatus</i>	<i>Paraconiothyrium</i> sp.	(Suzuki et al. 2019)
<b>Brown</b>		
<i>Fucus serratus</i>	<i>Lindra</i> , <i>Lulworthia</i> , <i>Engyodontium</i> , <i>Sigmoidea marina</i> , <i>Acremonium fuci</i> .	(Zuccaro et al. 2008)
<i>Desmarestia anceps</i>	<i>Geomyces pannorum</i> , <i>M. australis</i>	(Loque et al. 2010)

TABLE 2 (Continued)

Macroalgae	Fungi isolated	References
<i>Adenocystis utricularis</i>	<i>Antarctomyces psychrotrophicus</i> , <i>G. pannorum</i> , <i>Oidiiodendron</i> sp, <i>Penicillium</i> sp, <i>Phaeosphaeria herpotrichoides</i> , <i>M. australis</i> , <i>Rhodotorula mucilaginosa</i> , <i>Rhodotorula mucilaginosa</i>	(Loque et al. 2010)
<i>Sargassum ilicifolium</i>	<i>Aspergillus terreus</i>	(Murali, 2011)
<i>Turbinaria</i> sp.	<i>Alternaria</i> sp., <i>Aspergillus</i> sp., <i>Colletotrichum</i> sp, <i>Curvularia tuberculata</i> , <i>Drechslera</i> sp., <i>Fusarium</i> sp., <i>Phaeotrichoconis</i> sp., <i>Paecilomyces</i> sp., <i>Nigrospora</i> sp.,	(Murali, 2011)
<i>Stoechospermum marginatum</i>	<i>Alternaria</i> sp.	(Murali, 2011)
<i>Sargassum wightii</i>	<i>Alternaria</i> sp., <i>Aspergillus</i> sp., <i>Cladosporium</i> sp., <i>Curvularia</i> sp., <i>Emericella nidulans</i> , <i>Trichoderma</i> sp., <i>Pestalotiopsis</i> sp., <i>Cladosporium cladosporioides</i>	(Murali, 2011) (Hulikere et al. 2017)
<i>Enteromorpha flexuosa</i>	<i>Penicillium daleae</i>	(Iswarya & Ramesh, 2019)

Seaweed associated-fungi, *Aspergillus* spp. and *Penicillium* were common colonizers and also serve as a potential source of pharmacologically active compounds (Singh et al., 2015). *Aspergillus terreus* from the tissues of *Caulerpa scalpelliformis*, *C. sertularioides*, *G. edulis*, *Sargassum ilicifolium* and *U. lactuca* produced metabolites which have insecticidal activity (Suryanarayanan et al., 2010). *Xylaria* sp. isolated from red alga *Bostrychia tenella* synthesize cytochalasin D, a known antibiotic and antitumor compound (de Felício et al., 2015) whereas *Aspergillus niger* EN-13, isolated from brown alga, *Colpomenia sinuosa*, produces a sphingolipid and their corresponding glycosphingolipid named Asperamides A and B, where compound A exhibits antifungal activity against *Candida albicans* (Zhang et al., 2007) (Fig. 3).

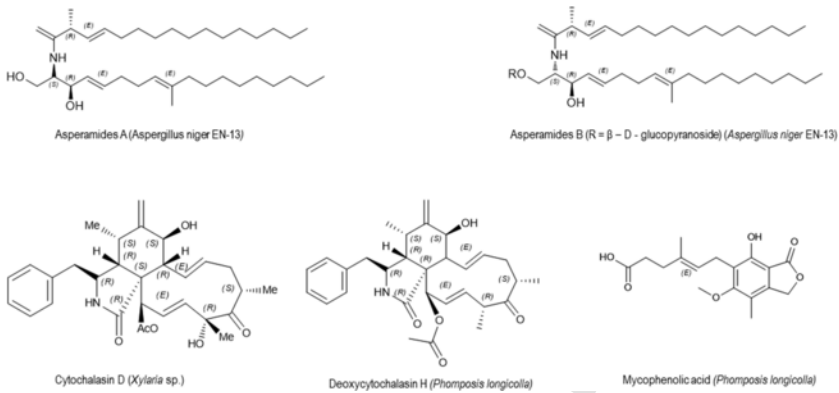


Fig. 3. Bioactive metabolites from the macroalgal associated fungi.

