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Microbial Surface Colonization and Biofilm Development in Marine Environments

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SUMMARY

Biotic and abiotic surfaces in marine waters are rapidly colonized by microorganisms. Surface colonization and subsequent biofilm formation and development provide numerous advantages to these organisms and support critical ecological and biogeochemical functions in the changing marine environment. Microbial surface association also contributes to deleterious effects such as biofouling, biocorrosion, and the persistence and transmission of harmful or pathogenic microorganisms and their genetic determinants. The processes and mechanisms of colonization as well as key players among the surface-associated microbiota have been studied for several decades. Accumulating evidence indicates that specific cell-surface, cell-cell, and interpopulation interactions shape the composition, structure, spatiotemporal dynamics, and functions of surface-associated microbial communities. Several key microbial processes and mechanisms, including (i) surface, population, and community sensing and signaling, (ii) intraspecies and interspecies communication and interaction, and (iii) the regulatory balance between cooperation and competition, have been identified as critical for the microbial surface association lifestyle. In this review, recent progress in the study of marine microbial surface colonization and biofilm development is synthesized and discussed. Major gaps in our knowledge remain. We pose questions for targeted investigation of surface-specific community-level microbial features, answers to which would advance

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our understanding of surface-associated microbial community ecology and the biogeochemical functions of these communities at levels from molecular mechanistic details through systems biological integration.

INTRODUCTION

Numerous kinds of surfaces with distinct physicochemical and biological properties exist in marine environments. These surfaces include living animal and algal surfaces, various kinds of particles and aggregates, inert or bioreactive mineral substrata, and submerged constructs and vessel surfaces. Diverse aquatic microorganisms are capable of colonizing surfaces of various kinds, leading to the formation of biofilms and to the development of specialized processes within these structures (1, 2). Surface association appears to be an ancient, universal, and fundamental survival mechanism that provides microorganisms with critical advantages, including greater access to nutritional resources, enhanced organism interactions, and greater environmental stability. These features are of particular importance in natural aquatic environments in which nutrients are often growth limiting and ambient conditions are highly dynamic and sometimes deleterious (1, 3, 4). Alterations (usually stimulation) of microbial activities by surfaces in soil environments were first reported more than a century ago (5, 6), and a similar surface-associated stimulation of microbial activities was subsequently found to be prevalent in marine environments as well (7). Key genetic and ecophysiological processes and mechanisms that are fundamental to the life of marine bacteria on surfaces have been revealed. Some up-to-date reviews on marine biofilm- or particle-associated microorganisms are available (e.g., see references 8–16). These reviews, albeit insightful, focus mostly on specific microbial groups, processes, functions, or colonizable substrata. Systematic reviews on the surface-associated microbiota and particularly the mechanisms that control the formation and development of surface-colonizing microbial communities in the marine environment are currently lacking. Because *Bacteria* are the most diverse and important (compositionally, dynamically, and functionally) microorganisms on marine surfaces and early colonizers may determine the structure, dynamics, and function of mature biofilm communities (17, 18), this review focuses on *Bacteria* and their processes and mechanisms related to early surface colonization, biofilm formation, and biofilm functions.

Physiological Advantages and Ecological Functions of Microbial Surface Association

Surfaces submerged in marine water are rapidly colonized by microorganisms (13). As stated above, surface colonization and subsequent biofilm formation provide these organisms with important advantages. Perhaps the most critical of these advantages in the context of the marine environment is access to resources. Charged and hydrophobic materials tend to accumulate on submerged surfaces, and biogenic particles such as phytoplankton detritus, zooplankton fecal pellets, and marine snow are generally rich in organic matter, resulting in enhanced availability of inorganic macronutrients, organic carbon and energy sources, micronutrients, and electron donors or acceptors in otherwise strongly nutrient-limited milieus (1, 3, 19–22). Surfaces have been shown to be "hot spots" of microbially catalyzed, biogeochemically important activities, as described in greater detail below. Surface colonization and the production of the shielding biofilm matrix, antiprotozoal factors, and stress response products also promote protection from predators, viruses, antibiotics, and other chemical toxins and deleterious environmental pressures (1, 3, 13, 19, 21–28). The biofilm matrix and the development within it of specific microenvironments promote the maintenance of extracellular enzyme structural integrity and activities (23, 29) as well as improved opportunities for physiological homeostasis of the bacteria (1, 3, 23).

Interactions of microorganisms in close spatial juxtaposition within the biofilm matrix facilitate metabolic cooperation (1, 3, 19, 21, 22, 26, 30) and genetic exchanges due to both the physical structure of the biofilm and community-level communication among organisms (21, 22, 30, 31). Biofilms often feature open-channel and pore structures, enhancing solute and microbial transport and promoting frequent cell-cell contacts (29, 32). The establishment of high microbial densities and the sensing, signaling, and adaptive responses of these dense assemblages of surface-associated microbiota in turn promote within-population microbial diversification, between-population niche specialization, and higher-level microbial community organization (13, 21–23, 26, 30, 33–39). The enhanced and sometimes unique ecophysiological activities of surface- and biofilm-associated microbial communities lay the foundations for biogeochemical functions that can sharply differ from those of free-living (i.e., planktonic) microbial communities in marine environments. For example, biofilm-associated microbial communities may thrive in extreme or hostile environments where individual microorganisms would find the maintenance of activity and growth, even survival, challenging (40–42). Biofilm formation also contributes to the development of organic aggregates and high-molecular-weight (HMW) complexes that have dynamics distinct from those of their constituents. In addition, the stabilizing effects of life in biofilms facilitate the decomposition of sinking particles by surface-associated microbial communities, altering carbon sequestration efficiency and thus the climate modulation capacity of the ocean via the "biological pump" mechanism (i.e., the vertical transportation of photosynthetically produced organic carbon from the euphotic surface ocean to the dark deep ocean). Carbon remineralized during sedimentation reenters the carbon cycle and ocean-air exchange quickly, while carbon that is transported from the euphotic zone to the interior and sediments of the deep ocean may remineralize and circulate with a long residence time (43–46).

