

## Seaweeds Epibionts: Biodiversity and Potential Bioactivities

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In the recent years pathogenic bacteria resistant to multiple drugs have become a worldwide emergence both in terrestrial and aquatic ecosystems. The antibiotics produced by several marine organisms salt-stable make them more suitable to be used in the control of fish or shellfish pathogens in marine ecosystems where antibiotic efficacy reduction is due to high salt conditions [1].

The cell extracts and active constituents of various seaweeds have been shown to have antibacterial activities *in vitro* against Gram-positive and Gram-negative bacteria and wide range of their activities were related to algae microbial epibionts [2;3].

Thus, epibiotic bacteria from seaweed surfaces are receiving an increasing attention, since they play an important role for both human and animal health and should constitute several sources of bioactive substances.

In our investigations on bacterial communities of some green, red and brown algae, we revealed the high diversity and species specificities of bacterial communities associated with several seaweeds species and revealed their antibiotic activities against several microbial pathogens. Most of these epibionts produce biologically active compounds that may play a protective role to their host and must be taken in account for exploring bioactive potential of seaweeds.

The present work is a bibliographic review of epibiotic bacteria of seaweeds, bio-producing species identified and their bioactive metabolites that can be used with special interest in the pharmaceutical industry.

**Keywords** sea weeds; bacteria; bioactive, metabolite.

### 1. Introduction

The available varieties of marine macroalgae are commonly referred to as “seaweeds” with 221 species belonging to 32 Chlorophyta (green algae), 64 Phaeophyta (brown algae) and 125 Rhodophyta (red algae) and industry uses 7.5-8 millions metric tonnes of wet seaweeds annually, either from wild or cultivated crop for multi purpose uses in pharmaceutical industries, agriculture fertilizer, feed for aquaculture or human food additives which successfully conquered the market on account to the consumer preference of healthy food [1,2,3, 4].

In this context, several compounds from seaweeds [5] including carotenoids, polyphenols [6] as well as other antioxidant pigments [7] and polyunsaturated fatty acids [8] were exploited as functional ingredients. Recent studies showed that marine macroalgae represent main source of several structurally novel secondary metabolites with promising area of functional ingredients studies [9,10,11].

Macroalgae as many marine organisms, often carry significantly less macro and microepibionts on their thalli compared to co-occurring biofilms on inanimate substrata [12, 13]. Therefore, it has been assumed that macroalgae defend themselves against bacterial fouling by production of secondary metabolites that prevent attachment and growth of ubiquitous planktonic bacterial colonizers [14,15,16,17,18,19,20,21,22,23,24].

The delivery mechanisms of secondary metabolites to the algal tissue surface and into the surrounding water as well as their ecologically relevant effects on either planktonic or algal surface-bound bacteria are poorly understood so far [25] and such observations suggested specific relationships between hosts and their epi- and/or endobiotic bacteria [26]. Bioactive compounds from seaweeds have shown antimicrobial action against a number of gram positive and negative bacteria [27, 28,29]. The difference in the inhibitory action on the bacterial strains could be due to differences in the cell membrane of gram positive and negative bacteria. The compounds responsible for antimicrobial activity of seaweeds are terpenes, phenolic or lipophilic in nature. Phlorotannins extracted from *E. kurome*, *E. cava* and *F. vesiculosus* have been reported to have antibacterial activities against positive and negative Gram bacteria, suggesting a potential use as natural preservatives in the food industry or as antibacterial drugs [30, 31].

Besides antimicrobial effects of secondary metabolites emanating from the host, recent studies have increasingly demonstrated that epibiotic bacteria associated with the algae deter growth and attachment of co-occurring bacterial species or new epibiotic colonizers competing for the same niche as well-investigated for *Pseudoalteromonas tunicata*, which has been isolated from a tunicate and a green macroalga. *P. tunicata* has been found to produce at least five extracellular compounds that inhibit settlement of invertebrate larvae and algal spores, growth of other species of bacteria and fungi, and surface colonization by diatoms [32, 33, 34]. These studies well demonstrated how epibiotic bacteria growing on the surfaces of marine algae live in a highly competitive environment where space and access to nutrients are limited [35, 36,37,38, 39,40, 41].

Previously the detection and characterization of marine epibiotic bacteria bioactives have been limited by a number of obstacles, such as unsuitable culture conditions, laborious purification processes, and a lack of de-replication. Nowadays, many of these limitations are being overcome due to improved microbial cultivation techniques, microbial (meta-genomic analysis and novel sensitive analytical tools for structural elucidation [41].