### 3.3. Microalgae

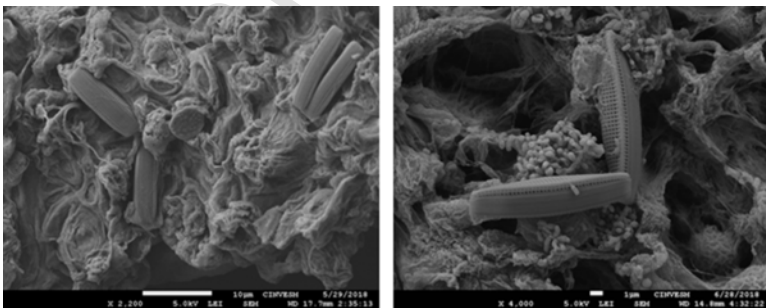
Table 3 illustrates the list of microalgae isolated from different macroalgal species. The epiphytic microalgal community is mostly dominated by benthic diatoms and a few centric species possessing an attached mode of life (Lage & Graça, 2016). As photosynthetic eukaryotes, diatoms can also serve as food for heterotrophic bacteria through specific interactions with growing diatoms as well as colonizing the sinking diatom and decomposing their organic matter. The interactions between diatoms and bacteria are generally confined and invariably, it is observed with *Proteobacteria* and *Bacteroidetes* phyla (Amin, Parker, & Armbrust, 2012). Diatoms release transparent exopolymer particles (TEPs) which are often colonized by bacteria and in response, bacteria produce exopolysaccharides probably to initiate attachment (Amin et al., 2012; Fukao, Kimoto, & Kotani, 2010; Schafer, Abbas, Witte, & Muyzer, 2002). The scanning electron micrographs of the red alga *Halymenia floresii* depict the association of different bacterial phylotypes with the surface attached diatoms (Fig. 4). The abundance and taxonomic composition of the diatoms on the macroalgae are highly affected by the architecture of the macroalgal thallus and its surface characteristics (Totti et al., 2009).

### 3.4. Virus

As ubiquitous components of marine holobionts, viruses are now emerging as pathogens or potential pathogens in various marine organisms including macroalgae (Beattie et al., 2018; Lachnit, Thomas, & Steinberg, 2016). Viruses can have both positive and negative impacts on the holo-

**TABLE 3** List of microalgae isolated from the macroalgae.

Macroalgae	Bacteria isolated	References
<i>Chaetomorpha linum</i>	<i>Leptocylindrus danicus</i> ; <i>Navicula distans</i> ; <i>Nitzschia hungarica</i> ; <i>Thalassionema frauenfeldii</i>	(Al-Harbi, 2017)
<i>Enteromorpha intestinalis</i>	<i>Chaetoceros fragile</i> ; <i>Gyrosigma fasciola</i> ; <i>L. danicus</i> ; <i>N. distans</i> ; <i>N. transitans</i> ; <i>Pleurosigma angulatum</i> ; <i>P. normanii</i>	(Al-Harbi, 2017)
<i>Ulva lactuca</i>	<i>Licmophora flabellata</i> ; <i>L. abbreviata</i> ; <i>P. normanii</i> ; <i>T. frauenfeldii</i>	(Al-Harbi, 2017)
<i>Laminaria</i> sp.	<i>L. danicus</i> ; <i>L. flabellata</i> ; <i>Navicula ramosissima</i> ;	(Al-Harbi, 2017)
<i>Padina fraseri</i>	<i>Cylindrotheca closterium</i> ; <i>Navicula</i> sp.; <i>Nitzschia</i> sp.; <i>Prorocentrum lima</i> ; <i>Cocconeis lineatus</i>	(Al-Harbi, 2017)
<i>Sargassum muticum</i>	<i>N. distans</i> ; <i>N. socialis</i> ; <i>N. vanhoeffeni</i>	(Al-Harbi, 2017)
<i>Turbinaria ornata</i>	<i>Leptocylindrus minimus</i> ; <i>L. danicus</i> ; <i>Bacillaria paxillifer</i> ; <i>N. hungarica</i> ; <i>T. frauenfeldii</i>	(Al-Harbi, 2017)
<i>Ecklonia maxima</i>	<i>Amphora</i> ; <i>Gomphoseptatum</i> ; <i>Navicula</i> , <i>Rhoicosphenia</i>	(Mayombo, Majewska, & Smit, 2019)
<i>Laminaria pallida</i>	<i>Amphora</i> ; <i>Gomphoseptatum</i> ; <i>Navicula</i> , <i>Rhoicosphenia</i>	(Mayombo et al. 2019)

**Fig. 4.** Diatoms embedded on the extracellular matrix of *H. floresii* (left) and associated with the macroalgal surface bacteria (right).

