REVIEW

Chemical interactions between marine macroalgae and bacteria

Franz Goecke, Antje Labes, Jutta Wiese, Johannes F. Imhoff*

Kieler Wirkstoff-Zentrum at the Leibniz Institute of Marine Sciences (IFM-GEOMAR), Am Kiel-Kanal 44, Kiel 24106, Germany

ABSTRACT: We review research from the last 40 yr on macroalgal-bacterial interactions. Marine macroalgae have been challenged throughout their evolution by microorganisms and have developed in a world of microbes. Therefore, it is not surprising that a complex array of interactions has evolved between macroalgae and bacteria which basically depends on chemical interactions of various kinds. Bacteria specifically associate with particular macroalgal species and even to certain parts of the algal body. Although the mechanisms of this specificity have not yet been fully elucidated, ecological functions have been demonstrated for some of the associations. Though some of the chemical response mechanisms can be clearly attributed to either the alga or to its epibiont, in many cases the producers as well as the mechanisms triggering the biosynthesis of the biologically active compounds remain ambiguous. Positive macroalgal-bacterial interactions include phytohormone production, morphogenesis of macroalgae triggered by bacterial products, specific antibiotic activities affecting epibionts and elicitation of oxidative burst mechanisms. Some bacteria are able to prevent biofouling or pathogen invasion, or extend the defense mechanisms of the macroalgae itself. Deleterious macroalgal-bacterial interactions induce or generate algal diseases. To inhibit settlement, growth and biofilm formation by bacteria, macroalgae influence bacterial metabolism and quorum sensing, and produce antibiotic compounds. There is a strong need to investigate the bacterial communities living on different coexisting macroalgae using new technologies, but also to investigate the production, localization and secretion of the biological active metabolites involved in those possible ecological interactions.

KEY WORDS: Marine microoganisms \cdot Defense \cdot Beneficial communication \cdot Biofilms \cdot Oxidative burst \cdot Antibiotic activity \cdot Quorum sensing control

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INTRODUCTION

Over the past decades an intensive collaboration between chemists and ecologists has resulted in an increasing number of studies which have combined modern chemical techniques with ecologically relevant experiments and theories (Pawlik 2000, Hay 2009). Thousands of marine secondary metabolites have been identified (Hay 1996). These compounds have been shown to play a major role in mediation of diverse ecological interactions (Dworjanyn et al. 1999). Chemical ecology has provided significant insights into the ecology, evolution and organization of marine populations, communities, and also into the function of marine

ecosystems (Hay 2009). Selected aspects of marine chemical ecology have been frequently reviewed with a focus on specific taxonomic groups or systems (see Hay 2009 and references therein). Thus, the establishment and composition of communities on surfaces and on bodies of organisms (epibiosis, biofouling) and the processes involved have been described by several authors (Wahl 1989, 2008, Krug et al. 2006, Qian et al. 2007, Harder 2009, Hay 2009). Sessile invertebrates such as tunicates, cnidarians, bryozoans, barnacles, and sponges were the model systems for these experiments. With respect to the chemical ecology of algae, investigations were focused either on the capabilities of the macroalgae for chemical defense against grazers or

on the communication between algae, e.g. for reproductive purposes (see Cronin & Hay 1996, Paul & Puglisi 2004, Amsler 2008 and references therein, Macaya & Thiel 2008, Paul & Ritson-Williams 2008). A few interesting studies have been presented on fungi, microalgae and protozoa as associates of macroalgae (see Harder 1999, Hellio et al. 2002, Raghukumar 2002, Kohlmeyer & Volkmann-Kohlmeyer 2003, Lam et al. 2008b). Detailed knowledge of the interaction of algae with their associated microbes and among microbes on algal surfaces and tissues is still lacking (Steinberg et al. 1997, Steinberg & de Nys 2002, Kubanek et al. 2003). Therefore, this review will focus on specific interactions between macroalgae and bacteria.

COLONIZATION OF MACROALGAL SURFACES BY MARINE MICROBES

Microbial epibiosis

Microorganisms are an essential component of earth's biosphere (Whitman et al. 1998). Their number in aquatic environments is enormous. Seawater contains up to 10⁷ viruses, 10⁶ bacteria, 10³ fungi, 10³ microalgae, and 10 to 100 microscopic larvae and spores per ml (Cole 1982, Jensen & Fenical 1994, Engel et al. 2002, Harder 2009). The aquatic environment favors the development of microbes and the formation of biofilms on surfaces (Weinberger 2007). Macroalgae are especially susceptible to epibiosis because they live in an environment with strong competition for space amongst benthic organisms (Hellio et al. 2001, Harder et al. 2004, Potin et al. 2002, Lam et al. 2008b). In addition, algal surfaces provide a habitat rich in organic material. Macroalgae release large amounts of organic carbon into the surrounding environment, providing nutrients for microorganisms (Khailov & Burlakova 1969, Kong & Chan 1979, Bouvy et al. 1986, Armstrong et al. 2001, Lane & Kubanek 2008) and triggering chemotactic behaviour of bacteria (Bell & Mitchell 1972, Paul & Puglisi 2004). Most primary metabolites such as carbohydrates, amino acids, peptides, and proteins are inducers of microbial colonization (Steinberg et al. 2002). Hence, the surface of a macroalga provides a protected microniche favorable for bacterial colonization and reproduction (Byappanahalli et al. 2003, Beleneva & Zhukova 2006, Mahmud et al. 2007, Englebert et al. 2008). For this reason, marine macroalgae are continuously challenged by microorganisms as well as by grazers (Weinberger et al. 1997, Bouarab et al. 2001).

The resulting marine microbial communities covering macroalga are complex and highly dynamic ecosystems, consisting of a diverse range of organisms

(Holmström et al. 2002, Honkanen & Jormalainen 2005, Krug et al. 2006). Bacteria are dominant among the primary colonizers of algal surfaces, followed by diatoms and fungi (Qian et al. 2007, Lam et al. 2008a).

While some macroalgae are heavily colonized, other algal species in the same habitat remain almost free of epibionts. Such differences may even be found in closely related species living in the same habitat, e.g. in *Fucus evanescens* which show little epibiosis and *F. vesiculosus* which are heavily fouled (Wikström & Pavia 2004). This indicates the presence of an established antifouling defense in only some macroalgal species (de Nys et al. 1993, Steinberg & de Nys 2002, Bhadury & Wright 2004, Nylund & Pavia 2005) and, on the other hand, species-specific contact mechanisms between algae and bacteria.

Bacterial communities associated with macroalgae

Descriptive studies of bacteria isolated from the surface of macroalgae were reported as early as 1875 (Johansen et al. 1999). The interest in bacterial populations living in association with macroalgae has increased during recent decades. We 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 yr (Table 1 & Appendix 1). Bacterial-macroalgal associations were shown to be widely distributed in marine habitats (Appendix 1). The number and complexity of these studies increased significantly during the past decade. This increase can be attributed to the combined use of improved methods in bacterial culture, microscopy and molecular biology (Fig. 1). However, many questions concerning the occurrence, distribution, persistence and ecological function of the associated bacteria remain unresolved.

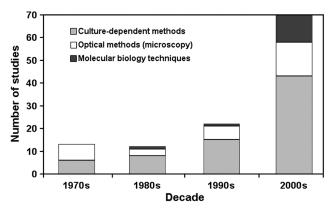


Fig. 1. Worldwide studies of bacterial communities associated with macroalgae in the last 4 decades, showing the methodology used for the analysis. Data refers to Table 1 & Appendix 1

Table 1. Macroalgae as source of new bacterial species. Quotation marks indicate proposed but not yet validated species

Macroalga	Bacterial species	Source
Chlorophyta		
Acrosiphonia sonderi (Kütz.) Kornm.	Algibacter lectus Formosa agariphila Mesonia algae Pibocella ponti Winogradskyella epiphytica	Nedashkovskaya et al. (2004e) Nedashkovskaya et al. (2006a) Nedashkovskaya et al. (2003) Nedashkovskaya et al. (2005a) Nedashkovskaya et al. (2005c)
Avrainvillea riukiuensis Yamada	Zobellia russellii Tenacibaculum amylolyticum	Nedashkovskaya et al. (2004b) Suzuki et al. (2001b)
Capsosiphon fulvescens (Agardh) Setchell & Gardner		Park et al. (2001b)
Caulerpa sp.	Microbulbifer epialgicus	Nishijima et al. (2009)
Enteromorpha linza (L.) J. Agardh	Erythrobacter longus	Shiba & Simidu (1982)
Ulva fenestrata Ruprecht	Algibacter lectus Arenibacter certesii Arenibacter palladensis Maribacter ulvicola Pseudozobellia thermophila Roseivirga ehrenbergii Ulvibacter litoralis	Nedashkovskaya et al. (2004e) Nedashkovskaya et al. (2004a) Nedashkovskaya et al. (2006b) Nedashkovskaya et al. (2004d) Nedashkovskaya et al. (2009) Nedashkovskaya et al. (2005b) Nedashkovskaya et al. (2004c)
Ulva lactuca L.	Pseudoalteromonas ulvae	Egan et al. (2001a)
Heterokontophyta, Phaeophyceae Chorda filum (L.) Stackhouse	Arenibacter latericius Winogradskyella thalassocola	Ivanova et al. (2001) Nedashkovskaya et al. (2005c)
Ecklonia kurome Okamura	Croceitalea dokdonensis Croceitalea eckloniae Flagellimonas eckloniae	Lee et al. (2008b) Lee et al. (2008b) Bae et al. (2007)
Fucus evanescens C. Agardh	Bacillus algicola Brevibacterium celere Formosa algae Pseudoalteromonas issachenkonii	Ivanova et al. (2004a) Ivanova et al. (2004b) Ivanova et al. (2004c) Ivanova et al. (2002b)
Fucus serratus L.	Cellulophaga baltica Cellulophaga fucicola	Johansen et al. (1999) Johansen et al. (1999)
Kjellmaniella crassifolia Miyabe	'Fucobacter marina'	Sakai et al. (2002)
Laminaria japonica Areschoug	Pseudoalteromonas bacteriolytica Winogradskyella eximia Zobellia laminariae	Sawabe et al. (1998b) Nedashkovskaya et al. (2005c) Nedashkovskaya et al. (2004b)
Lessonia sp.	Alteromonas atlantica	Akagawa-Matsushita et al. (1992)
Padina sp.	Roseibacillus ponti	Yoon et al. (2008)
Pocockiella sp.	Microbulbifer variabilis	Nishijima et al. (2009)
Saccharina latissima (L.) Lane et al.	Kiloniella laminariae	Wiese et al. (2009a)
Undaria pinnatifida (Harvey) Suringar	<i>'Gracilibacillus</i> sp.'	Tang et al. (2009)
Rhodophyta	7.1.11:	Dealers at al. (2004)
Delesseria sanguinea (Huds.) Lamour Gigartinaceae	Zobellia galactanovorans Lacinutrix algicola Lacinutrix mariniflava	Barbeyron et al. (2001) Nedashkovskaya et al. (2008) Nedashkovskaya et al. (2008)
Jania sp.	Shewanella alga	Simidu et al. (1990)
Polysiphonia japonica Harvey	Maribacter polysiphoniae	Nedashkovskaya et al. (2007)
Porphyra sp.	'Phycisphaera mikurensis'	Fukunaga et al. (2009)
Unidentified red algae	Luteolibacter algae	Yoon et al. (2008)
Unidentified macroalgae		
	Aeromicrobium tamlense Agarivorans gilvus Agrococcus jejuensis Ferrimonas marina Flavobacterium algicola Koreibacter algae Labedella gwakjiensis Mesonia phycicola Nitratireductor kimnyeongensis Paracoccus zeaxanthinifaciens Phycicocla gilvus	Lee & Kim (2007) Du et al. (in press) Lee (2008) Katsuta et al. (2005) Miyashita et al. (2010) Lee & Lee (in press) Lee (2007) Kang & Lee (2010) Kang et al. (2009) Berry et al. (2003) Lee (2006) Lee et al. (2008a)

Phylogenetic studies of epiphytic bacteria provided an insight into the complex bacterial communities associated with macroalgae (Penesyan et al. 2009). Bacterial communities living on marine macroalgae differ in number and composition of species from those occurring in seawater (Kong & Chan 1979, Lemos et al. 1985, Mow-Robinson & Rheinheimer 1985, Johnson et al. 1991, Steinberg et al. 2002, Longford et al. 2007). In most cases, the epiphytic bacterial communities are highly specific. Some microbes are found consistently as epiphytes, e.g. Leucothrix mucor (Bland & Brock 1973). Recently, the variability and abundance of the epiphytic bacterial community associated with Ulva australis was investigated using molecular methods. The results showed that members of the Alphaproteobacteria and the Bacteroidetes were a stable part of the associated bacterial population (Tujula et al. 2010). Bacterial-macroalgal associations comprised a number of new bacterial species, genera and even orders, proving that macroalgae represent a distinct and rich source of new microbial taxa (Genilloud et al. 1994). From 36 macroalgal species, 56 new bacterial species have been isolated (32% from Chlorophyta, 35% from Phaeophyceae, 12% from Rhodophyta, and 21% from undetermined algae) (Table 1).