After nearly a decade, metabolomics begun to acquire some credence in analytical bioresearch but though suggested comprehensive detection, the number of identifiable metabolites is currently limited even though multiple measurement technologies (mass spectrometry (MS) or nuclear magnetic resonance (NMR)) are combined.

Through available data, the list of seaweeds epibionts summarize more than one hundred species almost displaying bioactivities against several microbial bacteria and fungi. Geographical repartition data of these epibionts indicated Mediterranean availability and local rich diversity interfering with climatic changes and locations. The present review discusses the importance of seaweeds bacterial epibionts exploring metabolomic data available for most potentially rich bioactive species, and highlights the significance of considering chemical ecology and environmental data to understand marine microorganism-host associations for the targeted isolates and bioactive producing microorganisms.

## 2. Seaweeds bacterial epibionts and bioactivities

Epibiosis is a typical aquatic phenomenon where the distinctive role of water as a food vector for sessile organisms represent the main reason of surface attachment, fouling and hence epibiotic associations predominate in aquatic environments and causes a variety of beneficial effects to the basibiont, such as the induction of morphogenesis in macroalgae by symbiotic bacteria [42, 43] as the interaction between macroalgae and nitrogen-fixing bacteria [44] and the protection of seaweed surfaces from bacterial colonizers by associated bacteria [45].

To successfully compete in biofilms, many representatives of bacterial genus *Pseudoalteromonas* release anti-bacterial products that aid the cells in the colonization of host surfaces. Through the production of agarases, toxins, bacteriolytic substances and other enzymes, bacterial cells are assisted in their competition for nutrients and space as well as in their protection against predators grazing on surfaces [32]. The antifouling mechanisms of *Ulva reticulata* (Chlorophyta) e.g. rely not only on compounds released from the alga itself but also on those produced by epibiotic bacteria, such as a thallus-associated *Vibrio sp.* [34, 38].

Furthermore, chemically driven interactions are very important in the establishment of cross-relationships between marine surface-associated microorganisms and their eukaryotic hosts since it has been demonstrated that microorganisms produce antimicrobial compounds that may protect the host surface against colonization in return for a nutrient rich environment [41]. Epibiotic bacteria are fast colonizers, highly adaptive and capable of rapid metabolism of host exudates and therefore play a key role in the colonization and biofouling process e.g. on macroalgae [46].

### 2.1. Seaweeds epibionts biodiversity

In aquatic environments bacteria have a strong affinity for a variety of substrates including animal and plant surfaces, but information about bacterial biofilms on aquatic macrophytes still scarce [47,48]. Almost bacterial communities are heterotrophic types which largely contribute to the overall nutrient cycling and interact in various ways by relocating nutrients, converting degradation products, restoring growth forms of macroalgae, facilitating spore attachment, and preventing grazing [49].

Previously, cultivation-dependent techniques were used first to study such microbial communities [50] and recently, the development of molecular and genomic analysis, provided new tools and data about microbial communities in their natural environments. First to distinguish the epibiotic bacterial community from potential bacterial endobionts scanning electron microscopy was used in combination with culture-independent denaturing gradient gel electrophoresis of bacterial 16S ribosomal RNA gene fragments [51]. Then, cloning and sequencing of 16S rRNA genes is being used to explore the microbial diversity from complex samples. Using the high-throughput sequencing of the V1–V3 region of the 16S rRNA gene [52], showed that algae host characteristic bacterial communities were more diverse than those associated with other marine organisms as corals.

Present data described more than one hundred twenty seven associated bacteria specified both by culturing methods and 16S rDNA sequencing for the most green, red and brown algae provided mainly from the northern coast in Tunisia (Table 1). The main groups are from Gamma-proteobacteria, Firmicutes and Alpha-proteobacteria isolated from *Ulva rigida*, *Ulva intestinalis*, *Jania rubens* and *Padina pavonica*. At the opposite, the almost available bibliographic data dealt with red and brown algae associated bacteria indicated dominance of alpha-proteobacteria among the algae associated bacterial communities [53, 54, 55, 40, 56, 57]. More recent data described higher biodiversity epibionts bacteria with marine algae *Sargassum sp* comprising groups of cyanobacteria, plantomycetes, actinobacteria, firmicutes, bacteroidetes and proteobacteria [58]. Ultimately, characterization of composition for bacterial communities associated with four major ecological functional groups of benthic algae was released [52]: encrusting calcifying algae (CCA), upright calcareous algae (*Halimeda opuntia*), fleshy macroalgae (*Dictyota bartayresiana*) and turf algae and indicated that benthic reef algae have characteristic microbial communities associated with their tissues.