Considering the substantial physiological advantages of surface colonization and biofilm formation, it is not surprising that the surface lifestyle plays important roles in microbial adaptation to and biogeochemical functioning in marine environments (3). Specific regulatory networks that modulate the expression of numerous genes and metabolic pathways in surface-associated cells dictate the biogeochemical functions that result (3, 22, 47–49). Consequently, differences in physiological status and activities between surface-associated and free-living cells of the same taxon are often observed (e.g., see references 1, 6, and 47). Surface colonization may be particularly important for the expression and secretion of biopolymer-targeted extracellular enzymes and for the transition of microbial cells to the competent state, in which the uptake and incorporation of extracellular DNA (eDNA) are effective (31, 50, 51). Surface-associated microorganisms play important roles in numerous critical marine processes, including organic matter remineralization (23, 52–54), nutrient regeneration

and element cycling (23, 52, 53, 55), contaminant (such as heavy metal) concentration and transfer in food webs (23), induction of benthic invertebrate larval settlement (10, 13, 56), and xenobiotic compound biodegradation (21, 30, 32, 57). The unique genetic, physiological, and ecological processes, mechanisms, and functions associated with the surface-associated microbiota make their study a fascinating and productive area in microbiology, with important implications for basic marine science and for applied biotechnology and bioengineering.

Physiological Challenges and Deleterious Effects of Microbial Surface Association

Surface-associated microorganisms also face challenges that free-living microorganisms may avoid (27, 58, 59). High cell densities on surfaces, and particularly in biofilms, promote intense competition for nutrients and other resources as well as progressive deterioration of conditions due to depletion of resources and accumulation of metabolic wastes. This may force some microorganisms into inactive states or even kill them (27, 59–62). Resource limitation and waste accumulation due to encapsulation in the biofilm matrix are of particular importance in deeper biofilm layers (35, 39). Thus, the spatial heterogeneity of biofilms and the activities of neighboring microorganisms can contribute to the formation of optimal, suboptimal, and adverse microniches for a given microorganism within the biofilm three-dimensional structure. Changes in the distributions of chemical species and other biota in a biofilm may also change the microenvironments and thus influence the activities of a surface-associated microorganism. Marine particles are prone to concentrate viruses (63), and viral attack is sometimes augmented in surface-associated microbial communities due to their high cell densities or enhanced virus production induced by the quorum sensing (QS) mechanism (64–66). Surfaces and biofilms also have the tendency to absorb heavy metals and toxic organic compounds (23, 32, 67). Surface-associated microorganisms generally switch off the expression of genes involved in motility and switch on the expression of genes involved in adhesion and biofilm development (36). Thus, biofilms may become inhibitory if the microorganisms cannot escape when conditions become deleterious (68). In spite of these challenges, surface association is a major mode of microbial life. In addition to the direct benefit provided by surface-associated growth-stimulating nutrient enrichment, the advantages provided by cell-cell interactions may be a driving force behind the common surface association lifestyle.

Microbial surface colonization and surface-associated metabolic activities also exert macroscale deleterious effects, including biofouling (13, 56), biocorrosion (18, 55, 69), and the persistence and transmission of harmful or pathogenic microorganisms and virulence determinants (23, 33, 70). Biocorrosion is a particularly important consequence of biofilm development in marine environments and has major impacts on marine engineering, causing extensive damage and economic losses worldwide (71, 72). In many coastal marine environments, there is a particularly severe carbon steel corrosion phenomenon called accelerated low water corrosion (ALWC) (73, 74). The rate of this intensified corrosion is usually 10 times that of common carbon steel corrosion in seawater (75). Despite its severity and ubiquity and numerous investigations of this phenomenon, the process and mechanism of ALWC remain poorly understood. Neither the causative organisms nor the environmental inducers of this process are completely resolved (74–76). Sulfur-oxidizing bacteria (SOB) and sulfate-reducing bacteria (SRB) were originally proposed to be the key microorganisms responsible for ALWC (76, 77). However, as ALWC occurs in the photic zone (just above the extremely low water level) where bulk anoxic conditions usually do not exist due to photosynthetic oxygen production in the daytime, SRB may not contribute to ALWC prior to the development of a thick corroding biofilm and anoxic microenvironments (18). Recently, it was found that the microaerophilic, neutrophilic, marine iron-oxidizing bacteria (FeOB) in the newly defined *Zetaproteobacteria* lineage (78–80) contribute to carbon steel corrosion in natural and simulated coastal environments (81, 82). Marine *Zetaproteobacteria* FeOB may also play an important role in the initiation of ALWC (18). A key environmental factor for the induction of ALWC appears to be elevated concentrations of seawater inorganic nitrogen compounds (especially nitrate) (75, 83, 84). Single-cell genomic analyses showed that nitrogen acquisition is particularly important for the marine iron-oxidizing *Zetaproteobacteria*, which usually harbor nitrate reductase genes (85). Some *Zetaproteobacteria* FeOB also harbor nitrogen fixation genes, and diazotrophy has been confirmed for some of these bacteria (85). The importance of nitrogen acquisition to the iron-oxidizing activity of marine *Zetaproteobacteria* FeOB stresses the importance of environmental nitrate (and other nitrogenous nutrients) for the induction of ALWC.