Considering all available evidence, including our own observations (Staufenberger et al. 2008, Lachnit et al. 2009, Wiese et al. 2009a,b), it is reasonable to conclude that a highly specific association of bacterial communities with marine macroalgae exists. It has been proposed that the physiological and biochemical properties of macroalgae predetermine the composition of the adhering microbial communities (Beleneva & Zhukova 2006). Different species of marine algae growing under the same environmental conditions bear different bacterial communities, varying in number and composition. This assumption was investigated, using a molecular approach, by Lachnit et al. (2009) regarding the bacterial populations on Delesseria sanguinea, Fucus vesiculosus, Saccharina latissima (formerly Laminaria saccharina), and Ulva compressa growing in 2 different habitats. In that study, it was demonstrated that bacterial communities derived from macroalgae belonging to the same species but originating from a different habitat were more similar than those from different species inhabitating the same ecological niche. Similar results were obtained by Nylund et al. (2010), who analyzed 2 localities on the west coast of Sweden with respect to the bacteria associated with the red macroalgal species Bonnemaisonia asparagoides, Lomentaria clavellosa and Polysiphonia stricta.

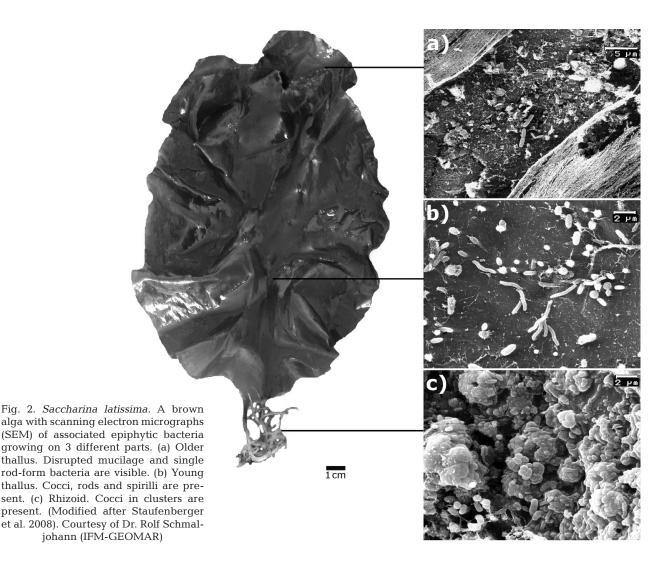
In general, a stable association between host and microorganisms is observed (Kong & Chan 1979, Shiba & Taga 1980, Lewis et al. 1985, Johnson et al. 1991); however, over the seasons or over the life span of the

basibiont the composition of the bacterial communities may change (Laycock 1974, Hornsey & Hide 1976a, Sakami 1996, Staufenberger et al. 2008). This has been demonstrated for bacteria associated with Ascophyllum nodosum, Fucus vesiculosus, Sargassum natans and Ulva australis (Sieburth & Conover 1965, Sieburth & Tootle 1981, Hellio et al. 2004, Tujula et al. 2010). Furthermore, it was reported that the composition of the bacterial communities varies on different parts of the thallus, e.g. for Ascophyllum nodosum (Cundell et al. 1977), Chara vulgaris (Ariosa et al. 2004), and Saccharina latissima (Staufenberger et al. 2008) (Fig. 2). In addition to different structural features of the specific parts of the algal thallus, these differences may be explained by a lack of vascular connections in the algal tissue and by the resulting deficit in efficient resource translocation (Honkanen & Jormalainen 2005). Various biological activities (for example antibacterial and antiherbivory activities) were found in extracts from different parts of macroalgae which was shown by unequal concentrations of the different secondary metabolites throughout the thallus (Hornsey & Hide 1976b, Meyer & Paul 1992, Vlachos et al. 1999, Freile-Pelegrin & Morales 2004, Macaya et al. 2005). This effect was shown for a number of metabolites, such as soluble phlorotannins and halogenated organic compounds (Mehrtens & Laturnus 1997, Koivikko et al. 2005). In the brown alga Dictyota ciliolata, for example, the secondary metabolites 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). The same phenomenon was observed in the red macroalga Neorhodomela larix regarding its content of bromophenols such as lanosol (Phillips & Towers 1982, Carlson et al. 1989). Therefore, different allocation and concentration of the chemical compounds may lead to different microbial communities at the different parts of macroalgae (Fig. 2).

Although some of the bacterial-algal interactions have been discussed earlier, the ecological relevance of most naturally occurring bacterial communities on macroalgae remains unclear and in most cases the bacterial species involved have not yet been identified (Duan et al. 1995, Ivanova et al. 2002a). For example, many coenocytic green macroalgae such as Caulerpa, Codium, Bryopsis and Penicillus spp. have been shown to harbour endosymbiotic bacteria, as shown by microscopic studies (Burr & West 1970, Turner & Friedmann 1974, Dawes & Lohr 1978, Rosenberg & Paerl 1981). However, only in Caulerpa taxifolia could it be shown, using molecular approaches, that Herbaspirillum sp.related bacteria are host-specific endosymbionts (Meusnier et al. 2001, Delbridge et al. 2004). The characterization of microorganisms associated with algae is still at an early stage of development and detailed molecular studies on microbial communities associated with macroalgae are rare (Staufenberger et al. 2008). Studies of macroalgal-microbial interactions have lagged, mainly for methodological reasons (Largo et al. 1997, Kohlmeyer & Volkmann-Kohlmeyer 2003). Suitable tools for the analysis of epiphytic bacterial communities including culture-independent approaches were not available until molecular techniques were introduced to this field of research (Fig. 1) (Ashen & Goff 1998, 2000, Meusnier et al. 2001, Ohkubo et al. 2006, Tujula et al. 2006, Weinberger 2007, Burke et al. 2009). Until now, most of the available information about bacterial-macroalgal interactions was obtained from culture studies (Fisher et al. 1998, Skovhus et al. 2004). If we consider that only ca. 1 to 10% of the associated bacteria have been cultivated (Jensen et al. 1996), it is reasonable to assume that most of the ecologically relevant bacteria are not known so far. The same is true for their possible susceptibility to naturally

released algal metabolites (Paul et al. 2006). However, an increasing number of results demonstrate that chemical interactions determine the bacterial-algal relationships. The substances on the surface of a macroalga include exuded secondary metabolites and extracellular exopolymers. As soon as algal metabolites are degraded by the associated bacteria, the chemical cocktail may be further enriched (Lachnit et al. 2010). Many bacterial taxa obtained from algal tissue are able to degrade sugars produced by algae, such as alginate, cellulose and manitol (Table 2). They are considered to be involved in the decay process of algal fronds (Johnson et al. 1971, Lewis et al. 1985, Uchida & Nakayama 1993, Jensen et al. 1996, Sakami 1999, Ivanova et al. 2005). Probably, this is one reason for specific macroalgal-bacterial interactions (Kong & Chan 1979, Lu et al. 2008).

Numerous studies on antifouling activity of extracts and isolated substances from macroalgae have shown that algae are a rich source of bioactive compounds



 $\begin{tabular}{ll} Table 2. Enzymatic activities detected in marine bacteria that are relevant to the degradation of macroalgal cell walls. *Bacteria isolated from algae \\ \end{tabular}$

Enzyme	Bacteria	Source
Agarases	Acinetobacter sp. Agarivorans spp. Alterococcus spp. Alteromonas spp.* Bacillus sp. Cellulophaga baltica*, C. fucicola* Cytophaga spp. Flavobacterium spp Glaciecola agarilytica Marinilabilia spp. Microbulbifer spp.* Microscilla spp. Phycisphaera mikurensis* Pseudoalteromonas agarivorans* P. antarctica*, P. gracilis* Pseudomonas atlantica* Persicobacter spp. Pseudozobellia thermophila* Saccharophagus spp. Thalassomonas spp. Vibrio spp.* Zobellia galactanovorans*, Z. laminariae*, Z. russellii*	Yaphe (1957), Quatrano & Caldwell (1978), Vera et al. (1998), Allouch et al. (2003), Johansen et al. (1999), Romanenko et al. (2003), Schroeder et al. (2003), Nedashkovskaya et al. (2004b), Jam et al. (2005), Michel et al. (2006), and literature therein Flament et al. (2007), Yong et al. (2007), Fukunaga et al. (2009), Nedashkovskaya et al. (2009), Fu & Kim (2010)
Carrageenases	Alteromonas fortis Cytophaga (Cytophaga drobachiensis*) Marinilabilia spp. Microbulbifer sp.* CMC-5 Microbulbifer elongates* Pseudoalteromonas carrageenovora* Zobellia galactanivorans*	Yaphe & Baxter (1955), Sarwar et al. (1983), Potin et al. (1991), Nakagawa & Yamasato (1996), Barbeyron et al. (1998, 2000), Michel et al. (2006), and literature therein, Jam et al. (2005), Khambhaty et al. (2007), Jonnadula et al. (2009)
Alginases	Alcaligenes spp.* Alginomonas spp. Alginovibrio (A. aquatilis) Alteromonas atlantica*, A. carrageenovora*, A. sp.* Cytophaga diffluens Deleya marina* Flavobacterium sp.* Glaciecola sp. Gracilibacillus spp.* G halotolerans* Halomonas marina, H. sp. AW4* Moraxella sp.* Ochrobactrum sp.* Pseudoalteromonas sp.* Pseudomonas alginovora* Streptomyces sp. ALG-5* Vibrio spp. (V. fischeri*, V. harveyi*)	Ando & Inoue (1961), Davidson et al. (1976), Stevens & Levin (1977), Quatrano & Caldwell (1978) and references therein, Preston et al. (1986), Boyen et al. (1990), Brown et al. (1991), Tseng et al. (1991), Akagawa-Matsushita et al. (1992), Ramaiah & Chandramohan (1992), Sawabe et al. (1992), Uchida & Nakayama (1993), Uchida et al. (1995), Sakami (1999), Sawabe et al. (1997, 1998a), Kraiwattanapong et al. (1999), Ivanova et al. (2002a,b), Uchida et al. (2002), Wang et al. (2006), Sawabe et al. (2007), An et al. (2008, 2009), Tang et al. (2008), Zhou et al. (2008), Kim et al. (2009), Tang et al. (2009)
Fucoidanases	Arenibacter spp.* Flavobacterium algicola* Fucobacter marina* Fucophilus fucoidanolyticus* Gramella sp. Maribacter sp. Mesonia algae* Pseudoalteromonas citrea* P. issachenkonii* Sphingomonas paucimobilis Vibrio sp. Zobellia sp.*	Furukawa et al. (1992), Bakunina et al. (2000, 2002), Ivanova et al. (2002a), Sakai et al. (2002, 2003, 2004), Kusaykin et al. (2006), Urvantseva et al. (2006), Kim et al. (2008), Miyashita et al. 2010)
Fucanases	Alteromonas sp. SN-1009 Mariniflexile fucanivorans	Colin et al. (2006), Descamps et al. (2006), Barbeyron et al. (2008)
Mannanase	Aeromonas sp. F-25 Bacillus subtilis Pseudomonas sp. PT-5* Streptomyces lividans Vibrio sp.*	Yamaura et al. (1990), Moreira & Filho (2008), Tanaka et al. (2009)
Cellulases & pectinases	Acinetobacter spp. Alteromonas spp. Flavobacterium spp. Pseudoalteromonas sp.* Vibrio spp.*	Araki et al. (1992), Ramaiah & Chandramohan (1992), Yamasaki et al. (1998), Ivanova et al. (2002a), Yoshimura et al. (2006)