Several bacterial species have been isolated from the spot-wounded fronds of *Laminaria japonica* [54], the surface of *Fucus serratus* and the rotten thallus of *Fucus evanescens* [59, 60]. Some brown algae-associated bacteria may degrade algal polysaccharides, such as fucoidan, or alginate [61, 62]. On the other hand, brown algae can produce biologically active compounds that are capable of killing bacteria or inhibiting bacterial growth [63, 64, 65]. Bacteria associated with kelp are believed to be critically important in many processes in kelp forest ecosystems. Several studies have addressed the flow of matter in kelp forests in South Africa [66, 67, 68] and these findings highlighted the important role of heterotrophic bacteria as secondary producers utilizing kelp-produced carbon. Experimentally, kelp partially degraded by naturally associated bacteria has been provided as better food source than undegraded kelp for amphipods living in kelp forests [69]. These studies have not been able to identify specifically the kinds of bacteria responsible for these processes [56].

## 2.2. Seaweeds epibionts main bioactive groups

From 1997 to 2008 around 660 new marine bacterial compounds were identified and most of these compounds originated respectively from the classes of Actinobacteria (40%), Cyanobacteria (33%), members of the Proteobacteria (12%), representatives of the Firmicutes and Bacteroidetes 5% each [70]. Interestingly, marine archaea may also be a source of new secondary metabolites [71].

The present data (Table 1) showed dominance of the Gammaproteobacteria within bioactive group of epibionts for different types of algae and mainly *Pseudoalteromonas* genus which display antimicrobial, cytotoxic and antifouling activities. Besides the Firmicutes group *Bacillus* genus (mainly *B. pumilus* and *B. cereus*) are dominant and present within most types of algae. These species display large antibacterial and antifungal profiles. The alphaproteobacteria group (several species) was mainly isolated from the green algae group (*U. rigida*). Marine aerobic heterotrophic bacteria of the genus [72] comprise one of the most abundant groups of proteobacteria, widely distributed in the marine environment [73, 74, 75]. Bacterium of *Pseudoalteromonas* and *Alteromonas* sp were previously isolated mainly from *Laminaria* fronds produced extra and intra-cellular alginate lyases and utilized alginate as its sole carbon source. The enzyme was purified from the culture supernatant of one strain, its substrate specificity was characterized and molecular mass estimated was of 32 kDa [76].

An aerobic, polarly flagellated marine bacterium that produces a prodigiosinlike pigment was isolated from the red-spotted culture beds of *Laminaria japonica*. Five isolates had unique bacteriolytic activity for both Gram-positive and -negative bacteria, which had never been observed among *Alteromonas* or related species. The isolates were identified as the causative agent of red spot disease of *L. japonica* seeds. The phenotypic features of the isolates were similar to these of *Pseudoalteromonas rubra* ATCC 29570T, but they could be differentiated using 10 traits (growth at 37°C, requirement for organic growth factors, bacteriolytic activity, utilization of sucrose, N-acetylglucosamine, fumarate, succinate, D-galactose, L-proline and acetate). The G+C content of DNAs from the isolates was 4446 mol/o. The isolates constitute a new species, distinct from the other *Alteromonas* and *Pseudoalteromonas* species, as shown by DNA-DNA hybridization experiments and phylogenetic clustering of 16S rRNA gene sequences, for which the name *Pseudoalteromonas bacteriolytica* sp. nov. (Type strain = IAM 145953 is proposed. A set of phenotypic features which differentiate this new species from closely related *Pseudoalteromonas* and *Akeromonas* species is provided [77]

Non-pigmented strains of Gram-negative, aerobic, marine bacteria with polar flagella were isolated from the thallus of the brown alga *Fucus evanescens* in the Kraternaya Bight of the Kurile Islands in the Pacific Ocean with bacteriolytic, proteolytic and haemolytic activities and degraded algal polysaccharides, synthesizing a number of glycoside hydrolases (fucoidanases, laminaranases, alginases, agarases, pullulanases, *b*-glucosidases, *b*-galactosidases, *b*-Nacetylglucosaminidases and *b*-xylosidases). By 16S rDNA analysis, the bacteria were shown to belong to a distinct species, *Pseudoalteromonas issachenkonii* sp. Nov [47].