The importance of environmental nitrate for the development of ALWC is also highlighted by other lines of experimental evidence. Nitrate inhibits the sulfate reduction activity of SRB and thus is often employed to control oil reservoir souring caused by SRB sulfidogenesis (86–91), but at the same time, it usually accelerates the biocorrosion rate (especially via pitting corrosion as in ALWC) (92–94). Furthermore, many marine FeOB are facultative iron-oxidizing nitrate reducers (95–99), which may carry out iron corrosion using nitrate as a terminal electron acceptor under anoxic conditions (100, 101). It is likely that some FeOB that carry out nitrate reduction-coupled iron oxidation may play an important role in exacerbating ALWC before SRB take a part in further steel corrosion. It is reasonable to hypothesize that sequential steel surface colonization and ordered biogeochemical activities by different functional groups of microorganisms may thus play a critical role in the initiation and development of ALWC in marine environments. In-depth investigations of the surface physicochemical and nutritional microenvironment and the composition and dynamics of surface-associated microbiota on submerged steels may help to fully resolve the mechanism of ALWC and provide solutions limiting damage due to this process.

Biogeochemical Contributions of Marine Surface-Associated Microbiota

Surfaces are clearly "hot spots" of microbial activities (53, 102–105). Compared to their free-living counterparts, surface-associated microorganisms usually possess distinct compositions (generally more diverse or more surface specific) (104, 106–110), morphologies (usually larger cells) (102, 106, 111, 112), abundances (often enriched) (53, 102, 106, 107, 109, 113), dynamics (often greater seasonal compositional variations and diel and even hourly activity changes) (102, 105, 114, 115), and functions (e.g., often higher per-cell exoenzymatic activities) (53, 102, 105–107, 110, 112, 116–118). It has been proposed that surface-associated microorganisms are mainly copiotrophic, whereas free-living bac-

teria are mainly oligotrophic (119–121). However, some studies have shown similar or only slightly different particle (surface)-associated and free-living microbial communities (122–124). These studies were conducted in estuaries that are eutrophic and in which most suspended particles are old and composed mainly of inorganic matter having terrestrial or sediment origins. Particles in estuarine waters of this kind are generally less rich in organic matter than those in pelagic waters, except during algal bloom events (118). This would tend to minimize the advantage of particle colonization. Indeed, it has long been recognized that nutrient-enriched conditions inhibit bacterial irreversible adhesion to surfaces and biofilm formation (2, 125). Supplementation of seawater with a high concentration of glucose induces convergence of the biofilm and free-living microbial communities, which were originally quite different when no glucose or low concentrations of glucose were supplied (126). On the other hand, environmental microorganisms tend to form biofilms under oligotrophic or starvation conditions (2). In non- and less-eutrophic marine environments such as pristine estuaries and offshore waters, where the majority of the particles are biogenic and thus organically enriched (123), significantly different community structures of particle-associated and free-living microorganisms are commonly found (108, 114, 127–129). Particle-associated bacterial communities are frequently enriched in the marine *Roseobacter* clade (MRC) bacteria of the *Alphaproteobacteria*; the *Alteromonadaceae* and *Vibrionaceae* groups of the *Gammaproteobacteria*; as well as the *Deltaproteobacteria*, *Bacteroidetes*, and *Planctomycetes* (108, 127, 130–137). Many of these bacteria produce extracellular enzymes for biopolymer degradation, and some require suboxic or anoxic microniches within particles to support microaerophilic or anaerobic metabolism. The contrasting nutritional conditions between particles and seawater have strong impacts on microbial lifestyle differentiation, particularly in oligotrophic environments. It is reasonable to hypothesize that the significance of the difference between the surface-associated and free-living microbial communities may increase from the eutrophic and terrigenous particle-dominated riverine estuaries to the biogenic particle-dominated oligotrophic open oceans, caused by the differences in organic matter content and nutrient bioavailability between particles in these two distinct environments. This hypothesis is consistent with a recent ecophysiological study of the marine group II *Euryarchaea* and numerous studies on marine bacteria (138).