against colonizing organisms (see section below on antibiotic activities of macroalga-associated bacteria and Table 5) (Steinberg et al. 1998, Bhadury & Wright 2004, Dobretsov et al. 2006b, Lane & Kubanek 2008, and references therein, Nylund et al. 2008). In addition to being defense mechanisms, these substances can trigger specific interactions between macroalgae and colonizers. Macroalgae without their own chemical defense are considered to rely on the secondary metabolites produced by their associated bacteria (Holmström et al. 1992, Egan et al. 2000 and references therein). Dobretsov & Qian (2002) showed that the antifouling mechanisms of Ulva reticulata (Chlorophyta) rely not only on compounds released from the alga itself but also on those produced by epibiotic bacteria, e.g. by a thallus-associated Vibrio sp. (Harder et al. 2004).

Fouling organisms have negative effects on host growth and reproduction. Hence, evolutionary pressure on marine macroalgae has favored the development of mechanisms to defend their surfaces against biofilms (Wahl 1989, Steinberg & de Nys 2002).

DETRIMENTAL BACTERIAL-MACROALGAL INTERACTIONS — DISEASES

Quantification of bacterial epiphytes on different marine macrophytes showed that healthy individuals carry 10⁴ to 7 ×10⁵ bacteria per gram algal fresh weight (Laycock 1974, Jensen et al. 1996). By contrast, the number of bacteria and saprophytes was increased by more than 2 orders of magnitude (440 times) in diseased macroalgae (Weinberger et al. 1994). Despite some beneficial aspects of epibiosis (see Wahl 1989, 2008), biofilm formation produces a permanent threat to macroalgae (Steinberg et al. 1997, Potin et al. 2002, Honkanen & Jormalainen 2005, Nylund & Pavia 2005, Medeiros et al. 2007). Epibiosis may lead to increased hydrodynamic drag on the basibiont. It may reduce the buoyancy and elasticity of the tissue, attract grazers, and thereby increase tissue loss of the host or may even result in its destruction. In additon, bacteria compete with algae for nutrients and may even be more efficient in uptake and assimilation of nutrients (Berland et al. 1972). Biofilms may also inhibit gaseous exchange as well as reducing incident light and thereby decrease photosynthetic activity (Provasoli & Pintner 1980, Sieburth & Tootle 1981, Wahl 1989, 2008, Steinberg et al. 1997, Mindl et al. 2005). Bacterial biofilms may enhance the attachment and growth of a range of other fouling organisms, such as diatoms, invertebrate larvae, and algal spores (Joint et al. 2002, Tait et al. 2005, Huggett et al. 2006). The host may even be damaged directly by the bacterial community

due to the production of toxins, digestive enzymes, inhibitors or waste products (Weinberger et al. 1997, Ivanova et al. 2002a,b, Patel et al. 2003, Rao et al. 2006) (Table 2).

Microorganisms that are common on the surface of macroalgae might become detrimental if they are able to enter the algal tissue. In order to attack the frond tissues, a pathogen must penetrate the cuticle layers of the macroalga (Craigie et al. 1992). Algal cell walls and cuticles contain a great diversity of polysaccharides, which make them chemically and structurally more complex and heterogeneous than those of terrestrial plants (Polne-Fuller & Gibor 1987). Bacteria capable of degrading the macroalgal cell wall are important factors for the damage of algal tissue and provide an entrance for pathogenic and opportunistic bacteria (Buschmann et al. 1997, Ivanova et al. 2005). Not only bacteria but also algal endophytes are able to breach the cuticula and cell wall and facilitate secondary infections. An example of this is the green endophytic alga Acrochaete operculata. It causes cellular damage to Chondrus crispus (Rhodophyta) and leads to secondary bacterial infections by facultative pathogens from the Cytophaga/Flavobacterium group (Correa & McLachlan 1994, Craigie & Correa 1996). Vibrio species have been reported as one of the opportunistic pathogens from diseased Porphyra and Laminaria fronds (Wang et al. 2008). Usually, the secondary bacterial infection contributes to further disintegration of the infected tissue, finally leading to thallus rupture.

Bacterial decomposition of dead and drying macroalgae on the beaches is rapid, indicating the abundant presence of decomposing bacteria in the living algal community (Uyenco et al. 1981, Delille & Perret 1991). A large proportion of bacteria in coastal waters are able to decompose macroalgal thalli (Uchida 1995, Uchida et al. 2002, Yoshimura et al. 2006). As bacteria are able to utilize algal nutrients selectively, they play a key role in the biotransformation (Chesters et al. 1956, Ramaiah & Chandramohan 1992). They release a variety of compounds which are subsequently used by other organisms (Yaphe & Baxter 1955, Yaphe 1962, Dimitrieva & Dimitriev 1996, Sawabe et al. 1998b, Ivanova et al. 2002a,b, Sakai et al. 2002, Romanenko et al. 2003). Biotransformation and nutrient recycling is initiated by bacterial enzymes such as cellulases, alginases, fucoidanases, pectinases and agarases. Many of these enzymes have biotechnological applications (Yamasaki et al. 1998, Wong et al. 2000, Descamps et al. 2006, Wang et al. 2006, Kim et al. 2009). Despite the large number of associated bacteria, these lytic activities have been found only in a small number of genera (Table 2).

Pathogenic bacteria in host-associated biofilms cause significant mortality to their hosts or cause sig-

nificant degradation of algal host tissue (Littler & Littler 1995, Correa & Sánchez 1996, Steinberg et al. 1997). Despite the prevalence of microbes in the ocean and the nature of pathogen-borne epidemics, diseases among marine macroalgae are rare (Table 3). This is even more remarkable, considering that algae do not have cell-based immune systems (Potin et al. 1999, Kubanek et al. 2003). However, evidence for induced defense reactions of algae upon pathogen recognition is emerging (Potin et al. 2002, Steinberg & de Nys 2002, Weinberger et al. 2005, Weinberger 2007).

Bacterial infections of macroalgae may cause obvious but non-necrotic changes in morphology, appearance of holes in the thallus, or discolorations causing light or dark areas. It is also possible that they may not affect the visible appearance of the alga at all (Andrews 1976, Uyenco et al. 1981, Correa 1997). The association of bacteria with abnormal tissue growth (galls) on marine macroalgae is well known and has been found in more than 20 species of red and brown macroalgae (McBride et al. 1974, Tripodi & Beth 1976, Tsekos 1982, Apt 1988 and literature therein). For example, bacterial symbionts of the *Roseobacter* group are able to cause such gall formations in the red macroalga *Prionitis* spp. (Ashen & Goff 2000). The metabolic consequences of gall formation for the macroalgae and its bacterial inhabitants remain unknown. But apparently the hypertrophic growth of gall-induced algal cells provides a suitable microhabitat for proliferation of the 'symbiont' (Apt & Gibor 1989, Ashen & Goff 1998).

Table 3. Macroalgal diseases caused by bacteria. (-) not specified

Macroalgae	Disease	Pathogen	Source
Heterokontophyta, Phaeoph	ıyceae		
Cystoseira nodicaulis	_	Unidentified <i>Proteobacteria</i>	Pellegrini & Pellegrini (1982)
Laminaria japonica	Hole-rotten disease	Pseudoalteromonas, Vibrio, Halomonas	Wang et al. (2008)
Laminaria japonica	Summer sporelings disease	Micrococcus sp.	Wu (1990)
Laminaria japonica	Red spot disease	Pseudoalteromonas bacteriolytica	Ezura et al. (1988), Sawabe et al. (1998b), Yumoto et al. (1989a,b)
Laminaria japonica	Spot-wounded fronds	Pseudoalteromonas elyakovii	Sawabe et al. (2000)
Undaria pinnatifida	Green decay diseases	Vibrio logei	Jiang et al. (1997)
Rhodophyta Chondrus crispus	-	Cytophaga/Flavobacterium group	Correa & McLachlan (1994), Craigie & Correa (1996)
Gracilaria conferta	-	Cytophaga/Flavobacterium and Vibrio group	Weinberger et al. (1997), Weinberger & Friedlander (2000b
Gracilaria gracilis	_	Undetermined bacteria	Jaffray & Coyne (1996)
Gracilaria gracilis	_	Pseudoalteromonas gracilis	Schroeder et al. (2003)
<i>Gracilaria</i> sp.	Rotten thallus syndrome	Vibrio sp.	Lavilla-Pitogo (1992)
Gracilaria verrucosa	Rotten thallus syndrome	Vibrio sp.	Beleneva & Zhukova (2006)
Hydrolithon, Sporolithon, Lithophyllum, Titanoderma and other coralline algae	Thallus holes	Plectonema terebrans	Ghirardelli (1998, 2002), Tribollet & Payri (2001)
Kappaphycus alvarezii	Ice-ice whitening	<i>Cytophaga-Flavobacterium</i> group <i>-Vibrio</i> group	Largo et al. (1995, 1999), Vairappan et al. (2008)
Mazzaella laminarioides	Deformative disease	Pleurocapsa sp.	Buschmann et al. (1997), Correa et al. (1993)
Porolithon onkodes and other coralline algae	Coralline lethal orange disease (CLOD)	-	Aeby (2007), Littler & Littler (1994, 1995)
Porphyra leucosticta	White rot disease	Vibrio sp.	Tsukidate (1977, 1983)
Porphyra leucosticta	Suminori	Flavobacterium sp.	Kusuda et al. (1992)
Porphyra yezoensis	Green spot rotting	Vibrio sp., Pseudomonas sp.	Fujita et al. (1972), Nakao et al. (1972)
Porphyra yezoensis	Anaaki	Flavobacterium sp.	Sunairi et al. (1995)

BENEFICIAL BACTERIAL-MACROALGAL INTERACTIONS

The role of epiphytic bacteria in maintaining the health of the host has received little attention. Though beneficial associations between bacteria and their host have been identified (Cole 1982, Weinberger et al. 1997, Dobretsov & Qian 2002, Rao et al. 2006), the advantages for algae are less obvious (Marshall et al. 2006).