## 3. Metabolomic seaweeds epibionts

A significant increase in number of natural products from marine microorganisms was reported earlier in recent decade with 62% in 2007 compared to 2006 [78]. Such rise was judged spectacular compared with number of identified microbial metabolites in 2007 to average of 1965 to 2005 resulting in a 600% rise. Approximately 3000 natural products were identified from marine microorganisms by the end of 2008 [79]. Else, an increasing interest in exploration of marine bacteria and fungi for microbial secondary metabolites provide promising new lead structures for drug discovery [80, 81]. Advances are made in identification of antimicrobial and antitumor compounds as sources for new anti-infectives [82] and drugs for treatment of cancer diseases [84], respectively. Further, increasing evidence is accumulating that marine bacteria synthesize new compounds valuable for discovery of pharmaceutical drugs [83, 85, 86, 87].

Nevertheless, few metabolites have been isolated from seaweeds epibionts [88, 89,90]. Most frequently reported bioactive bacterial metabolites have been isolated from species of the genus *Alteromonas*, *Bacillus* and *Pseudoalteromonas*. Another very productive genus is *Streptomyces* but none of these species have been isolated from our seaweeds surfaces.

### 3.1. *Pseudomonas sp.*

A well known toxin Tetrodotoxin (TTX), because of its unique chemical structure and the specific action of blocking sodium channels of excitable membranes have been isolated from *Pseudomonas sp.* from different sources [91]. The toxin is a genuine product of *Pseudomonas sp.*, and is transmitted through its host such as the red alga *Jania sp.*, sponges or other marine organisms. An antibacterial compound magnesidin has been isolated from associated bacteria *Pseudomonas magnesorubra* to the green alga *Caulerpa peltata*. This compound displayed strong activity against *Staphylococcus* and *Bacillus* strains [92].

### 3.2. *Pseudoalteromonas*

Five korormicins have been isolated from a marine *Pseudoalteromonas sp.* [93]. These compounds are selective inhibitors of the primary sodium pump and showed antibiotic activities against obligate marine Gram-negative bacteria.

Else, a brominated biphenol that has been described from *Pseudoalteromonas phenolica* and was shown to have a remarkable activity against a methicillin-resistant *Staphylococcus aureus* strain [94]. Violacein the purple pigment with antiprotozoal activity was isolated from *P. tunicate*. PCR-amplification of the putative *vioA* gene and biochemical analysis of cell extracts revealed that violacein is synthesized by another *Pseudoalteromonas* species found in *Ulva australis* biofilms: *P. ulvae* [95]. Predominance of biosynthesis of this pigment by biofilm population versus planktonic cells was analysed [96] and demonstrated that cells extracted from biofilms contained 3 to 59 (depending on species) times more violacein per protein biomass than the corresponding plankton extracts.

### 3.3. *Roseobacter sp.*

The *Roseobacter* clade seems to be specific marine and showed an interesting metabolic capacity in the past. Tropodithietic acid is an antibacterial compound metabolized by the *Roseobacter* clade against pathogenic bacteria [96]. Since most microorganisms produce molecules that prevent the attachment, growth and/or survival of competing organisms, research on microbe–microbe interactions has led to the discovery of many antibiotic compounds [83]. Chemically-mediated intra- and interspecies communication was postulated for pelagic microbes [97] and appears to be particularly important for surface-attached microorganisms and those living in biofilms due to the high cell density in these habitats [98].

In terms of biotechnological exploitation of these conditions, efforts should be made to develop much improved techniques to better mimic surface-associated lifestyles and competitive cultivation. Growth of a marine alga-associated *Roseobacter sp.* under static conditions for example resulted in enhanced biofilm formation and the production of antibacterial compounds [57].