Due to steep gradients of key geochemical parameters (e.g., O_2, pH, sulfide, and redox potential) and to enrichment of nutrients (e.g., organic and inorganic substrates, electron donors, and electron acceptors) (6, 139–141), surfaces usually support diverse and elevated microbial metabolic and biogeochemical activities (102, 107, 111, 117). Surface-associated marine microbiota participate in a plethora of C cycling processes. Photosynthetic and chemolithoautotrophic CO_2 fixation (102, 142–148), aerobic anoxygenic phototrophic energy conservation (149–151), seawater methane production and oxidation (143, 146, 147, 152), degradation of biopolymers and other organic matter (102, 117, 145, 153), and heterotrophic respiration (102, 104, 113, 145) are all enhanced on surfaces. N cycling processes such as N_2 fixation (154, 155), nitrification (142, 143, 156–158), denitrification (158–161), dissimilatory nitrate reduction (158, 159), anaerobic ammonium oxidation (anammox) (158, 162, 163), and nitrogenous organic compound degradation (158, 164–166) are also activities associated with surfaces and can be particularly important at specific depths in the water column. For example, in the oxygen minimum zone (OMZ) of the Eastern Tropical North Pacific, particles contribute 100% of the activity reducing nitrate to nitrite and 53 to 85% of N_2 production by denitrification and anammox (167). P cycling processes such as eDNA secretion (168, 169) and particulate organic phosphorus degradation (153, 170, 171) are enhanced on marine particles, as are microbial S cycling activities such as sulfate reduction (133, 141, 147, 153, 172), sulfur oxidation (133, 146-148, 153), and organic S compound (e.g., the algal osmolyte dimethylsulfoniopropionate [DMSP]) transformation and degradation (153, 173–175). As noted above, surface- and particle-associated microorganisms also contribute substantially to marine iron cycling processes, such as iron oxidation and reduction (78, 147, 176–178), siderophore-mediated iron solubilization and uptake (153, 179–181), iron transport among different oceanic environments (182), and biocorrosion (18, 69, 72, 81). Silica regeneration from diatom detritus (183, 184), H_2 production, H_2 oxidation-related energy metabolism and dark primary production (185), as well as many other biogeochemical cycling processes are driven by surface-associated microbial activities. The biogeochemical cycling processes of almost all of the environmentally important elements are highly complex and dynamic in the ocean, involving both free-living and surface-associated microbiota as drivers (186, 187). Cycles of the various elements are intrinsically interconnected, and microbial processes foster this connectivity via the metabolic intersection of different pathways and via functional cooperation between different microbial groups (188). For example, the cooperation of archaeal anaerobic methane oxidation and bacterial sulfate reduction in natural microbial aggregates plays a critical role in coupled marine C and S cycling in anoxic methane-rich environments and thus in the control of ocean methane emissions (189–191). Particles and biofilms in marine environments provide favorable niches for the coupling of different metabolic pathways and biogeochemical cycles. Particularly in oxic marine waters, some of these microbial processes and activities happen only within the suboxic and anoxic microenvironments within particles or biofilms, which thus define surfaces and surface-associated microbial activities as unique niches and biogeochemical processes that differ from those in bulk seawater (172).

Although it is generally accepted that surface-associated microorganisms play important roles in nutrient regeneration, element cycling, biological productivity, and food web energetics, the contributions of the surface-associated microbiota to the total microbial metabolic activities in different marine ecosystems are poorly quantified, and controversies remain. For example, metabolic activities of the particle-associated microbiota vary widely. This has several causes, including particle quality and quantity (16). There are many different types of particles in the marine environment, such as suspended riverine or sediment particles, phytoplankton detritus, zooplankton and fish fecal pellets, aggregates, marine snow, macrogels, transparent exopolymer particles (TEPs), microgels, and colloidal microparticles (186). These particles differ in their origins, spatiotemporal distributions, and quality as microbial resources. The quantity of suspended riverine particles in estuaries is directly related to the seasonal pattern of riverine discharges, and these particles are usually rich in minerals and poor in organic matter. The quantity of resuspended sediment particles usually has both tidal and seasonal patterns in coastal waters, and these particles are generally poor in organic matter due to long-

term remineralization. Marine snow, fecal pellets, and phytodetrital aggregates from algal blooms constitute the major types of biogenic particles that contribute the most to the biological pump export and sequestration of carbon in the ocean (16). The abundance and spatiotemporal distribution of these biogenic particles, which are rich in organic matter, depend on epipelagic primary productivity and food webs (16). While biogenic particles constitute the major colonizable surface type in open oceans, in estuarine and coastal seas, the surface types are usually more complex, consisting of both biogenic and abiogenic particles, each with various age distributions. The distinct nutritional conditions of different surface types certainly contribute to the metabolic variability of the surface-associated microbiota, leading to quantitative differences in microbial activities. In addition, although individual surface-associated microorganisms are typically much larger than free-living microorganisms, the level of activity of surface-associated microorganisms is highly variable and sometimes, even on a per-cell basis, lower than that of free-living microorganisms (111, 192). Only a fraction of the surface-associated microorganisms may be active at a given time or under specific environmental conditions (129). For example, the attached microbial community may be more active at night, while the free-living community dominates activity during the day (114). This can be explained by higher rates of activity of particle-associated microaerophilic and/or anaerobic microorganisms that can be more active during the night when dissolved O_2 levels are lower due to the absence of photosynthesis and to night community respiration (140). This switch to more suboxic conditions may result in niche segregation and functional separation between the surface-associated and free-living microorganisms. In some environments, marine particles are sites of enhanced extracellular hydrolytic enzyme activity but low substrate incorporation activity, indicating that surface-associated bacteria may be actively dissolving particulate organic matter (POM) without significant increases in their growth rates (44, 118). The activities of surface-associated microorganisms also influence the composition, abundance, dynamics, and ecophysiological functions of the surrounding free-living microorganisms via the release of nutritional resources and extracellular hydrolytic enzymes from colonized surfaces. This contributes to distributed networks of metabolite exchange and other forms of cooperation that involve both surface-associated and free-living microbial communities (105, 147, 186, 193, 194). It is clear that the variability of biogeochemical contributions of surface-associated microbiota is high and should be considered in an ecosystem context.