Nutritional aspects and growth factors

Beneficial relationships may be based on the algal capacity to produce organic compounds and oxygen which are utilized by bacteria (Brock & Clyne 1984, Coveney & Wetzel 1989). In turn, bacteria mineralize organic substrate, supplying the algae with carbon dioxide, minerals and growth factors (Croft et al. 2005, 2006). Several studies indicated that marine epiphytic bacteria are important sources of fixed nitrogen for algae. Diverse epiphytic Cyanobacteria (Calothrix sp., Anabaena sp., and Phormidium sp.) that fix nitrogen and supply it to Codium species (Chlorophyta) have been described from certain locations (Dromgoole et al. 1978, Rosenberg & Paerl 1981). Another nitrogen fixer, Dichothrix fucicola, was located in association with populations of Sargassum natans and S. fluitans in the Sargasso Sea and the Gulf Stream (Carpenter 1972, Carpenter & Cox 1974). The nitrogen supply of Caulerpa taxifolia is provided by an endosymbiotic bacterium from the Agrobacterium-Rhizobium group, living in the algal rhizoids (Chisholm et al. 1996). A significant nitrogenase activity was attributed to the nitrogen-fixing Azotobacter sp., present on the macroalga Codium fragile subsp. tomentosoides (Head & Carpenter 1975), indicating nitrogen fixation within the association.

These associations secure the supply of dinitrogen to the macroalgae and might be one of the reasons for the successful invasion of these noxious macroalgae (like *Caulerpa taxifolia* or *Codium fragile*) into oligotrophic environments (Chisholm et al. 1996). Indeed, in other aquatic environments, some epiphytic Cyanobacteria like *Nostoc* sp., *Calothrix* sp. and *Anabaena* sp., living on the green macroalga *Chara vulgaris* seem to be the main nitrogen contributors (Ariosa et al. 2004).

In addition to nitrogen fixation, microbes play a role in the protection of the macroalga against toxic compounds such as heavy metals (Riquelme et al. 1997, Dimitrieva et al. 2006) or crude oil (Semenova et al. 2009). Microorganisms are able to detoxify, for example, heavy metals by precipitation, adsorption, or transformation to less toxic forms (Yurkov & Beatty 1998).

Bacteria also supply macroalgae with growth factors, e.g. by involvement in the production and turnover of various phytohormones and biostimulators of cell growth and development (Berland et al. 1972, Bolinches et al. 1988, Meusnier et al. 2001). For example, a favorable growth-promoting effect by the bacterium Pseudoalteromonas porphyrae was observed on Laminaria japonica (Dimitrieva et al. 2006). Plant hormone production seems to be widespread in various genera of marine bacteria. Maruyama et al. (1990) demonstrated that bacteria produce more cytokinin-type and auxin-type hormones when associated with macroalgae as compared to planktonic bacteria. Previous studies showed the ability of bacteria living on Ulva spp. (formerly Enteromorpha) to convert tryptophan into the phytohormone indole-3-acetic acid (IAA) (Fries 1975). In the macroalga *Prionitis lanceolata*, the gall formation mentioned above is associated with a bacterium of the Roseobacter group. IAA is overproduced in those algal galls in comparison to the rest of the thallus. Although the role of the bacterium in the physiology of the macroalga is not well understood, a coevolution has been suggested (Ashen et al. 1999, Ashen & Goff 2000).

Impact on macroalgal morphology

Beside nutrititional and growth promoting effects, bacteria affect the morphology and life cycle of macroalgae. Marine foliaceous green macroalgae such as Ulva spp. drastically lose their typical morphology when cultured aseptically (Fries 1975, Provasoli & Pintner 1980, Tatewaki et al. 1983). This phenomenon was also observed in the red macroalgae Dasya pedicellata C. Agardh and Polysiphonia urceolata (Dillwyn) Greville (Provasoli & Pintner 1972). Addition of adequate marine bacteria or their culture filtrates restored the typical morphology of these macroalgae (Nakanishi et al. 1999). Actually, morphogenesis in such macroalgae (Ulvaceae and Monostromaceae) is controlled by a restricted group of bacteria of the Bacteroidetes phylum, mainly Cytophaga and Flavobacterium spp. (Hanzawa et al. 1998, Nakanishi et al. 1999, Matsuo et al. 2005, Marshall et al. 2006). Furthermore, morphogenic effects on macroalgae were also demonstrated for members of the genera Caulobacter, Vibrio, Pseudomonas, Deleya, Escherichia and some Gram-positive bacteria (Nakanishi et al. 1996). These bacteria lose their ability to induce morphogenic effects when grown alone for several generations in marine media containing rich organic sources, but regain it under co-cultivation with Ulva in synthetic mineral media. Both 'partners' apparently depend on the metabolites produced by the other (Provasoli & Pintner 1980).

Thallusin was the first compound identified to induce thallus differentiation in macroalgae. It was produced from an epiphytic marine bacterium isolated from the alga *Monostroma* sp. (Matsuo et al. 2003). In order to maintain the common algal morphology, this compound has to be constantly supplied by the bacterium. Thallusin exemplifies a fundamental symbiotic chemical communication between macroalgae and epiphytic bacteria in the marine environment (Matsuo et al. 2005). However, the mechanism of modulation of algal morphology by thallusin is not yet understood (Marshall et al. 2006).

Effect on spore germination and macroalgal colonization

Recently, it was discovered that bacterial biofilms play a role in spore germination and subsequent colonization of new substrates by algae. A set of diverse bacterial species isolated from marine surfaces colonized by Ulva spp. either stimulated or inhibited the zoospore settlement of this green macroalgae (Patel et al. 2003, Tait et al. 2005). Phylogenetic analysis revealed that the isolated bacteria belonged to the Gammaproteobacteria, the Cytophaga-Flavobacteria-Bacteroidetes group and Alphaproteobacteria. Most of these microorganisms revealing stimulating effects were strains of Vibrio and Shewanella species. Effects on spore settlement were strain- but not species-specific, and the activity varied with the age of the biofilm. A positive correlation between zoospore settlement of Ulva linza and bacterial biofilm density indicates the important role of bacterial biofilms in the development of algal communities (Marshall et al. 2006).

It appears that these are not isolated cases. Of the 192 bacterial strains isolated from the surfaces of seaweeds from China, 63 isolates were shown to be inhibitory against the settlement of algal spores (Ma et al. 2009). Also, a number of diverse bacterial metabolites affect the germination of spores of various macroalgae (Egan et al. 2001b, Matsuo et al. 2003, Dimitrieva et al. 2006) (Table 4). For example, an antialgal peptide that inhibited spore germination was produced by Pseudoalteromonas tunicata isolated from Ulva australis (Egan et al. 2001b). The fatty acids cis-9-oleic acid and 2-hydroxymyristic acid produced by the bacterium Shewanella oneidensis (Bhattarai et al. 2007) as well as a peptidic compound produced by the bacterium Alteromonas sp. (isolated from the red alga Rhodymenia sp.) exhibited activity against spores of *U. lactuca* (Silva-Aciares & Riquelme 2008).

As mentioned, bacterial biofilms play an important role in initiation of colonization processes. A preferential settlement of spores on specific bacterial biofilms producing morphogenic compounds may facilitate a close association of the developing macroalgae with these specific bacterial 'episymbionts' (Joint et al. 2002, Patel et al. 2003). As we discuss later, these epibionts play a protective role by releasing compounds into the surrounding seawater that prevent extensive biofouling of the surface or act against microbial pathogens (Armstrong et al. 2001, Wiese et al. 2009b).

CHEMICAL INTERACTIONS

Since the 1970s it has been known that chemical compounds are the basis of many aspects of communication and molecular interaction between aquatic organisms (Bhakuni & Silva 1974, Scheuer 1978, Hay 2009). However, studies on these chemical interactions within marine communities are relatively new as compared to the analyses of feeding relationships (Paul & Puglisi 2004). More intense investigations of the large variety of interactions between hosts and microbes and between different microbes should reveal the different communication pathways, which include the production of defensive or deterrent compounds, pheromones, attractants and other signal substances. Some of these compounds act in a general way while others have highly specific modes of action (Davies et al. 1998, Rasmussen et al. 2000, Da Gama et al. 2002). Chemically mediated interactions like fertilization, allelopathy, and prey detection between macroalgae and other marine organisms fundamentally depend on the sensing of chemicals at or near surfaces (Steinberg & de Nys 2002). It has been demonstrated that the microbial colonization of various host organisms might be controlled by host-derived molecules (Wahl et al. 1994, Rao & Fujita 2000). However, little is known about the potential role of secondary metabolites in the regulation and development of associations. Other chemically mediated types of microbial behaviors such as chemotaxis, adhesion, swarming and biofilm formation are much better understood (Parsek & Greenberg 2000, Ren et al. 2002, Qian et al. 2007).

Antibiotic activities of macroalga-associated bacteria

Antimicrobial activity is widespread among algaassociated bacteria. Wiese et al. (2009b) showed that almost 50% of a total of 210 isolates of the epiphytic bacterial community of *Saccharina latissima* (Baltic Sea, Germany) inhibited the growth of at least one microorganism from a panel covering Gram-negative and Gram-positive bacteria. Burgess et al. (1999) demonstrated that 35% of the surface-associated bacteria isolated from various macroalgae and invertebrates in

Table 4. Bioactive compounds produced by macroalgal associated bacteria. AF = antifungal activity, AP = antiprotozoal activity, AS = antisettlement activity, GNI = antibiotic activity against Gram-negative bacteria, GPI = antibiotic activity against Gram-positive bacteria, MG = morphogenesis activity, PH = photosynthetic compound

Compound	Chemical class	Activity	Producing bacterium	Macroalgae	Source
2,4 dibromo-6- chlorophenol	Halogenated phenol	GPI	Pseudoalteromonas luteoviolacea	Padina australis	Jiang et al. (2001)
2,4-diacetyl phloroglucinol	Phenol	GPI	Pseudomonas sp.	Ceratodyction spongiosum	Isnansetyo et al. (2001)
Chlorophyll d	Pyrrole	PH	Acaryochloris sp.	Ahnfeltiopsis flabelliformis	Murakami et al. (2004)
Cyclo-[isoleucyl- prolylleucyl-alanyl]	Tetrapeptide	GPI	Pseudoalteromonas sp.	Digenea sp.	Rungprom et al. (2008)
Cyclo-(L-prolyl- L-glycine)	Diketopiperazines	GPI	Pseudoalteromonas luteoviolacea	Padina australis	Jiang et al. (2001)
Cyclo-(L-phenyl alanyl-4R)- hydroxy-L-proline	Diketopiperazines	GPI	Pseudoalteromonas luteoviolacea	Padina australis	Jiang et al. (2001)
Haliangicin	β -methoxyacrylate	AF	Haliangium luteum	Undetermined algae	Fudou et al. (2001)
Korormicin	γ -lactone derivate	GNI	Pseudoalteromonas sp. F-420	Halimeda sp.	Yoshikawa et al. (1997)
Macrolactines G, M	Lactones	GPI	Pseudomonas sp.	Red algae	Gerard et al. (1997)
Macrolactines G, M, A, F	Lactones	GPI	<i>Bacillus</i> sp. PP19-H3	Schizymenia dubyi	Nagao et al. (2001)
Massetolide A	Lipopeptide	GPI	Pseudomonas sp.	Red algae	Gerard et al. (1997)
Pelagiomycin A	Phenazine	GPI, GNI	Pelagiobacter variabilis	Pocockiella variegata	Imamura et al. (1997)
-	Peptide	AS	Pseudoalteromonas tunicata	Ulva lactuca	Egan et al. (2001b)
-	Peptide	AS	<i>Alteromonas</i> sp. Ni1-LEM	Rhodymenia sp.	Silva-Aciares & Riquelme (2008)
Protein 30,7 kDa	Protein	GPI	Bacillus licheniformis	Fucus serratus	Jamal et al. (2006)
Thallusin	Pyridine	MG	Cytophaga/ Flavobacterium/ Bacteroidetes group	Monostroma sp.	Matsuo et al. (2003)
Violacein	Alkaloid	AP	Pseudoalteromonas tunicata, P. ulvae	Ulva australis	Matz et al. (2008)
YP1	Tambjamine	AF	Pseudoalteromonas tunicata	Ulva australis	Franks et al. (2006)

Scottish waters produced antimicrobial substances. From a total of 280 strains isolated from 7 macroalgae, 21% showed antibacterial activity (Boyd et al. 1999b). Of the isolates from 9 brown macroalgae, 20% were antibiotically active as were 33% of the isolates from 9 red algae collected from Japanese waters of the Pacific Ocean (Kanagasabhapathy et al. 2006, 2008). Penesyan et al. (2009) obtained 325 bacterial isolates from the surface of *Delisea pulchra* and *Ulva australis* in Australia and demonstrated antibiotic activity of 12% of the strains. *Microbulbifer* sp. was the dominant biological active bacterium in this study.