biont which either may spread diseases among hosts or may be a part of the holobiont immune system (Ying et al., 2018). Lachnit et al. (2016) reported the viruses associated with a red macroalga, *D. pulchra*, identify-

ing diverse morphotypes of virus-like particles from icosahedral to bacilliform to coiled pleomorphic as well as bacteriophages. The virome sequencing revealed the presence of a diverse group of dsRNA viruses affiliated to the genus *Totivirus*, known to infect plant pathogenic fungi. Furthermore, a ssRNA virus belonging to the *Picornavirales* order with a close phylogenetic relationship to a pathogenic virus infecting marine diatoms was also identified in association with *D. pulchra*. Viruses have a large potential effect by not only infecting the host but also other microorganisms, like bacteriophages which regulate the bacterial community composition, thus adding a complexity to the holobiont structure (Gachon, Sime-Ngando, Strittmatter, Chambouvet, & Kim, 2010; Ying et al., 2018). Table 4 includes the viruses isolated from different macroalgae.



#### 4. ROLE OF MICROBIOME: MICROBIAL INTERACTIONS AND THEIR HOSTS RESPONSE

The microbiome performs a ‘protective’ role with epibiotic bacteria present on surfaces that release chemicals that prevent biofouling by other organisms (Armstrong, Yan, Boyd, Wright, & Burgess, 2001). Similarly, macroalgal growth and development are shown to depend

**TABLE 4** List of viruses isolated from the macroalgae.

Macroalgae	Viruses	References
<i>Delisea pulchra</i>	<i>Totivirus</i> ; <i>Picornavirales</i>	(Lachnit et al. 2016)
<i>Chondrus crispus</i>	<i>Totivirus-like entities</i>	(Rousvoal, Bouyer, López-Cristoffanini, Boyen, & Collén, 2016)
<i>Ectocarpus siliculosus</i>	<i>Ectocarpus</i> DNA virus	(Lanka, Klein, Ramsperger, Müller, & Knippers, 1993)
<i>Heterosigma akashiwo</i>	<i>Phycodnaviridae</i>	(Nagasaki, Shirai, Tomaru, Nishida, & Pietrokovski, 2005)
<i>Ecklonia radiata</i>	<i>Siphoviridae</i> ; <i>Myoviridae</i> ; <i>Inoviridae</i> ; <i>Podoviridae</i>	(Beattie et al. 2018)
<i>Laminaria</i> sp. and <i>Saccharina</i> sp.	<i>Phaeovirus</i>	(McKeown et al. 2017)

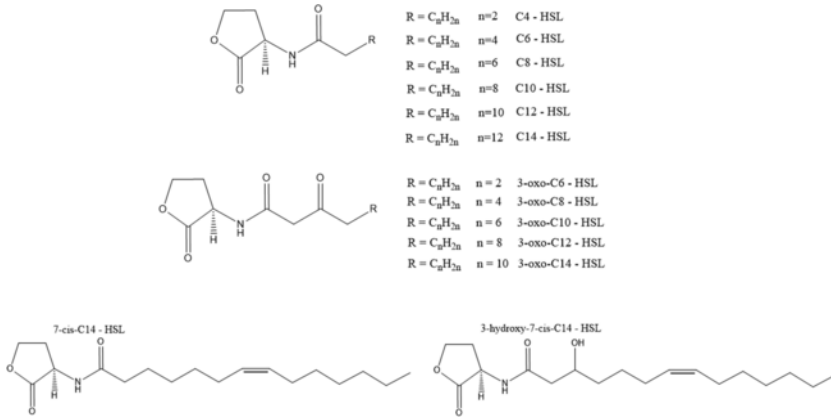
on associated microorganisms, particularly on bacterial communities (Singh & Reddy, 2014; Wichard et al., 2015). With such an obligate association, a fraction of epiphytic bacterial communities can be regarded as 'core microbial species' (Singh & Reddy, 2016). The group of a microbial community which are consistently present on the surface of different individuals of the macroalgae is known as a 'core community' (Burke et al., 2011). The interactions between the macroalgae and the microbiota are extremely diverse (van der Loos, Eriksson, & Falcão Salles, 2019). As the microorganisms in the diverse marine environment are concentrated on microscale patches, their closeness, proximity suggests many potential cell-cell communications (Amin et al., 2012; Azam & Malfatti, 2007). The interactions of macroalgae and bacteria are mainly for nutrient exchange, signal transduction and gene transfer (Kouzuma & Watanabe, 2015).