Surface-associated microbiota may also play distinct roles at different depths in the water column. Surface-colonizing microorganisms themselves participate actively in biopolymer hydrolysis, fixed carbon remineralization, and microbial secondary production near the ocean surface, where they also help retain N, P, and Fe within the upper mixed layer of marine waters (Fig. 1) (144, 186). Based on their behavior in the water column, marine particles can be crudely divided into two categories: sinking particles and nonsinking particles (195). While nonsinking particles show nearly constant concentrations throughout the dark ocean, concentrations of sinking particles such as biogenic aggregates and fecal pellets decrease exponentially with depth (46). On the one hand, organic matter degradation and decomposition of sinking particles decrease the biological pump carbon sequestration efficiency (43–46). On the other hand, microbial particle colonization may potentially increase the stability, the specific density, and hence the settling velocity of the colonized sinking particles via the production and release of polymeric substances. This moderates, to a certain degree, the decomposition rate of the sinking particles and thus the biological pump efficiency (46). Marine snow plumes generated by surface-associated microbial activities contain high concentrations of nutrients and dissolved organic matter (DOM), also stimulating the activity and growth of free-living microorganisms in the deep ocean (44, 196, 197). The surface-associated and free-living microorganisms above the thermocline are adapted to warm ambient temperatures, whereas in deep waters, free-living microorganisms show optimal activity at *in situ* temperatures, implying long residence at depth (198). The distinct temperature optima of the transient deepwater surface-associated and resident free-living microorganisms provide a reasonable explanation for findings of limited species exchange between particle-associated and free-living microbial communities throughout the water column (104, 128, 199). It seems likely that the sinking particle-associated microbial communities are composed mainly of microorganisms that originated from surface seawater, and they lose substantial amounts of activity in the cold deep water (200, 201). This is consistent with observations that the metabolic activity and growth rate of deepwater surface-associated microbial communities are usually lower than those of the surrounding free-living microbial communities, although the surface-associated microorganisms are almost exclusively responsible for the production and activity of the extracellular hydrolytic enzymes required for nutrient and labile organic matter production from POM. Marine snow is most abundant in surface waters and decomposes substantially (~90%) in the twilight zone of the water column (202, 203). The dynamics of the nutritional composition of sinking particles may influence the succession and function of the surface-colonizing microbiota thereon. The marine snow particles that reach deeper waters are generally older and more recalcitrant to microbial utilization because these particles are progressively processed as they sink, and their C/N ratios and refractory matter percentage increase with depth (202, 204, 205). Surface colonization on these recalcitrant particles may prove to be of little benefit to the newly colonizing microorganisms. This provides an alternate explanation to the limited species exchange found between particle-associated and free-living microbial communities in the ocean (104). The particle origin, degree of decomposition, nutritional status, and environmental temperature may determine the composition, succession, and activity of the sinking-particle-colonizing microbial community, which may select in favor of a surface-associated composition distinct from that of the free-living community (104). Thus, extracellular enzymes are likely produced by surface water particle-colonizing microorganisms soon after the colonization event. While the sinking of the particles into deep water will decrease the physiological activity of the particle-associated microorganisms (200), the hydrolytic activities of the secreted extracellular enzymes may be retained (to a large extent), and thus, the resident free-living microorganisms may have a better opportunity to utilize the majority of the nutrients and organic matter released by enzymatic hydrolysis of sinking POM (44, 196, 197). This "uncoupled" hydrolysis (44, 117, 206) predicts that the separation of extracellular enzyme activity from the physiological activity of the enzyme producers and the allochthonous particle-associated microbial activity from the autochthonous free-living microbial activity during the sinking of particles from the surface into the