Antimicrobial active isolates from all mentioned macroalgae were phylogenetically assigned to diverse genera comprising *Pseudomonas, Pseudoalteromonas, Stenotrophomonas, Vibrio, Aeromonas, Shewanella, Streptomyces* and *Bacillus* species (Wiese et al. 2009b). Many *Bacillus* species are efficient producers of antimicrobial compounds and therefore highly successful colonizers of macroalgal surfaces (Trischman et al. 2004, Kanagasabhapathy et al. 2006). Most of the isolates with high antifouling activity obtained by Burgess et al. (2003) were identified as *Bacillus* species, i.e. *B. pumilus, B. licheniformis* and *B. subtilis*. Besides

Bacillus species, Pseudoalteromonas spp. are commonly found on marine macroalgae (Wang et al. 2008). Many of them also produce biologically active molecules (Holmström et al. 1998, Kalinovskaya et al. 2004, Skovhus et al. 2007). For example, 3 epiphytic strains of Pseudoalteromonas sp. isolated from Ulva lactuca were able to inhibit the growth of a variety of bacteria and fungi (Egan et al. 2000, 2001a,b): P. tunicata was able to prevent biofouling by growth inhibition of other surface-associated microorganisms. For this purpose, it produced at least 5 target-specific compounds (Holmström et al. 1992, James et al. 1996) (Table 4), including a large antibacterial protein (James et al. 1996), a small polar heat-stable anti-larval molecule (Holmström et al. 1992), a putative antialgal peptide (Egan et al. 2001b), an antifungal alkaloid (Franks et al. 2006) and also violacein, a purple pigment that inhibits protozoan grazing (Matz et al. 2008). This chemical arsenal has been shown to be important for the survival of P. tunicata in its highly competitive marine surface environment (Rao et al. 2005, 2007, Thomas et al. 2008, and references therein). Production of a range of compounds active against a variety of target organisms is a characteristic feature of these bacteria and may largely promote their competition and colonization of algal surfaces (Holmström & Kjelleberg 1999, Patel et al. 2003, Rao et al. 2005).

Bacteria producing antibiotic substances reflect an important part of bacterial communities on surfaces of marine organisms as compared to free-living bacterial communities (Mearns-Spragg et al. 1998, Zheng et al. 2005, Kanagasabhapathy et al. 2008). However, we still have a long way to go in understanding how bacteria really protect their hosts and what kind of compounds they may produce under the multifactorial natural conditions in situ (Bode et al. 2002). For example, a marine actinomycete (SS-228) was shown to produce an antibiotic compound only when the growth medium was supplemented with Laminaria sp., a macroalgae common in the habitat from which the strain was obtained (Okazaki et al. 1975). Inhibitory activities against other epiphytic bacteria are of great importance in microhabitats such as an algal surface, where competition for an attachment site is frequent (Lemos et al. 1985, Mearns-Spragg et al. 1998, Yan et al. 2002, Rao et al. 2007).

Chemical defense of macroalgae against microorganisms

The defending interaction of macroalgae with biofilms is well documented and the surfaces of many macroalgae remain relatively free of epibiosis. However, few studies have investigated if secondary

metabolites are released from macroalgae and affect planktonic bacteria directly (Nylund & Pavia 2005, Paul et al. 2006, Dubber & Harder 2008, Lam et al. 2008a). Lu et al. (2008) showed that macroalgae like Ulva clathrata have an inhibitory effect on Vibrio anguillarum, a fish and mussel pathogen, although not reducing the total amount of heterotrophic bacteria. This effect was explained by some unknown chemical substances, either released from U. clathrata or produced by the alga-associated microorganisms. Recently, Pang et al. (2006a) observed that in polycultures with the red macroalga Gracilaria textorii the total number of Vibrio species (V. alginolyticus and V. logei) was controlled. Even more, after inoculation of V. parahaemolyticus into cultures of the red macroalga Grateloupia turuturu, the bacterium was inhibited in its growth and finally disappeared from the cultures (Pang et al. 2006b).

Antibiotic activities of macroalgal extracts and metabolites

Given that algae lack cell-based immune responses and are continuously exposed to a broad array of potentially deleterious microorganisms, it is reasonable to hypothesize that the production of bioactive secondary metabolites acts as a fundamental mechanism of antimicrobial defense to deter microbial attack (Engel et al. 2002). Macroalgae may secrete antifouling compounds into the surrounding seawater and retain antigrazing compounds within the thallus structure (Armstrong et al. 2001). The production of inhibitory substances from macroalgae was noted as early as in 1917 (Ara 2001) and since then the antibacterial activity of extracts of macroalgae has been described in many studies around the world (Yan et al. 2003, Bhakuni & Rawat 2005, Puglisi et al. 2007, Dubber & Harder 2008, and literature therein) (Table 5). Many different compounds produced by macroalgae exhibit antibiotic activity, for example fatty acids, phenols, acetylenes, various terpenes, coumarins, carbonyls, and polysaccharides (Bhakuni & Silva 1974, Hoppe et al. 1979 and literature therein, Ballantine et al. 1987, Lustigman et al. 1992, Lobban & Harrison 1996, Steinberg et al. 1997, Potin et al. 1999, Ara 2001, Sandsdalen et al. 2003; Table 5). These biological activities might have a protective function by elimination or control of the number of pathogens, epiphytes or endophytes (Hornsey & Hide 1976b, Hoppe et al. 1979, Smit 2004, Plouguerne et al. 2008).

While a large proportion of the literature deals with antimicrobial activities of marine macroalgal extracts and secondary metabolites (Table 5), little is known about how these compounds act in an ecological con-

Table 5. Examples of antimicrobial and antifouling compounds isolated from macroalgae. AV = antiviral, AE = antifouling, AF = antifungal activity, GNI = antibiotic activity against Gram-negative bacteria, GPI = antibiotic activity against Gram-positive bacteria

Macroalga	Compounds	Activity	Source
Chlorophyta			
Avrainvillea nigricans	5'-hydroxy isoavrainvilleol	GPI	Colon et al. (1987)
Caulerpa spp.	Sesquiterpenoids	GPI, GNI	Paul et al. (1987)
Codium iyengarii	Iyengaroside-A, clerosterol galactoside	GPI, GNI	Ali et al. (2002)
Penicillus capitatus	Capisterones A, B	AF	Puglisi et al. (2004)
Tydemania expeditionis	Sulphated triterpenoids	AF	Jiang et al. (2008)
Úlva fasciata	Labdane diterpenoids	GNI	Chakraborty et al. (2010)
Heterokontophyta, Phaeophyceae			
Canistrocarpus cervicornis	Diterpenes	AE	Bianco et al. (2009)
Cystoseira spinosa var. squarrosa	Tetraprenyltoluquinol	GPI, GNI	Amico et al. (1988)
Cystoseira tamariscifolia	Methoxybifurcarenone	GNI	Bennamara et al. (1999)
Dictyotaceae	Dolabellane derivatives	AF	Tringali et al. (1986)
Dictyopteris zonarioides	Zonarol & isozonarol	AF	Fenical et al. (1973)
Dictyota menstrualis	Dictyol D, pachydictyol A	AE	Schmitt et al. (1995)
Dilophus guineensis	Dilophic acid	GPI	Schlenk & Gerwick (1987)
Dilophus okamurai	Spatane-type diterpenes	AE	Kurata et al. (1988)
Fucus vesiculosus	Polyhydroxylated fucophlorethol	GPI, GNI	Sandsdalen et al. (2003)
Landsburgia quercifolia	1,4-naphthoguinone	GPI, AF	Perry et al. (1991)
Lobophora variegata	Lobophorolide	AF	Kubanek et al. (2003)
Sargassum spp.	Polyphenols	AE, GNI	Sieburth & Conover (1965)
Stoechospermum marginatum	Spatane diterpenoids	GPI	De Silva et al. (1982)
Stoechospermum marginatum	Sulfated fucan	AV	Adhikari et al. (2006)
Rhodophyta			
Asparagopsis armata	Halomethanes, haloether, haloacetales	GPI, GNI	Paul et al. (2006)
Bonnemaisonia hamifera	Poly-brominated 2- heptanone	GNI	Nylund et al. (2008)
Callophycus serratus	Bromophycolides	AF	Lane et al. (2009
Dasya pedicellata var. stanfordiana	P-hydroxybenzaldehyde	GPI, GNI	Fenical & McConnell (1976)
Delesseriaceae	Almazole D	GNI	N'Diaye et al. (1996)
Delisea pulchra	Halogenated furanones	AE	Maximilien et al. (1998)
Delisea pulchra	Halogenated furanones	GPI, GNI	Wright et al. (2006)
Grateloupia indica	Galactan sulphate	AV	Chattopadhyay et al. (2007)
Laurencia chilensis	3-hydroxi-4-methyl acetophenone	GPI, GNI	Valdebenito et al. (1982)
Laurencia majuscula	Brominated sesquiterpenes	GPI, GNI	Vairappan et al. (2010)
Laurencia pannosa	Pannosanol, pannosane	GNI	Suzuki et al. (2001a)
Laurencia spp.	Laurinterol, isolaurinterol	GNI	Vairappan et al. (2001b)
Laurencia spp. Laurencia spp.	Brominated sesquiterpenes	GPI, GNI	Bansemir et al. (2004)
Osmundaria serrata	Lanosol ethyl ether	GPI, GNI, AF	Barreto & Meyer (2006)
Rhodomela confervoides	Bromophenols	GPI, GNI	Xu et al. (2003)
Sphaerococcus coronopifolius	Bromosphaerone,	GPI, GIVI	Etahiri et al. (2001)
Spinaerococcus coronophonus	12S-hydroxybromosphaerodiol	GII	Lami et al. (2001)

text (Engel et al. 2002). Engel et al. (2006) explored the antimicrobial effects of extracts from several marine macroalgae against algal saprophytes, parasites, and pathogens. It was concluded that the antimicrobial metabolites selectively target marine microorganisms, although the susceptibility of ecologically relevant bacteria has rarely been studied (Yoshikawa et al. 1997, Puglisi et al. 2007, Kanagasabhapathy et al. 2008).