#### 4.1. Quorum sensing

Quorum Sensing (QS), an essential language of bacteria, is a cell density-dependent communication system that regulates a diverse array of physiological activities such as symbiosis, virulence, competence, conjugation, antibiotic production, motility, sporulation, and biofilm formation. This phenomenon relies on the accumulation of signal molecules in the surrounding environment up to threshold concentrations, at which the target genes are activated (Romero, Martin-Cuadrado, Roca-Rivada, Cabello, & Otero, 2011; Williams, Winzer, Chan, & Cámara, 2007). These QS signals, otherwise known as Auto Inducers (AIs), broadly fall into three categories. Acyl Homoserine Lactones (AHLs) are the major group of auto inducer signals in gram-negative bacteria (Di Cagno, De Angelis, Calasso, & Gobetti, 2011) (Fig. 5); Auto Inducer Peptides (AIPs) are the major auto inducers in gram-positive bacteria (Thoendel, Kavanaugh, Flack, & Horswill, 2011; Zhang & Li, 2016), whereas, regardless of gram-positive or gram-negative bacteria, Auto inducer 2 (AI 2) known as universal language, is used for intra- and inter-species communication (Lowery, Dickerson, & Janda, 2008). Besides, there have been cyclic dipeptides, bradyoxetin, AI -3 in *E. coli* and diffusible signal factors, documented in different QS systems (Gonzalez & Keshavan, 2006).

Apart from defending the attached basibiont the surface-associated bacteria also assist the host in growth and morphogenesis. AHLs, N-





**Fig. 5.** Different homoserine lactones with differing chain length produced by the bacteria.

acyl homoserine lactones, produced by the macroalgae-associated bacteria facilitates the settlement of zoospores in *Ulva spp.* (Joint et al., 2002; Singh et al., 2015; Williams, 2007). The bacterial isolates, *Shewanella algae*, *P. aeruginosa*, *Photobacterium sp.*, *P. lutimaris*, *Vibrio gallicus*, *Vibrio fluvialis*, *V. parahaemolyticus*, associated with green macroalgae *Ulva* (*U. fasciata* and *U. lactuca*) and red macroalgae *Gracilaria* (*G. corticata* and *Gracilaria dura*), induced carpospore liberation from cyto-carps of *G. dura* by producing different AHLs (Singh et al., 2015). The AHLs produced by *Acrochaetium sp.* control spore release in the red alga, *G. chilensis* whereas its production was inhibited in the brown alga, *C. sinuosa* (Kanagasabhpathy, Yamazaki, Ishida, Sasaki, & Nagata, 2009; Weinberger et al., 2007). The motile zoospores of *Enteromorpha* exploit the diffusible signal molecules produced by bacterial biofilms for temporary settlement on the surface (Joint et al., 2002).

QS-mediated interactions widely influence algal-bacterial symbiotic relationships, which in turn determine community organization, population structure, and ecosystem functioning (Zhou, Lyu, Richlen, Anderson, & Cai, 2016). In *U. mutabilis* the chemical communication signals between the associated bacteria, *Roseobacter* and *Cytophaga*, up-regulate the growth and thallus morphogenesis (Spoerner et al., 2012). A chemical elicitor protein, probably a quorum signal N-acyl homoserine lactone produced by a gram-positive probiotic *Lysinibacillus xylanilyticus* associated with a red alga *G. edulis* promotes the growth of the host (Suvega & Arunkumar, 2019).

## 4.2. Quorum quenching

Quorum Quenching (QQ), is defined as any interference on the QS communication system either by enzymatic degradation of the AHLs, or by production of inhibitors or antagonists of signal reception. QQ strategy plays an important role in preventing microbial disease and affecting beneficial bacteria (Chen, Gao, Chen, Yu, & Li, 2013). Many algae use defense strategies to protect themselves from the potentially opportunistic pathogens associated with them by altering their QS communication systems i.e. quenching their signal molecules.

The first QS inhibitory activity was reported by the halogenated furanones from the red alga *D. pulchra* which exhibited antibiofilm activity against *Bacillus subtilis*, *P. aeruginosa* and *E. coli*, and these compounds were released at the surface at concentrations capable of inhibition (Givskov et al., 1996; Ren et al., 2002, 2001; Steinberg & de Nys, 2002). In particular the brominated furanones significantly inhibited the settlement of cyprid larvae of *Balanus amphitrite* (de Nys et al., 1995). A number of halogenated furanones from this alga antagonize the bacterial AHLs and interfere with their associated biological activity, such as competitively inhibiting swarming motility (Givskov et al., 1996). A mixture of relatively less lipophilic compounds, floridoside, betonicine and isethionic acid, isolated from the red alga *Ahnfeltiopsis flabelliformis* was observed to inhibit the exogenous QS signaling molecule, N-octanoyl-DL-homoserine lactone (OHL), in the quorum-sensing inhibition assay (Kim, Kim, Seo, & Park, 2007). The methanolic extract of the red alga, *Asparagopsis taxiformis*, showed quorum sensing inhibitory activity against the reporter strain, *Chromobacterium violaceum* CV026 (Jha, Kavita, Westphal, Hartmann, & Schmitt-Kopplin, 2013) whereas the polar extracts of the green alga *U. fasciata* and *Codium* sp. exhibited QS inhibitory activity on *C. violaceum* CV017 (Batista, Carvalho, Costa, Coutinho, & Dobretsov, 2014). In the brown alga *Laminaria digitata*, QQ activity was demonstrated by the inactivation of AHLs based on the enzymatic production of the oxidized halogen HOBr which reacts specifically with 3-oxo-acyl HSLs (Borchardt et al., 2001; Romero et al., 2011). The polar and non-polar extracts of the different brown algae, *Sargassum* spp. *S. vulgare*, *S. furcatum*, showed anti-quorum sensing activity on the reporter strain, *C. violaceum* CV017 (Batista et al., 2014);