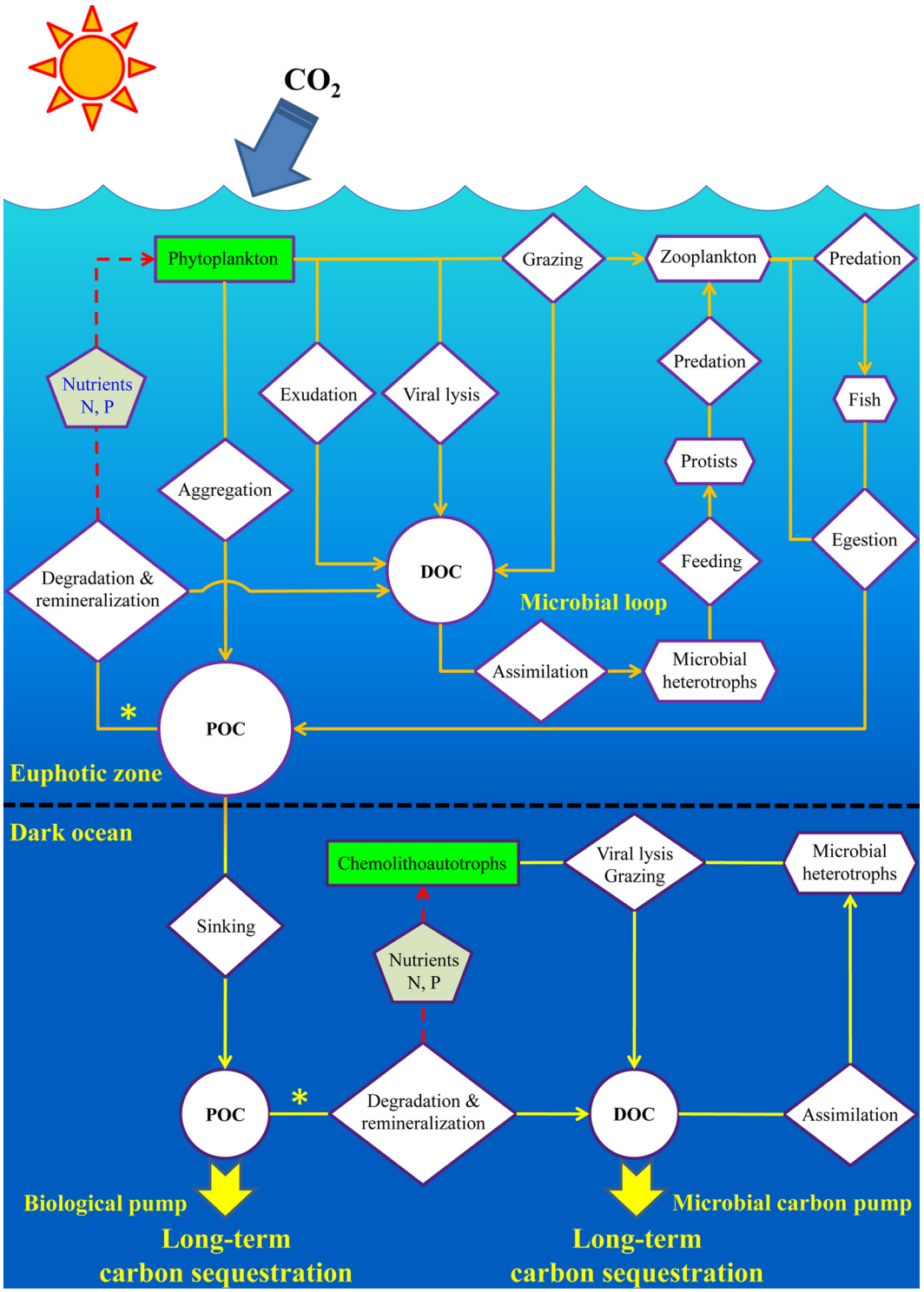

FIG 1 Key processes of the marine carbon cycle. Microorganisms colonize the surfaces of most marine organisms, such as phytoplankton, zooplankton, protists, and fish, and marine particles, including phytoplankton detritus, zooplankton and fish fecal pellets, and marine snow. The surface-associated microbiota participate in mutualistic or antagonistic interactions with algae or zooplankton. They also play important roles (indicated by asterisks) in the degradation and remineralization of particulate organic matter and in the enhancement of primary production (via inorganic nutrient regeneration to fuel phytoplankton in the euphotic zone and chemolithoautotrophic microbial communities in the aphotic zone). The surface-associated microbiota also influence long-term carbon sequestration in the ocean via both the biological pump and the microbial carbon pump mechanisms. All the respiration terms are omitted so that the graph is not too cluttered. Abbreviations: POC, particulate organic carbon; DOC, dissolved organic carbon.

deeper waters may have significant implications for microbial functions and biogeochemical processes in the deep ocean.

The distinction between surface ocean and deep ocean surface-associated microbial activities is also related to the importance of the surface-associated microorganisms for free-living chemolithoautotrophic activity in the deep ocean. It has long been recognized that deep ocean waters maintain high levels of nitrate, presumably produced by decomposition and nitrification (207). Furthermore, it was recently suggested that chemolithoautotrophic productivity in the mesopelagic and bathypelagic zones of the ocean may represent a substantial contribution to the ocean's total primary production (46, 146, 208, 209). In deep waters of the ocean, *Archaea* generally constitute a substantial fraction (10 to 40%) of the prokaryotic community (210–212). The deep ocean *Archaea* are mainly chemolithoautotrophic ammonia-oxidizing *Thaumarchaeota* (211, 213–215), which may also participate in the heterotrophic or mixotrophic uptake of organic substrates such as amino acids and carboxylic acids (211, 216–218). The autotrophic CO_2 fixation activity of the ammonia-oxidizing *Thaumarchaeota* has been verified in diverse marine environments (211, 219–221), and it has been estimated that this group of marine *Archaea* fixes ~400 Tg C year^{-1} (208). Marine ammonia-oxidizing *Thaumarchaeota* are also capable of producing recalcitrant organic carbon (i.e., glycerol dialkyl glycerol tetraether membrane lipids) (222) and may facilitate long-term carbon sequestration in the deep ocean and sediments (208). The source of deep ocean ammonia is generally accepted to be decomposing sinking POM (142, 165, 214). Bacteria are the major producers of extracellular enzymatic activity in the deep ocean down to the bathypelagic layers (223), although in surface waters, marine group II *Euryarchaea* are also preferentially particle associated and contribute to the catabolism of HMW substrates (138). POM enzymatic hydrolysis by *Bacteria* transforms marine particles into nutrient islands, with NH_4^+ concentrations usually being >2 orders of magnitude higher than those in the surrounding seawater (139, 224). Ammonia-oxidizing *Thaumarchaeota* likely do not produce extracellular enzymes in sufficient quantities for degradation of POM in the deep ocean (223) and may rely on extracellular enzymatic activities of *Bacteria* for obtaining ammonia for activity and growth (142, 165). Metabolic cooperation, in a broad sense, between surface-associated *Bacteria* and free-living *Archaea* may play a substantial role in deep ocean nitrification and dark CO_2 fixation (Fig. 1). Similarly, the release of NH_4^+ from sinking particles into the water column by surface-associated bacterial extracellular enzymatic activities may fuel anammox-mediated nitrogen loss and chemolithoautotrophic CO_2 fixation in the OMZs of the world's oceans (225). In order to advance our understanding of the biogeochemical contributions of surface-associated microbiota, more studies, particularly of chemolithoautotrophic activities, are needed.