From an ecological perspective, antimicrobial defense mechanisms of marine macroalgae may reduce epibiosis, inhibit premature decomposition and directly provide resistance to infectious diseases (Engel et al. 2006). The required defense substances may be expressed constitutively or may be induced in response

to contact with the target organisms and their chemical signals, respectively (Cronin & Hay 1996, Amsler & Fairhead 2005). The inducible defense allows metabolic cost savings and is advantageous due to a lower risk of autotoxicity and resistance adaptation (Macaya et al. 2005, Medeiros et al. 2007, Macaya & Thiel 2008). An increasing number of studies is related to the induced defense mechanisms of macroalgae against herbivores. Research on the induced defense mechanisms against microbial pathogens or epibiosis is still limited. Recently, Vairappan et al. (2010) were the first to demonstrate the highly selective antibiotic activity of extracts from the epiphytic macroalga *Laurencia majuscula* against 6 algal pathogenic bacteria. They

were able to identify 4 halogenated compounds whose concentration increased more than 120% during an ice-ice disease outbreak in the host basibiont, the macroalga *Kappaphycus alvarezii* (Table 5). Interestingly, in another species of these red macroalgae, *Laurencia obtusa*, the dynamics of vesicle transport from *corps en cerise* (specific structures where those macroalgae accumulate these halogenated secondary metabolites) and their eventual exocytosis were shown to be induced in relation to bacterial biofilms (Paradas et al. 2010). The authors suggested a direct correlation with this process and the inhibition of microfouling on the macroalgal surface.

Oxidative burst—an antibacterial response of macroalgae

In addition to the production of antibiotic compounds, macroalgae are able to use oxidative burst as a defense mechanism as described for higher plants (Weinberger et al. 1999, 2002, Dring 2005, Ar Gall et al. 2008). This process is a non-specific defense response against surface colonization typically characterized by a rapid activation of reactive oxygen species causing death of the pathogen (Bouarab et al. 1999, Weinberger & Friedlander 2000a,b, Steinberg & de Nys 2002, Potin 2008). The oxidative burst is triggered by cell-cell recognition, involving the perception of signal molecules or cell wall compounds from the invading organism by the algal cell membrane (Küpper et al. 2006). Common elicitors of non-specific host responses are oligosaccharides, glycoproteins, and glycopeptides (Küpper et al. 2001). Recently, other compounds such as methyl jasmonate and free fatty acids (in particular arachidonic and linolenic acid) were also found to be strong triggers of an oxidative burst in Laminaria digitata (Küpper et al. 2009). In particular, the elicitation of defense mechanisms by oligosaccharides has been studied in macroalgae (e.g. Potin et al. 1999, Ar Gall et al. 2008). This involves the degradation of the host cellwall polysaccharides by enzymes released from various pathogens, comprising epiphytic bacteria (Weinberger et al. 1999, Weinberger & Friedlander 2000a,b, Küpper et al. 2002) and algal endophytes (Bouarab et al. 1999, Küpper et al. 2002). This was shown for the brown alga L. digitata, where oligosaccharides derived from alginate elicit a distinct oxidative burst in the cortical cells of sporophytes and thereby control the populations of epiphytic bacteria (Küpper et al. 2001). Küpper et al. (2002) investigated 45 species of brown algae with regard to their ability to respond to oligoalginates with an oxidative burst. They found that a total of 15 macroalgal species reacted, all of them belonging to an alginate-rich group with complex thallus morphology. But there is also evidence for a constitutive release of hydrogen peroxide in red macroalgae e.g. *Solieria chordalis*, as a mechanism to prevent both the establishment of bacterial biofilms and the subsequent development of algal epiphytes (Ar Gall et al. 2008). In addition to algal elicitors, Küpper et al. (2006) demonstrated that components of the outer membranes of Gram-negative bacteria may be considered as exogenous elicitors in brown macroalgae. In the red agarophyte *Gracilaria conferta* bacterial elicitors are presumably represented by a low-molecular weight peptide (Weinberger & Friedlander 2000a).

These results demonstrate that defense pathways exist in marine macroalgae which are similar to those known from animals and land plants (Bouarab et al. 2004, Weinberger 2007). Interestingly, the oxidative burst is known to direct a variety of secondary defense responses like the generation and release of volatile halogenated compounds and the peroxidation of fatty acids (Küpper et al. 2001, 2006, Weinberger et al. 2002, Cosse et al. 2007, Potin 2008). Induction of the oxidative burst within red and brown macroalgae is followed by a rapid increase in emission of iodine-containing halocarbons, molecular iodine, and also in the brominating activity (Weinberger et al. 1999, Palmer et al. 2005).

Quorum sensing and its role in bacterial-macroalgal interactions

Quorum sensing (QS) is a cell to cell communication mechanism that allows bacteria to coordinate swarming, biofilm formation, stress resistance, and production of secondary metabolites in response to an excess of the threshold of QS signals (Paul & Ritson-Williams 2008, Dobretsov et al. 2009). Gram-negative bacteria, such as *Pseudomonas* or *Vibrio* strains, produce N-acyl homoserine lactones (AHLs) as signalling compounds. *Pseudomonas* spp. are also known to produce diketopiperazines acting as QS signals (Dickschat 2010). The signal molecules γ -butyrolactones and oligopeptides are known to be synthesized by Gram-positive bacteria, e.g. members of the genera *Streptomyces* or *Bacillus* (reviewed by Dobretsov et al. 2009).

The interaction between zoospores of eukaryotic green macroalgae (Ulvales) with *Vibrio anguillarum* indicates algal susceptibility to quorum sensing AHL molecules (Joint et al. 2002, Wheeler et al. 2006). Although the specific mechanism regulating these responses to AHLs is not known, it was shown that the AHL molecules affect the calcium influx into the spores of *Ulva* sp., affecting their motility towards the surfaces where they eventually settle (Diggle et al. 2007, Joint et al. 2007). In addition, it has been demonstrated that

life cycle completion and spore release in the red epiphytic alga *Acrochaetium* sp. strongly depend on AHLs, which are produced by bacteria associated with the algal basibiont *Gracilaria chilensis* (Weinberger et al. 2007). These findings of AHL perception in green and red algae confirm that AHL signalling is more widespread among eukaryotes than previously thought. This indicates a more general importance of the associated microbial communities in interactions with macroalgae. As we mentioned before, bacterial biofilms play an important role in the development of macroalgal communities. Hence, the ability to exploit a bacterial sensory system makes an important contribution to the ecological success of macroalgae (Tait et al. 2005, Joint et al. 2007).

Algae reduce harmful effects by controlling bacterial colonization by interfering with the bacterial QS systems, which regulate several bacterial traits related to colonization (Gram et al. 1996, Steinberg et al. 1997, Dworjanyn et al.1999). During the past decade it has been shown that various macroalgae are able to stimulate, inhibit or inactivate QS signals in bacteria by producing QS inhibitors or analogues thereof (Maximilien et al. 1998, Joint et al. 2007, Kanagasabhapathy et al. 2009, Table 6). The Australian red macroalga Delisea pulchra produces halogenated furanones, structural analogues to N-acyl homoserine lactones. These furanones protect the algal surfaces by interfering with AHL-regulated processes and selectively inhibit bacterial colonization and biofilm formation (Maximilien et al. 1998, Rasmussen et al. 2000, Manefield et al. 2002). In addition to the furanones of *D. pulchra*, a variety of

bacteria and eukaryotes have been shown to produce cyclic dipeptides that can act as AHL mimics and affect QS-regulated behaviour in other bacteria (Dobretsov et al. 2009, Dickschat 2010). Recently, Kanagasabhapathy et al. (2009) suggested that certain epibiotic bacteria from the brown macroalgae Colpomenia sinuosa may play a role in defense mechanisms and suppress the settlement of other competitive bacteria by producing quorum sensing inhibitors (QSI) or QSI-like compounds. AHL-antagonists and inhibitors of the AHL regulatory system lead to an inhibition of bacterial colonization in an entirely different way from antibiotic substances (Givskov et al. 1996, Manefield et al. 1999, 2002). Their action results in lower bacterial abundance on the algal surface relative to other surfaces that are not controlled by such or similar mechanisms (Maximilien et al. 1998, Steinberg & de Nys 2002).

BIOSYNTHETIC ORIGIN OF BIOLOGICALLY ACTIVE METABOLITES

Macroalgae are prolific natural product synthesizers. Until now, approximately 2000 secondary metabolites have been isolated from these algae, most of them displaying biological activities (Medeiros et al. 2007). Nevertheless, marine microorganisms have also been shown to be an important source for novel natural products (Fenical 1993, Penesyan et al. 2010). Considering that so far virtually all macroorganisms collected and extracted for chemical studies include the associated microorganisms, questions about the true biosyn-

Table 6. Quorum sensing (QS) inhibitors observed in algae (modified from Dobretsov et al. 2009). AHL = N-acyl homoserine lactones

Algae	Compound	Activity	Source
MICROALGAE Chlorophyta Chlamydomonas reinhardtii	Lumichrome	Mimic AHL signals	Rajamani et al. (2008), Teplitski et al. (2004)
MACROALGAE Chlorophyta Caulerpa sp.	Not identified (algal extract)	AHL inhibitors	Skindersoe et al. (2008)
Heterokontophyta, Phaeophycea			
Laminaria digitata	Hypobromous acid	Deactivates AHL by interfering with QS genes	Borchardt et al. (2001)
Rhodophyta		3	
Ahnfeltiopsis flabelliformis	Betonicine, floridoside and isethionic acid	Compete with AHL signals	Kim et al. (2007)
Delisea pulchra	Halogenated furanones	Mimic AHL signals, inhibit gene expression	Manefield et al. (1999)
Galaxauraceae	Not identified (algal extract)	AHL inhibitors	Skindersoe et al. (2008)
Laurencia sp.	Not identified (algal extract)	AHL inhibitors	Skindersoe et al. (2008)
Unidentified red algae	Not identified (algal extract)	AHL inhibitors	Skindersoe et al. (2008)

thetic origin of molecules isolated from macroalgae need to be addressed. In several cases, it has already been proven that metabolites initially assigned to the basibionts are in fact of microbial origin (Jensen & Fenical 1994, Schmidt 2005, Dobretsov et al. 2006a, König et al. 2006, Egan et al. 2008, Jones et al. 2008, Lane & Kubanek 2008, Rungprom et al. 2008). Chlorophyll d, for example, is not a constituent of red algae as was described for more than 60 yr. In fact, it does not even occur in eukaryotes at all, but is produced by the cyanobacterium Acaryochloris spp. (Murakami et al. 2004, Larkum & Kühl 2005; Table 4). Further studies like this including labelling experiments and genetic studies of biosynthetic genes will reveal the producing part of the association for other macroalga-epibiontsystems.