Carvalho, Batista, Dobretsov, & Coutinho, 2017; Schwartz, Dobretsov, Rohde, & Schupp, 2017).

By interfering with the AHL signaling of *Vibrio anguillarum*, the settlement of *Enteromorpha*, an important fouling organism, can be prevented (Joint et al., 2002). In aquaculture systems, several algal species were used for controlling pathogenic bacteria by disrupting the quorum sensing communication between them, for example, *Vibrio harveyi* (Natrah, Bossier, Sorgeloos, Yusoff, & Defoirdt, 2014; Ramanan, Kim, Cho, Oh, & Kim, 2016). The halogenated furanones of *D. pulchra* protect both shrimp and fish from vibriosis by interfering with their AHL signaling system (Rasch et al., 2004; Torres et al., 2019). A QS antagonist, (5Z)-4-bromo-5-(bromomethylene)-3-butyl-2(5H)-furanone (furanone) from the *D. pulchra* was found to inhibit the formation of the siderophore produced by *Pseudomonas putida* and *P. aeruginosa* (Ren, Zuo, & Wood, 2005). QQ is a promising approach for very effective next-generation antibacterial drugs which block the QS-mediated pathogenic infection by interfering with the bacterial communication (Chen et al., 2013).

### 4.3. Positive effects: symbiotism

There are many beneficial functions for the macroalgal host, for example, normal growth, morphological development, spore germination and nitrogen fixation activity. This is despite the low average microbial density ( $10^5$  to  $10^6$  cells per gram of seawater), the closeness, proximity and the heterogeneous distribution that suggest their interaction is across multiple spatial scales (Amin et al., 2012). Generally, the associated microorganisms were assumed to use the readily available range of organic carbon sources produced by the macroalgae in the form of complex diversified polysaccharides (Martin, Portetelle, Michel, & Vandenbol, 2014). The microbial metabolites produced by these symbiotic microorganisms help in chemical defenses of the macroalgae and its biological interactions with foulers and pathogens (Chakraborty et al., 2017a; Wahl et al., 2012). In such a microhabitat, the macroalgae supply bacteria with oxygen and fixed carbon, and the bacteria supply  $\text{CO}_2$ , minerals, vitamins and growth factors. The microbial community on the surface of the macroalgae was mainly formed by bacteria but also included different eukaryotes in a ratio of 640:4:1 of bacteria:diatoms: flagellates (Lage & Graça, 2016; Railkin, 2003).

Epiphytic bacteria are known to maintain the health of the host. Several algal species need specific vitamins for their growth and bacteria may be partly responsible for the production of these substances (Villarreal-Gómez, Soria-Mercado, Guerra-Rivas, & Ayala-Sánchez, 2010). Conversely, bacterial colonization could be especially rapid if the surface is a potential source of nutrients, such as polysaccharides in exudates of seaweeds that may serve as a source of carbon for heterotrophic bacteria living on the surface. For example, Kelp exudates could shape bacterial community composition, and create communities that are kelp-specific rather than randomly assembled from the surrounding seawater (Collen & Davison, 2001; Michelou et al., 2013). Bacteria may degrade algal polysaccharides such as for fucoidan (Nedashkovskaia et al., 2002) or alginates (Brown, Preston, & Ingram, 1991; Preston, Romeo, & Bromley, 1986).