Impacts of Surface-Associated Microbiota on Ocean Carbon Sequestration

The settling of biogenic and physically coaggregated particles and especially the macroscopic aggregates designated marine snow contributes substantially to the flux of organic carbon from surface seawater to the deep oceans and sediments (226, 227). Although there seems to be little consistency across the world's oceans regarding the mechanisms that control the spatiotemporal variability of particulate export to the deep ocean, preferential microbial remineralization of POM P and N (versus C) is commonly found (228). Surface-associated microbial activities may enhance ocean carbon sequestration by disproportionally utilizing and recycling C, N, and P. Organic matter of all descriptions is usually the major constituent of large marine particles, which also contain inorganic materials such as silt, clay, and calcite accumulated from the surrounding water (102, 111). TEPs, formed mainly by large, sticky, and acidic algal polysaccharides, usually serve as the glue that facilitates large-particle formation, leading to rapid particle sinking from surface waters to the deep ocean (229–231). Surface attachment stimulates bacteria to produce their own exopolysaccharides, also enhancing aggregation (232). Particulate organic carbon (POC) contained in marine particles forms the second largest organic carbon pool (up to 30 Pg C) in modern oceans (233), contributing to the drawdown of atmospheric CO_2 and modulation of climate variability on a global scale (43–46). Particle-associated microorganisms have major impacts on marine POC dynamics and carbon sequestration (Fig. 1).

Although some surface-colonizing bacteria may increase diatom aggregate formation, the particle sinking rate, and, thus, the potential efficiency of the marine biological pump (234, 235), it is commonly accepted that POC degradation by surface-colonizing microorganisms generally decreases the carbon sequestration efficiency of the ocean (44, 46, 113, 209, 236). The extracellular hydrolytic enzymes produced by surface-associated microbial assemblages usually have compositions and substrate ranges that differ from those of free-living microbial assemblages, likely due to differences in microbial composition (108, 237, 238). The elevated quantity and activity of surface-associated hydrolytic enzymes are likely influenced by the involvement of the QS regulatory mechanism in surface-associated microbial communities (239–241), and the higher enzyme specificity is likely due to the capability for sensing, recognition, and regulatory responses toward available substrates on the surface by specific surface-associated microorganisms (53, 242).

Some surface-associated microorganisms possess astonishing carbon cycling capabilities. For example, *Alteromonas* species are widespread in the ocean and are common surface- and particle-colonizing bacteria in both shallow and deep waters (243–246). *Alteromonas* species are metabolic generalists capable of rapid responses to an environmental disturbance (247–249). They are also large bacteria with large genomes and are copiotrophic, with high specific metabolic activities. They can degrade and utilize a broad spectrum of organic substrates, including deep-sea recalcitrant organic matter (245, 250–252). *Alteromonas* produces and secretes a variety of extracellular enzymes that contribute to the hydrolysis of biopolymers, including polysaccharides (253–257), proteins (258, 259), nucleic acids (260, 261), and lipids (262), the major components of marine POM. *Alteromonas* and related species respond rapidly to phytoplankton blooms and especially to elevated POC concentrations (109, 263–265). Algal exudates from a variety of phytoplankton can be utilized by *Alteromonas*, making them a major microbial group in algal phycospheres (266–268). Some *Alteromonas* strains also possess algicidal activity (269), reflecting their intimate association with marine algae. *Alteromonas* sp. strain AltSIO was recently shown to be capable of utilizing as diverse a catalog of dissolved organic carbon (DOC) substrates as the entire *in situ* microbial assemblage (270). In addition to their surprisingly high carbon cycling capability, bacteria in this group were also found to be important in marine iron cycling and trans-

port, an ecophysiological trait likely related to their surface association capabilities (182, 271). Metabolic versatility and surface association accord the *Alteromonas* group bacteria great carbon cycling potential and make these bacteria a member of the marine master recyclers (249, 272).

The release of labile DOC from POC degradation by particle-associated microorganisms may not only fuel the microbial loop (198, 273, 274) but also facilitate the priming effect that stimulates the degradation of recalcitrant organic matter (275, 276). Furthermore, deep-water microorganisms usually have large genomes and inventories of genes contributing to surface association (199). Higher levels of cell-specific extracellular enzymatic activity, microbial production, and cellular respiration were found to be linked to the utilization of deep ocean recalcitrant organic matter (277, 278), indicating an important role of particle-associated microorganisms in deep-sea carbon cycling (132, 279–281). On the other hand, POC degradation by surface-colonizing microorganisms may also release recalcitrant DOC (209), facilitating carbon sequestration by the microbial carbon pump mechanism (Fig. 1) (272, 282–285). DOC (up to 662 Pg C) forms the largest organic carbon pool in the modern ocean, and a substantial fraction (~97%) of DOC consists of refractory and ultrarefractory molecules that persist for thousands of years in the marine environment (286). The quantitative contributions of surface-associated microorganisms to the size and dynamics of the ocean's POC and DOC reservoirs and the influence of spatiotemporally different environmental conditions on surface-associated microbial processes and activities are still poorly understood, especially under anthropogenic perturbation and global change scenarios (16, 284–286). In-depth studies of the marine surface-associated microbiota are fundamental for a mechanistic and predictive understanding of the marine carbon cycle.