APPLIED ASPECTS OF BACTERIAL-MACROALGAL INTERACTIONS

The development and expansion of macroalgal farming stresses the need for understanding the relationship between macroalgae and symbiotic as well as pathogenic microorganisms in both wild and cultivated populations (Correa 1996). The extensive farming of brown, red and green macroalgae in Asia has shown that all are susceptible to disease (Craigie & Correa 1996). In aquaculture, secondary bacterial infections contribute to disintegration of the infected tissue, finally leading to thallus rupture, breaking-off of macroalgae from culture lines and massive biomass loss (Vairappan et al. 2001a, 2008). Infectious diseases in macroalgae might be highly destructive as in the case of the green spot rot of Undaria spp. and the white rot in Nereocystis spp. (Lavilla-Pitogo 1992, Correa et al. 1993, Park et al. 2006, and references therein). Red rot disease is caused by the fungal pathogen Phytium porphyrae affecting different Porphyra species, one of the most popular edible and extensively cultivated macroalga, especially in Asia. In Japan, the disease causes losses of about 40 to 60 million US\$ every year (Woo et al. 2002). Despite some knowledge of the pathogens and diagnosis of the diseases, little is known concerning the ecology of microbial pathogens of these macroalgae (Andrews 1976, Jaffray & Coyne 1996, Correa 1997; Table 3). The growing use of macroalgae and their products enforces the need to understand the nature and severity of diseases that can be anticipated in macroalgal mariculture (Apt 1984). The development of appropriate strategies will provide adequate and improved protection of the macroalgae in order to lower commercial risks (Park et al. 2006). For this purpose, pathogens of macroalgae have to be identified and characterized at the species level and strategies have to be developed to prevent infection of macroalgae by such pathogens.

On the other hand, there is an increasing interest in algae-associated microorganisms as a source for natural bioactive substances (Egan et al. 2008). Algaassociated bacteria represent an important potential source of new substances and have been identified as a promising source of new bioactive and antimicrobial metabolites (Yan et al. 2002, Penesyan et al. 2009). Novel infectious diseases of humans, reemerging diseases, and the widespread distribution of multidrugresistant pathogenic bacteria clearly indicate a strong need to develop new antibiotics (Fenical 1993, Skindersoe et al. 2008). Table 4 provides a comprehensive overview of compounds produced by macroalgaassociated bacteria. Most of these compounds including peptides or diketopiperazines were produced by members of *Pseudoalteromonas*.

CONCLUSIONS AND PERSPECTIVES

Epibiotic bacteria are fast colonizers, highly adaptative and capable of rapid metabolization of algal exudates, and therefore play a key role in the colonization and biofouling process on macroalgae (Lachnit et al. 2009). Chemical interactions between different species of bacteria affect the production and secretion of secondary metabolites in these microorganisms (Jensen & Fenical 1994, Burgess et al. 1999, Rao et al. 2005). The competition for space between epibiotic bacteria based on compounds may provide an antifouling protection to the algal basibiont (Armstrong et al. 2001, Rungprom et al. 2008). Since symbiotic bacteria, pathogens, and foulers first select, then settle, and finally attach to the host, macroalgae may prevent damage by also producing secondary metabolites that inhibit one or all of these steps. Such metabolites represent the chemical first line of defense against microbial challenge. 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 (Egan et al. 2000, Than et al. 2004, Rao et al. 2007, Lane & Kubanek 2008). 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 (Penesyan et al. 2010). The selection of these 'symbiotic' microorganisms might also be chemically mediated (Lachnit et al. 2010). However, after more than 20 yr of research on this topic, there is still no experimental evidence demonstrating if or how host organisms selectively attract and harbor such epibionts (Harder 2009). There is an enormous variety of different metabolites as possible mediators of interspecies interactions in the algal biosphere, including products of the algal host, pathogens, foulers, and symbionts. Although bacterial secondary metabolites are likely to participate in such interactions, little is known about the role of bacterial secondary metabolites in mediating such ecological interactions (Maximilien et al. 1998, Meusnier et al. 2001). An interesting aspect is the chemical interaction between hosts and their symbionts, the details, including host specificity, nutrients and metabolite exchange, and cell-cell communication have to be revealed by further studies.

In order to develop a better understanding of chemically mediated communication on and with the alga, it is important to detect the allocation of secondary metabolites within the host tissues (Dworjanyn et al. 1999, 2006, Sudatti et al. 2008). For such investigations, it is essential to measure the in situ concentrations and the methods of release of putative deterrents (Krug et al. 2006, Paradas et al. 2010). Only a few analyses have attempted to measure the concentration of these compounds in seawater and host tissues (de Nys et al. 1998, Maximilien et al. 1998, Dworjanyn et al. 1999, Manefield et al. 1999, Kubanek et al. 2003, Paul et al. 2006, Sudatti et al. 2006). The recent improvement of techniques for detecting natural products on tissue surfaces, such as desorption electrospray ionization mass spectrometry (DESI-MS), will provide new sensitive and effective approaches to resolve localization and origin of these compounds (Lane et al. 2009, Nyadong et al. 2009). Improved chemical and molecular biological methods coupled with ecologically relevant bioassays are likely to lead to new discoveries (Hay 2009) and to a better understanding of the development of complex chemical defense mechanisms against microbial threats. The results will enforce our knowledge of distinct functions of bacteria in various kinds of interactions between macroalgae and bacteria, as well as within the bacterial community.

In addition to the chemical point of view, we also need more detailed studies of the bacterial communities and their development, using new molecular approaches. Until now, most investigations have focussed on 1 or 2 different techniques to describe communities. From our point of view, a synopsis between culture-dependent and -independent methods is needed. Various authors have already shown that the diversity of a given bacterial community cannot be described by applying either genetic or culture-based methods (Jensen et al. 1996, Tujula et al. 2006, Longford et al. 2007, Penesyan et al. 2009). Since most studies presented qualitative information but did not analyze abundances and ratios that occur *in situ*, the

application of quantitative or semi-quantitative methods is required, such as cloning techniques, cytogenetic fluorescence in situ hybridization (CFISH), real time quantitative PCR (qPCR), denaturing gradient gel electrophoresis (DGGE), and terminal restriction fragment length polymorphism of DNA (T-RLFP), as well as metagenome studies. The genes used for these investigations should comprise phylogenetic markers as well as functional genes in order to obtain insight into biosynthetic pathways and their regulation, in particular of those used in the production of the interacting small molecules. Community description should be extended by studying the geographic distribution among different host populations with respect to the associated bacterial communities, which are necessary to clarify eventual effects (Wright et al. 2000).

To sum up, there is a strong need to integrate aspects of ecology, cell biology, and chemistry in further studies (Steinberg & de Nys 2002) in order to understand the production and the distribution of the bioactive molecules *in situ* as well as their ecological impact on the macroalgal-bacterial interactions.

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Appendix 1. Studies of bacterial communities attached to the surface of different macroalgae over the last 40 yr. CUD = culture dependent methods. Microscopical methods: EPF = epifluorescence microscopy, EM = electron microscopy, SEM = scanning electron microscopy, STE = stereoscopic microscopy, TEM = transmission electron microscopy. Molecular techniques: CLO = cloning, CFISH = cytogenetic fluorescence in situ hybridization, DGGE = denaturing gradient gel electrophoresis, FISH = fluorescence in situ hybridization, IFN = immunofluorescent detection, RQT = real time quantitative PCR, RFLP = restriction fragment length polymorphism, TRFLP = terminal restriction fragment length polymorphism of DNA

Macroalga	Methodology	Location	Source
Chlorophyta			
Chlorophyta spp.	STE	San Juan Island, USA	Bland & Brock (1973)
Caulerpa cupressiodes	DGGE, SEM	Tampa Bay, USA	Delbridge et al. (2004)
Caulerpa mexicana	DGGE, SEM	Tampa Bay, USA	Delbridge et al. (2004)
Caulerpa prolifera	DGGE, SEM	Tampa Bay, USA	Delbridge et al. (2004)
	EM, STE	Tampa Bay, USA	Dawes & Lohr (1978)

Appendix 1 (continued)

Macroalga	Methodology	Location	Source
Caulerpa racemosa	TRFLP, SEM	Hong Kong	Dobretsov et al. (2006b)
Caulerpa sertulariodes	DGGE, SEM	Tampa Bay, USA	Delbridge et al. (2004)
Caulerpa taxifolia	RFLP	Mediterranean, Tahiti,	
		Philippines, Australia	Meusnier et al. (2001)
Chaetomorpha brachygona	CUD	Tolo, Hong Kong	Kong & Chan (1979)
Chaetomorpha media	CUD	Anjuna & Baga, India	Ramaiah & Chandramohan (1992)
Chaetomorpha sp.	CUD	Vellar Estuary, India	Lakshmanaperumalsamy & Purushothaman (1982)
Chara aspera	FISH	Baltic Sea, Germany	Hempel et al. (2008)
Cladophora rupestris	CUD	France	Barbeyron & Berger (1989)
Codium cylindricum	CUD	Tolo, Hong Kong	Kong & Chan (1979)
Codium fragile	CUD	Scotland	Boyd et al. (1999a,b)
Enteromorpha compressa	CUD	Ria de Arosa & Pontevedra, Spain	Lemos et al. (1985)
Enteromorpha intestinalis	CUD	Ria de Arosa & Pontevedra, Spain	Lemos et al. (1985)
	CUD	-	, ,
Enteromorpha linza		Japan William Fatanama India	Shiba & Taga (1980)
Enteromorpha sp.	CUD	Vellar Estuary, India	Lakshmanaperumalsamy & Purushothaman (1982)
	IFN	Auckland, New Zealand	Booth & Hoppe (1985)
Halimeda copiosa	CUD, EPF	Bahamas Islands	Jensen et al. (1996)
Halimeda tuna	SEM, EM	Lecce, Italy	Colombo (1978)
Monostroma nitidum	CUD	Japan	Shiba & Taga (1980)
Monostroma undulatum	CUD	Puerto Deseado, Argentina	Gallardo et al. (2004)
Udotea petiolata	SEM, EM	Sardinia, Italy	Colombo (1978)
Ulva australis	DGGE, CLO	Shark Point, Australia	Longford et al. (2007)
	DGGE,CFISH	Shark Point, Australia	Tujula et al. (2010)
	DGGE, CLO	Sydney, Australia	Burke et al. (2009), Delbridge et al. (2004)
	CUD, EPF	Sydney, Australia	Rao et al. (2006, 2007)
	CUD	Sydney, Australia	Penesyan et al. (2009)
Ulva compressa	DGGE	Baltic & North Sea, Germany	Lachnit et al. (2009)
orva compressa	TRFLP	Chañaral, Chile	Moran et al. (2008)
Ulva fasciata	CUD	Anjuna & Baga, India	Ramaiah & Chandramohan (1992)
Ulva lactuca	CUD	Scotland	` '
Olva lactuca	CUD		Boyd et al. (1999a,b)
		Tolo, Hong Kong	Kong & Chan (1979)
	CUD	Spain	Lemos et al. (1985)
	CUD, TEM	Massachusetts, USA	Waite & Mitchell (1976)
	CUD, TEM	Sydney, Australia	Egan et al. (2000)
	RTQ, DGGE	Kattegat, Denmark	Skovhus et al. (2004)
	CFISH, DGGE	Shark Point, Australia	Tujula et al. (2006, 2010)
Ulva pertusa	CUD, SEM	Jiaozhou, China	Duan et al. (1995)
	CUD	Tuandao Bay, China	Wang et al. (2009)
Ulva reticulata	CUD, SEM	Malaysia	Vairappan & Suzuki (2000)
	CUD, SEM	Hong Kong	Dobretsov & Qian (2002)
Ulva rigida	CUD	Las Salinas Beach, Spain	Bolinches et al. (1988)
	CUD	Pleubian, France	Liot et al. (1993)
Ulva sp.	CUD	Japan	Shiba & Taga (1980)
Ulva spp.	RTQ, DGGE	Kattegat, Denmark	Skovhus et al. (2004)
	CUD, EPF	Uminokoven, Japan	Uchida & Murata (2004)
Ulvaria fusca	RTQ, DGGE	Kattegat, Denmark	Skovhus et al. (2004)
Heterokontophyta, Phaeoph	-		
Ascophyllum nodosum	CUD	Trondheimsfjord, Norway	Sieburth & Jensen (1967)
	SEM	Massachusetts, USA	Cundell et al. (1977)
	SEM	Camp Varnum, RI, USA	Sieburth & Tootle (1981)
Chordaria flagelliphormis	CUD	Sea of Japan, Russia	Beleneva & Zhukova (2006)
Colpomenia sinuosa	CUD	Awaji Island, Japan	Kanagasabhapathy et al. (2006, 2009)
Cystoseira sp.	CUD	San Sebastian, Spain	Genilloud et al. (1994)
Desmarestia viridis	CUD	Sea of Japan, Russia	Beleneva & Zhukova (2006)
Dictyota dichotoma	CUD	Gijon, Spain	Genilloud et al. (1994)
Ecklonia cava	CUD	Awaji Island, Japan	Kanagasabhapathy et al. (2006)