An overarching clade of bacteria such as *Proteobacteria* and *Bacteroidetes* are more likely to be associated with the green alga and furthermore, they are functionally equipped to be associated with them (Ramanan et al., 2015, 2016). The temperate green alga *U. lactuca* relies on the defense provided by the microbial community on its surface to regulate the fouling by colonizers (Kumar et al., 2011) and ‘73’ different bacterial strains were isolated from the surfaces of *U. lactuca*, *U. pertusa* and *Enteromorpha* sp. (Ma et al., 2009). In the green alga, *U. rigida* ‘71’ bacterial phylotypes were isolated from its surface which belongs to four phyla: *Proteobacteria*, *Bacteroidetes*, *Firmicutes* and *Actinobacteria* (Ismail et al., 2018). Different studies showed that induction of cell divisions, differentiation, wall formation, and normal morphogenesis in green algae belonging to Ulvophyceae depend on bacterial compounds (Grueneberg, Engelen, Costa, & Wichard, 2016; Matsuo, Imagawa, Nishizawa, & Shizuri, 2005; Wichard, 2015). *Pseudoalteromonas ulvae* and *P. tunicata* isolated from the surface of the green seaweed *U. lactuca* have shown the ability to reduce the adhesion of colonizing organisms and inhibit the germination of spores of this alga. This result was also observed in the red algae *Polysiphonia* sp. in the presence of *P. tunicata*. *Ulva* spores can be attracted by the emission of QS molecules from biofilms dominated by *Pseudoalteromonas*. In other species, spore germination may be inhibited by the presence of *P. tunicata*. *U. australis* is colonized by a very poorly diversified microflora, dominated by *Roseobacter gallaeciensis*, which facilitates the selective establish-

ment of the bacterium *P. tunicata*. The two bacteria use different strategies. *R. gallaeciensis* invades and disintegrates the biofilms of competing bacteria, with the exception of *P. tunicata*. *P. tunicata* takes advantage of its “immunity” to proliferate in the face of competition that it cannot manage alone and then forms spatially separated microcolonies. These bacterial behaviors on the surface of *U. australis* allow the algae to have an inexpensive metabolic control of the bacterial biofilm.

The red alga *Agarophyton vermiculophyllum* chemically ‘gardens’ and recruits protective epibacterial strains in order to strengthen its disease resistance against potentially pathogenic microbes (Saha & Weinberger, 2019). Twenty one phenotypically different bacterial strains were isolated from the red alga *A. armata* which belong to seven different genera: *Vibrio*, *Staphylococcus*, *Bacillus*, *Cobetia*, *Photobacterium*, *Shewanella* and *Alteromonadaceae* (Horta et al., 2019). Ma et al. (2009) isolated ‘88’ bacterial strains from the surfaces of the red algae: *Chondrus ocellatus*, *Dumontia simplex*, *Grateloupia filicina*, *Halymenia sinensis* and *Porphyra* sp.

A study by Ji, Zhang, Wang, and Zhao (2017) suggested a complementary and mutualistic relationship between the female gametophyte of the Brown seaweed *Saccharina japonica* and its microbiome, in which bacteria seem to benefit from seaweed polysaccharides, and the kelp profits from enhanced growth and nutrient uptake by bacterial bioactive compounds such as vitamins and hormones. Analysis of gene functions within this kelp epimicrobiome was mainly symbiosis-associated, indicating that selective pressures shape these microbiomes to sustain a mutual benefit for both kelp and bacteria (Ji et al., 2017). *F. vesiculosus* L. is recognized as an important habitat-forming macroalga and could be able to produce secondary metabolites that directly act on the invertebrate larvae to prevent fouling (Kersen, Kotta, Bučas, Kolesova, & Değere, 2011; Lachnit, Wahl, & Harder, 2010). Several species of marine bacteria have been isolated from brown algae such as the spot-wounded fronds of *Laminaria japonica* (Sawabe et al., 2000), the surface of *F. serratus* (Johansen et al., 1999; Lachnit et al., 2009) and from the rotten thallus of *Fucus evanescens* (Ivanova et al., 2004), *Undaria pinnatifida* (Lee, Jung, & Lee, 2006), *Padina arborescens*, *Padina pavonica*, *P. tetrastromatica* (Ismail et al., 2016), *Macrocystis pyrifera* (Michelou et al., 2013), *Ecklonia radiata* (Qiu et al., 2019), *Taonia otamaria* (Othmani, Briand, Ayé, Molmeret, & Culioli, 2016). Around ‘18’ different bacteria were iso-

lated from the surfaces of two different brown algae, *Sargassum thunbergii* and *Sargassum* sp. (Ma et al., 2009). Such a complex microbiome on the surface of macroalgae is regarded as an indirect defense mechanism which may strengthen the direct antifouling defense mechanism of the host against any macrofoulers (Nasrolahi et al., 2012).