Metabolites represent the chemical first line of defense against microbial challenge. The competition for space between epibiotic bacteria based on compounds may provide an antifouling protection to the algal host [33, 98]. If the bacterial attachment is not stopped successfully, other secondary metabolites may inhibit the growth, survival, virulence, or reproduction of possibly invading organisms. These second line compounds may be produced by the macroalgae or by epiphytic and endophytic microbes associated with them [99, 100, 101]. A mutualistic relationship can be postulated in which the bacterial community protects the host from biofouling, while the host surface may provide nutrients and physical protection to the bacteria [41]. However, after more than 20 years of research on this topic, there is still no experimental evidence demonstrating if or how host organisms selectively attract and harbor their epibionts. There is large variety of different metabolites as possible mediators of interspecies interactions in the algal biosphere, provided by bacterial secondary metabolites that likely participate in such interactions but little is still known about their roles [14, 102]. Chemical interactions between different bacterial species can affect the production and secretion of secondary metabolites in these microorganisms [39]. In addition, small molecules and also antibiotics at subinhibitory concentrations may act as signaling molecules and stimulate secondary metabolites production in other microorganisms [101].

Since the marine macroalgae are continuously exposed to many biotic and abiotic pressures which influence the organism's physiology leading to the production of multi-functional natural secondary metabolites that influence composition of their epibionts [103].

The characteristic nature of some of the algal associated *Bacteria* support the hypothesis that algae influence the types of *Bacteria* that can survive on the algal surface, and there are a variety of mechanisms that algae may employ to achieve this such production of toxic secondary metabolites by some algae to *Bacteria* [104, 105] or inhibit quorum sensing [107, 108], and physical mechanisms like mucus release and tissue sloughing likely affect the types of bacteria that survive on the algal surface [109]. Furthermore, release of organic compounds by algae may selectively promote growth of certain groups of bacteria, and it has been shown that algal DOM differentially stimulates bacterial growth based on the type of alga from which it originated [110].