Appendix 1 (continued)

Macroalga	Methodology	Location	Source
Ecklonia maxima	CUD	Oudekraal, South Africa	Mazure & Field (1980)
Ectocarpus siliculosus	CUD	Tolo, Hong Kong	Kong & Chan (1979)
Eisenia bicyclis	CUD	Japan	Shiba et al. (1979)
1	CUD, SEM	Japan	Sakami & Sugiyama (1994)
Fucus ceranoides	CUD	Spain	Lemos et al. (1985)
Fucus serratus	CUD	Scotland	Boyd et al. (1999a,b)
	DGGE	Baltic & North Sea, Germany	Lachnit et al. (2009)
Fucus sp.	EPF, CUD	White Sea, Russia	Semenova et al. (2009)
Fucus vesiculosus	SEM	Camp Varnum, RI, USA	Sieburth & Tootle (1981)
i deds vesiculosus	CUD	Gijon, Spain	Genilloud et al. (1994)
	CUD	Las Salinas Beach, Spain	Bolinches et al. (1988)
	IFN	Baltic Sea, Germany	Booth & Hoppe (1985)
	DGGE	Baltic & North Sea, Germany	Lachnit et al. (2009)
Himanthalia alangata	CUD	-	, ,
Himanthalia elongata		Scotland	Boyd et al. (1999a,b)
T	CUD	Gijon, Spain	Genilloud et al. (1994)
Laminaria digitata	CUD, SEM	Bay of Brest, France	Corre & Prieur (1990)
	CUD	Scotland	Boyd et al. (1999a,b)
	CUD	Roscoff, France	Salaün et al. (2010)
Laminaria hyperborea	DGGE, EPF	Bergen, Norway	Bengtsson et al. (2010)
Laminaria japonica	CUD, SEM	Jiaozhou, China	Duan et al. (1995)
	CUD	Primor'e, Russia	Dimitrieva & Dimitriev (1996)
	CUD	Shandong Province, China	Wang et al. (2008)
	CUD	Sea of Japan, Russia	Beleneva & Zhukova (2006)
	CUD	Tuandao Bay, China	Wang et al. (2009)
Laminaria longicruris	CUD	Nova Scotia, Canada	Laycock (1974)
Laminaria pallida	CUD	Oudekraal, South Africa	Mazure & Field (1980)
Laminaria saccharina	DGGE	Baltic & North Sea, Germany	Lachnit et al. (2009)
	DGGE, CLO	Baltic & North Sea, Germany	Staufenberger et al. (2008)
Lobophora variegata	CUD, EPF	Bahamas Islands	Jensen et al. (1996)
Macrocystis integrifolia	SEM	Bamfield Inlet, Canada	Roland (1975)
Nereocystis luetkeana	SEM	Bamfield Inlet, Canada	Roland (1975)
Padina arborescens	CUD	Awaji Island, Japan	Kanagasabhapathy et al. (2006)
Padina tetrastromatica	CUD	Anjuna & Baga, India	Ramaiah & Chandramohan (1992)
Pelvetia canaliculata	CUD		· · · · · · · · · · · · · · · · · · ·
		Spain	Lemos et al. (1985)
Petalonia fascia	CUD	Awaji Island, Japan	Kanagasabhapathy et al. (2006)
Pilayella littoralis	IFN	Auckland, New Zealand	Booth & Hoppe (1985)
	IFN	Baltic Sea, Germany	Booth & Hoppe (1985)
Sargassum cinereum	CUD	Anjuna & Baga, India	Ramaiah & Chandramohan (1992)
Sargassum filicinum	CUD	Awaji Island, Japan	Kanagasabhapathy et al. (2006)
Sargassum fusiformis	CUD	Awaji Island, Japan	Kanagasabhapathy et al. (2006)
Sargassum hemiphyllum	CUD	Tolo, Hong Kong	Kong & Chan (1979)
Sargassum horneri	CUD	Japan	Shiba & Taga (1980)
Sargassum linearifolium	CFISH	Shark Point, Australia	Tujula et al. (2006)
Sargassum seratifolium	CUD	Awaji Island, Japan	Kanagasabhapathy et al. (2006)
Sargassum sp.	CUD	Sao Paulo, Brazil	Menezes et al. (in press)
Scytosiphon lomentaria	CUD	Awaji Island, Japan	Kanagasabhapathy et al. (2006)
Undaria pinnatifida	CUD	Awaji Island, Japan	Kanagasabhapathy et al. (2006)
•	CUD	Wando, Korea	Kim et al. (2008)
	CUD	Korea	Lee et al. (2006)
	-		,
Rhodophyta			
Amphiroa anceps	CFISH	Shark Point, Australia	Tujula et al. (2006)
Antithamnion plumula	CUD		Barbeyron & Berger (1989)
-		France	2 0 1 /
Bonnemaisonia asparagoides	TRFLP, EPF	Skagerrak, Sweden	Nylund et al. (2010)
Camphylaephora hyphaeoides		Sea of Japan, Russia	Beleneva & Zhukova (2006)
Ceramium kondoi	CUD	Awaji Island, Japan	Kanagasabhapathy et al. (2008)
Ceramium rubrum	IFN	Baltic Sea, Germany	Booth & Hoppe (1985)
Ceramium virgatum	CUD	Skagerrak, Sweden	Nylund et al. (2008)
Chondrus crispus	SEM	Camp Varnum, RI, USA	Sieburth & Tootle (1981)
1	CUD	Gijon & Vigo, Spain	Genilloud et al. (1994)

Appendix 1 (continued)

Macroalga	Methodology	Location	Source
Chondrus oncellatus	CUD	Awaji Island, Japan	Kanagasabhapathy et al. (2008)
Clathromorphum sp.	STE	Oudekraal, South Africa	Johnson et al. (1971)
	SEM, CUD	Oudekraal, South Africa	Johnson et al. (1991)
Coralline algae	CUD, DGGE	Shark Bay, Australia	Huggett et al. (2006)
Corallina officinalis	CUD	Scotland	Boyd et al. (1999a,b)
Corumna ornemans	CFISH	Shark Point, Australia	Tujula et al. (2006)
Delesseria sanguinea	DGGE	Baltic & North Sea, Germany	Lachnit et al. (2009)
Delisea pulchra	DGGE, CLO	Sydney, Australia	Burke et al. (2009), Delbridge et al. (2004)
Densea puicina	DGGE, CLO	Bare Island, Australia	
		·	Longford et al. (2007)
	CUD	Bare Island, Australia	Penesyan et al. (2009)
	CFISH	Shark Point, Australia	Tujula et al. (2006)
Gelidium amansii	CUD	Awaji Island, Japan	Kanagasabhapathy et al. (2008)
Gelidium caulacantheum	IFN	Auckland, New Zealand	Booth & Hoppe (1985)
Gelidium pusillum	CUD	Anjuna & Baga, India	Ramaiah & Chandramohan (1992)
Gelidium sp.	CUD	San Sebastian, Spain	Genilloud et al. (1994)
Gracilaria changii	CUD	Morib Beach, Malaysia	Musa & Wei (2008)
Gracilaria conferta	CUD	Israel	Weinberger et al. (1997)
Gracilaria corticata	CUD	Anjuna & Baga, India	Ramaiah & Chandramohan (1992)
Gracilaria textorii	CUD	Tuandao Bay, China	Wang et al. (2009)
Gracilaria verrucosa	CUD	Sea of Japan, Russia	Beleneva & Zhukova (2006)
Gracilaria spp.	EPF	Philippines & Japan	Largo et al. (1997)
Grateloupia filicina	CUD	Awaji Island, Japan	Kanagasabhapathy et al. (2008)
Hormosira banksii	IFN	Auckland, New Zealand	Booth & Hoppe (1985)
Hypnea charoides	CUD	Tolo, Hong Kong	Kong & Chan (1979)
	CUD	0 0	, ,
Hypnea sp.	СОД	Vellar Estuary, India	Lakshmanaperumalsamy &
TT 1	CLID	A : 0.D I I:	Purushothaman (1982)
Hypnea valentiae	CUD	Anjuna & Baga, India	Ramaiah & Chandramohan (1992)
Kappaphycus alvarezii	EPF	Philippines & Japan	Largo et al. (1997)
	INF	Philippines	Largo et al. (1998)
Laurencia distichophylla	IFN	Auckland, New Zealand	Booth & Hoppe (1985)
Lithophyllum sp.	CUD, SEM	Bicheno, Tasmania	Lewis et al. (1985)
Lomentaria catenata	CUD	Awaji Island, Japan	Kanagasabhapathy et al. (2008)
Mesophyllum sp.	CUD, SEM	Bicheno, Tasmania	Lewis et al. (1985)
Osmundaria serrata	SEM	South Africa	Barreto & Meyer (2006)
Pachymeniopsis lauceolata	CUD	Awaji Island, Japan	Kanagasabhapathy et al. (2008)
Palmaria palmata	CUD	Scotland	Boyd et al. (1999a,b)
-	CUD	Pleubian, France	Liot et al. (1993)
Phycodrys rubens	DGGE	Baltic & North Sea, Germany	Lachnit et al. (2009)
Plocamium telfairiae	CUD	Awaji Island, Japan	Kanagasabhapathy et al. (2008)
Polysiphonia fucoides	CUD	Skagerrak, Sweden	Nylund et al. (2008)
Polysiphonia lanosa	CUD	Tolo, Hong Kong	Kong & Chan (1979)
i orysipiioina ianosa	SEM	Camp Varnum, RI, USA	Sieburth & Tootle (1981)
Dalasiah sais misassassa			
Polysiphonia nigrescens	IFN	Baltic Sea, Germany	Booth & Hoppe (1985)
Polysiphonia urceolata	CUD	Tuandao Bay, China	Wang et al. (2009)
Porphyra columbina	CUD	San Jorge Gulf, Argentina	Estevao Belchior et al. (2003)
Porphyra haitanensis	CUD, SEM	Jiaozhou, China	Duan et al. (1995)
Porphyra leucosticta	CUD	Oono-Chyo, Japan	Tsukidate (1971)
Porphyra sp.	CUD	Japan	Shiba & Taga (1980)
	CFISH	Shark Point, Australia	Tujula et al. (2006)
Porphyra yezoensis	CUD, SEM	Jiaozhou, China	Duan et al. (1995)
	CUD	Awaji Island, Japan	Kanagasabhapathy et al. (2008)
	CUD, DGGE	China	Yang et al. (2008)
Rhodomela confervoides	CUD	Skagerrak, Sweden	Nylund et al. (2008)
Schizymenia dubyi	CUD	Awaji Island, Japan	Kanagasabhapathy et al. (2008)
come y momu duby i		, I	9 1 1 , , ,
Sporolithon sp.	STE	Oudekraal, South Africa	Johnson et al. (1971)