#### 4.4. Negative effects: pathogenism

Any disturbance and disruption of the mutualistic association between host and microbiota are regarded as an 'Holobiont break-up' which can be caused by environmental stress (Ying et al., 2018). Such disturbances are widely caused by spatial and temporal effects. The spatial and temporal shifts of seaweed associated microbiota are induced by the changing environmental conditions and seaweed physiology. Such shifts may result in potential consequences provoked by the structural, functional and behavioral changes in the host posing a challenge for its fitness (Serebryakova, Aires, Viard, Serrão, & Engelen, 2018). This shifts the symbiotic relationship of the microbiota to a potential pathogenic relationship with its associated hosts. The interplay between temperature, the algal chemical defense mechanism and bacterial virulence demonstrates a complex environmental change impact on an ecosystem (Case et al., 2011). Though the epibacterial community structures on the surface of macroalgae are host-specific, they are highly prone to spatial and temporal variation (Wu, Liu, Zhang, & Xiao, 2014). A shift in the microbiome from a stable state to a disturbed state where the colonizers may become opportunist pathogens when the host system is stressed by abiotic or biotic challenges is referred to as 'dysbiosis' (Minich et al., 2018).

Pathogenic bacteria can cause severe degradation of algal host cells or even lead to seaweed mortality, causing major financial losses for seaweed mariculture every year (Correa, Flores, & Sanchez, 1993; Goecke et al., 2010; Vairappan et al., 2008). Also, biofouling forms a permanent threat to macroalgae as bacterial biofilms increase the hydrodynamic drag on their host and enhance the attachment of other fouling organisms and grazers. Biofilms may also compete for nutrients, inhibit gaseous exchange, or block light essential for photosynthesis.

Microbial colonization can lead to the degradation of algal tissue, decreased photosynthesis and gas and nutrient exchange and ultimately disease. Marine macroalgal diseases have been recognized for a long time, but identifying the causative agents and distinguishing them from

other opportunistic bacteria is still an obstacle for describing the virulence mechanism (Egan et al., 2013). Macroalgae are under constant colonization pressure from the millions of microorganisms within the surrounding seawater, some of which are potential pathogens. The primary biofilm undergoes a transition to a much more complex community which eventually ends in fouling on the surface (Bhadury & Wright, 2004). All such biofouling communities vary spatially and temporally (Fitridge, Dempster, Guenther, & de Nys, 2012). Due to the effects of environmental change on host organisms and their pathogens, temporal-mediated diseases can have severe consequences for marine macroalgal ecosystems (Campbell, Harder, Nielsen, Kjelleberg, & Steinberg, 2011).

#### 4.4.1. *Spatial effects*

The close spatial proximity of surface-associated microorganisms on macroalgae operates and controls specific intercellular interactions (Egan et al., 2008). The spatial distribution and the abundance of the epiphytes are largely determined by several abiotic and biotic factors which ultimately leads to uncontrolled growth (Kersen et al., 2011; Kotta, Paalme, Püss, Herkül, & Kotta, 2008; Kotta & Witman, 2009; Nylund & Pavia, 2005). Spatial variability of the epiphytic communities varies both on the large and small scale (Fitridge et al., 2012). The protective effects of the microbiome on the surface were affected by severe settlement pressure and stressful temperatures as observed in *F. vesiculosus* (Nasrolahi et al., 2012), in which the composition and dominance were significantly influenced by wave exposure and frond segment (Kersen et al., 2011). Also, reduced light conditions due to the uncontrolled colonization of the surface have detrimental effects on the growth of the macroalgae (Rohde et al., 2008). The occurrence and richness of the epiphytes were observed to be specific and different, according to the different parts of the host macroalgae (Kersen et al., 2011). The spatial distribution of epibiotic organisms is determined by their ability to tolerate desiccation during low tides (Molina-Montenegro et al., 2005). Multiple opportunistic pathogens, *Alteromonas* sp. BL110, *Aquimarina* sp. AD1 and BL5 and *Agarivorans* sp. BL7 rather than the previously identified *Nautella* R11, cause bleaching disease in a temperate red alga *D. pulchra* with loss of its photosynthetic pigments followed by tissue necrosis and death. Multiple opportunistic pathogens are involved in bleaching disease in *D. pulchra* (Campbell et al., 2011; Case et al., 2011; Fernandes et al.,

2011; Gonzalez & Keshavan, 2006; Kumar, Zozaya-Valdes, Kjelleberg, Thomas, & Egan, 2016).