**Table 1** Bioactive epibionts bacteria isolated from species of algae and their bioactivities

Bioactive species	Group of Bacteria	Source	Bioactivities(inhibitory activities and others)	References
<i>Acinetobacter johnsonii</i>	Gamma proteobacteria	<i>Ulva rigida</i>	Antibacterial and antifungal	[87]
<i>Actinobacteria spp</i>	Actinobacteria	<i>Dictyota bartaryresiana</i>	Antibacterial and antifungal	[52]
<i>Aquimarina sp.</i>	Bacteroides	<i>Jania rubens</i>	Antibacterial and antifungal	[87]
<i>Alteromonas marina</i>	Gamma proteobacteria	<i>Ulva rigida</i>	Antibacterial and antifungal	110
<i>Alteromonas macleodii</i>	Gamma proteobacteria	<i>Ulva rigida</i>	Antibacterial and antifungal	110
<i>Bacteroidetes bacterium</i>	Bacteroides	<i>Ulva rigida</i>	Antibacterial and antifungal	110
<i>Bacillus algicola</i>	Firmicutes	<i>Fucus evanescens</i>		[59]
<i>Bacillus cereus</i>	Firmicutes	<i>Sargassum serratifolium</i>	Antibacterial	[40]
<i>Bacillus cereus</i>	Firmicutes	<i>Sargassum fusiforme</i>	Antibacterial	[40]
<i>Bacillus cereus</i>	Firmicutes	<i>Scytosiphon lomentaria</i>	Antibacterial	[40]
<i>Bacillus cereus</i>	Firmicutes	<i>Petalonia fascia</i>	Antibacterial	[40]
<i>Bacillus pumilus</i>	Firmicutes	<i>Sargassum fusiforme</i>	Antibacterial	[40]
<i>Bacillus pumilus</i>	Firmicutes	<i>Colpomenia sinuosa</i>	Antibacterial	[40]
<i>Bacillus pumilus</i>	Firmicutes	<i>Ecklonia cava</i>	Antibacterial	[40]
<i>Bacillus pumilus</i>	Firmicutes	<i>Padina pavonica</i>	Antibacterial and antifungal	110
<i>Bacillus pumilus</i>	Firmicutes	<i>Jania rubens</i>	Antibacterial and antifungal	110
<i>Bacillus sp.</i>	Firmicutes	<i>Ulva rigida</i>	Antibacterial and antifungal	110
<i>Bacillus psychrodurans</i>	Firmicutes	<i>Undaria pinnatifida</i>	Antibacterial	[65]
<i>Brevibacterium celere sp</i>	Actinobacteria	<i>Fucus evanescens</i>		[59]
<i>Dinoroseobacter shibae</i>	Alphaproteobacteria	<i>Ulva rigida</i>	Antibacterial and antifungal	110
<i>Enterococcus mundtii</i>	Firmicutes	<i>Ulva rigida</i>	Antibacterial and antifungal	110
<i>Flavobacteriaceae</i>	Gamma proteobacteria	<i>Formosa algae</i>		[60]
<i>Labrenzia marina</i>	Alpha proteobacteria	<i>Ulva rigida</i>	Antibacterial and antifungal	110
<i>Nereida ignava</i>	Alpha proteobacteria	<i>Ulva rigida</i>	Antibacterial and antifungal	110
<i>Octadecabacter sp.</i>	Alpha proteobacteria	<i>Ulva rigida</i>	Antibacterial and antifungal	110
<i>Paracoccus sp.</i>	Alpha proteobacteria	<i>Jania rubens</i>	Antibacterial and antifungal	[87]
<i>Pseudoalteromonas aurantia</i>	Gamma proteobacteria	<i>Ulva lactuca</i>	Antibacterial and antifungal	[32]
<i>Pseudoalteromonas citrea</i>	Gamma proteobacteria	<i>Fucus sp</i>		[59]
<i>Pseudoalteromonas elyakovic</i>	Gamma proteobacteria	<i>Laminaria japonica</i>		[54]
<i>Pseudoalteromonas issachenkonii</i>	Gamma proteobacteria	<i>Algae</i>		[54]
<i>Pseudoalteromonas Tunicata</i>	Gamma proteobacteria	<i>Ulva lactuca</i>	Antifouling	[32]
<i>Pseudoalteromonas sp</i>	Gamma proteobacteria	<i>Digenaea sp</i>	Antimicrobial, cytotoxicity and e	110
<i>Pseudoalteromonas sp</i>	Gamma proteobacteria	<i>Ulva rigida</i>	Antibacterial and antifungal	110
<i>Pseudoalteromonas sp</i>	Gamma proteobacteria	<i>Padina pavonica</i>	Antibacterial and antifungal	110
<i>Pseudoalteromonas sp</i>	Gamma proteobacteria	<i>Jania rubens</i>	Antibacterial and antifungal	110
<i>Pseudomonas sp</i>	Gamma proteobacteria	<i>Digenaea sp</i>	Antimicrobial, cytotoxicity and e	110
<i>Pseudomonas sp</i>	Gamma proteobacteria	<i>Padina pavonica</i>	Antibacterial and antifungal	110
<i>Pseudomonas sp</i>	Gamma proteobacteria	<i>Jania rubens</i>	Antibacterial and antifungal	110
<i>Psychrobacter arctica</i>	Gamma proteobacteria	<i>Undaria pinnatifida</i>	N.D	[65]
<i>Psychrobacter arctica</i>	Gamma proteobacteria	<i>Undaria pinnatifida</i>	N.D	[65]
<i>Psychrobacter nivimaris</i>	Gamma proteobacteria	<i>Undaria pinnatifida</i>	N.D	[65]
<i>Psychrobacter pulmoris</i>	Gamma proteobacteria	<i>Undaria pinnatifida</i>	N.D	[65]
<i>Psychromonas arctica</i>	Gamma proteobacteria	<i>Undaria pinnatifida</i>	N.D	[65]
<i>Psychroserpens mesophilus</i>	Gamma proteobacteria	<i>Ulva rigida</i>	Antibacterial and antifungal	110
<i>Roseobacter sp</i>	Alpha proteobacteria	<i>Algae</i>	Antifouling	[27, 57]
<i>Rhodobacteraceae bacterium</i>	Alpha proteobacteria	<i>Ulva rigida</i>	Antibacterial and antifungal	110
<i>Ruegeria sp.</i>	Alpha proteobacteria	<i>Ulva rigida</i>	Antibacterial and antifungal	110
<i>Salagentibacter sp.</i>	Bacteroides	<i>Ulva rigida</i>	Antibacterial and antifungal	110
<i>Staphylococcus arlettae</i>	Firmicutes	<i>Ulva rigida</i>	Antibacterial and antifungal	110
<i>Stappia sp.</i>	Alpha proteobacteria	<i>Ulva rigida et Ulva intestina</i>	Antibacterial and antifungal	87,11

## 4. Conclusions

Seaweeds epibiotic bacteria diversity and their metabolomic have been reviewed in this paper. Available data indicated high diversity for bacteria communities related to several types of seaweeds with mainly alpha and gamma proteobacteria and firmicutes. Biological activities of these communities of associated bacteria were not completely investigated and almost metabolites remain to be well characterized taking in account variations in environment marine ecosystems.

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