#### 4.4.2. Temporal effects

The temporal variation of the macroalgal associated microbiome may be affected by biotic factors such as algal growth, exudation of macroalgal metabolites, the composition of the microbial community in the surrounding seawater and abiotic factors like temperature, wave action, light conditions and nutrient levels in seawater (Bengtsson et al., 2010). Different seasons affect the temporal variations of macroalgal surface-associated bacterial communities (Singh et al., 2015). As a result of climate change, environmental stress can render macroalgae susceptible to the presence of opportunistic pathogens which are otherwise commensal to them, but can still take advantage of the weakened host and this results in disease outbreak (Egan et al., 2014). As most of the biofilm seems to consist of bacteria utilizing carbon produced by the host (Bengtsson & Øvreås, 2010), microbiome dynamics are probably strongly linked to seasonal changes in the kelp metabolome and seawater temperature (Bengtsson et al., 2010).

The temporal shifts of bacterial communities associated with the brown alga *S. muticum* were reflected in a significant abundance of unidentified *Rhodobacterales* and *Laktonella* in September–March and the substantial prevalence of unidentified *Pirellulales* in the summer. Such changes were related to the temporally changing algal exudates (Serebryakova et al., 2018). In another brown alga *L. hyperborea*, the substratum and seawater temperature manifested a variation in their associated microbiome where *Planctomycetes* and *Alphaproteobacteria* were frequently detected throughout the year and *Verrucomicrobia*, *Cyanobacteria*, *Gammaproteobacteria*, *Betaproteobacteria*, and *Bacteroidetes* were more sporadically detected (Bengtsson et al., 2010). The kelp microbiome was most influenced by an elevated temperature exhibiting a reduction in the dominant kelp-associated Alteromonadales, which negatively affects its growth (Minich et al., 2018). Any temporal variations in the primary biofilm will cause major temporal changes in the marine invertebrate populations, particularly, seasonality (Fitridge et al., 2012).





## 5. FUTURE PERSPECTIVES

Increased physical disturbances and stress, resulting from changing environmental conditions, are known to affect the macroalgae-associated microbial composition (directly or via its physiological responses) and cause its structural, functional or behavioral changes. In the marine environment, changing climatic conditions such as ocean warming and acidification can have direct physiological effects on the marine-habitat forming macroalgal species, which sequentially, can have negative impacts on the associated microbial communities. The microbiome of the brown alga, *E. radiata*, was affected by warming, followed by acidification which resulted in disease-like symptoms in the host (Qiu et al., 2019). The characteristic 'core' microbial community was replaced by taxonomically diverse microbial communities following the host's stress (Marzinelli et al., 2015). Case et al. (2011) showed that temperate marine macroalga, *D. pulchra*, has become more susceptible to the temperature-enhanced bacterial virulence of *Ruegeria* sp. R11 as a result of high-water temperatures or increased solar radiation. This also affects the production or delivery of furanones potentially leading to *in situ* bleaching (Case et al., 2011). Ice-ice disease in the red alga *Euclima/Kappaphycus* is still a major problem in this seaweed cultivation where the changes in extreme environmental conditions make the alga susceptible to the infection of *Vibrio* sp. (Irmawati & Sudirjo, 2017).

Bioactive metabolites of macroalgae surface-associated bacteria open up a new approach as a novel source of therapeutic molecules. For instance, *A. armata*-associated bacteria revealed to be a potential source of compounds with antitumor and antibacterial activity (Horta et al., 2019). Marine bacteria can be a vast source of new antimicrobial molecules and antibiofilm molecules with a wide range of applications in human health and Industry (Desriac et al., 2018). In the future, beneficial bacteria identified from healthy seaweed holobionts could be applied to diseased plantlets in order to suppress the growth of detrimental ones and/or to prevent disease outbreaks in aquaculture settings. In addition to bacteria, these macroalgae frequently host endophytic fungi that may have protective functions for the algae (Dittami et al., 2019). Thus, metabolites of these bacteria will provide a new possibility of disease management in aquaculture systems.

The surface-associated microbiome of macroalgae is phylogenetically diverse and ecologically important. Thus, assessing the microbial functions and interactions has emerged as a critical need in macroalgal research. Massive sequencing of the 16S rRNA gene and using a metagenomic approach have been the main tools to explore these aspects. However, the complete understanding of the relationships between host and microorganisms, as well as the dynamics of the symbiotic community, probably requires the generation of comprehensive insights with another novel integrative “omics” approach, such as single-cell sequencing, metagenome binning, GeoChip, RNA-Seq, etc. To characterize the interactions of organisms with their environment, environmental metabolomics shall be further explored in this area (Bundy, Davey, & Viant, 2009). Bioactive compounds from macroalgae and its associated microbiome may provide candidates with a high-efficiency and have broad implications in disease control. Concentration and quantity are the two main challenges to be addressed here. Different biotechnological tools should be developed for the isolation and identification of these compounds even at lesser concentrations, which again are the biggest challenges in this field.

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