Environmental Change-Induced Surface-Associated Microbiota Responses and Impacts

Ocean warming and acidification induced by increasing anthropogenic CO_2 emission may lower the carbon sequestration efficiency mediated by the biological pump (287–289). Uncertainties remain because the complex, nonlinear behaviors of most ecological processes and the synergistic ecosystem responses to changing global environmental conditions (e.g., increasing temperature, ocean stratification, ocean acidification, ocean oxygen depletion, and ocean nutrient regime shift) are not well understood (290–292). For example, the remineralization depth of sinking POC becomes shallower in warmer waters, indicating that the vertical POC flux and, thus, the carbon sequestration efficiency of the biological pump will be attenuated with future increases in ocean temperature (45, 293). Ocean acidification can significantly change the ballast composition, reduce the settling velocity of sinking particles, and thus force the sinking particles to remain in the epipelagic and mesopelagic zones of the water column, with longer residence times and greater microbial decomposition (294). This may make the POC remineralization depth shallower as well. However, ocean acidification may enhance the production of TEPs (295), facilitating the formation of large sinking particles and thus increasing the POC remineralization depth. Other environmental factors can also affect the marine POC remineralization depth, such as seawater oxygen concentration, stratification, organic matter content and origin of the sinking particles, and particle-colonizing microbial community composition and activity (45). Many of these factors, and particularly their synergistic effects, are still not well studied or quantified.

As a result of the increasing impacts of anthropogenic activities and global warming, both coastal hypoxic zones and oceanic OMZs are expanding, and prevalent microbial biogeochemical pathways are correspondingly being altered (296–300). Marine particles provide suboxic and anoxic microhabitats (140, 141, 154, 281, 301), and the gradients of oxygen and other bioactive resources within marine particles and biofilms support microbial compositional and physiological heterogeneity and diversity (34, 147, 151, 153, 172). Oxygen-limited and oxygen-depleted conditions facilitate various microaerophilic and anaerobic chemolithoautotrophic carbon fixation and heterotrophic respiration and fermentation processes (147, 302, 303). Different respiration pathways have distinctly different energy conservation efficiencies (147, 304), and hypoxic and anoxic conditions usually exert a negative influence on respiratory efficiency and thus the carbon sequestration efficiency of the ocean (284, 285). Furthermore, the increasing impacts of anthropogenic activities and global warming have also caused estuarine and coastal waters (including polar ocean coastal areas) to become more eutrophic and conversely have caused open oceans, particularly the giant subtropical gyres of the Pacific and Atlantic Oceans, to become more oligotrophic (305–310). The enhanced nutrient status and elevated export from the surface waters of sinking particles in the polar ocean waters, and the ocean stratification effect on the increase of the ocean's deepwater residence time, lead to the deep oceans becoming more stagnant and nutrient rich; conversely, the surface waters of the open oceans become more oligotrophic (311, 312). The shift of the oceanic nutrient regime, changes in oceanic circulation, as well as ocean acidification and deoxygenation may have significant negative impacts on ocean carbon cycling. This, on the other hand, may exacerbate global climate change, as the ocean is the largest active carbon sink on Earth, and its change will no doubt disturb the atmosphere-ocean CO_2 exchange balance and the carbon sequestration capacity of the ocean.

Substantial evidence establishes the importance of marine surface-associated microbial communities in global carbon cycling. Microbial populations are enriched on marine snow relative to surrounding seawater free-living microorganisms, especially in oligotrophic open oceans (106, 313), and even these oligotrophic waters can produce very high concentrations of marine snow and diatom mats (314, 315). This indicates that even the microorganisms in oligotrophic oceanic waters have an abundance of substrata, though perhaps only intermittently, to colonize. The increased formation of colloidal, gelatinous, detrital, and aggregate particles due to escalated terrigenous nutrient and organic matter inputs and to algal and jellyfish blooms in estuarine and coastal oceans (312, 316–319); the augmented tendency of microbial surface associations in response to increasingly oligotrophic conditions in the open oceans (1, 2, 6, 7, 106); the enhanced activity of surface-associated microbiota in coastal waters of the polar oceans due to seawater warming, permafrost melting, enhanced primary production, and particle transport from the tundra (320, 321); and the elevated activity of surface-associated microbiota in deep waters due to nutrient enrichment (132, 199, 278–281) lead us to hypothesize that surface-associated microbial communities may play even greater roles in ocean carbon cycling under global change scenarios. However, the mechanisms by which surface-associated microbial processes impact the ocean's biogeochemical

processes and carbon sequestration capacity and the magnitude of this impact, especially under changing environmental conditions, are not well understood. A fundamental understanding of the mechanisms and impacts of microbial surface colonization, biofilm formation, and surface-associated activities in marine environments will be required to address profoundly important questions related to global climate change.

The processes of microbial surface colonization and biofilm community development are highly dynamic and complex. These processes usually start with a surface-sensing step, and diverse environmental cues are likely involved in the induction of the initial surface attachment event. Cell surface components play important roles in subsequent irreversible surface adhesion and, thus, true colonization. Microbial intra- and interspecies interactions, including cooperation and competition, shape the routes of community succession, biofilm development, and functional maturation, resulting ultimately in complex microbial communities. In the following sections, we examine (i) how the microorganisms sense and respond to environmental cues to initiate surface colonization and biofilm development, (ii) how the microorganisms interact with the substratum surface to carry out the actual colonization steps, (iii) how the microorganisms cooperate and compete to drive the development of the surface-colonizing and biofilm communities, (iv) how two key marine bacterial groups succeed as key surface colonizers, and (v) future directions in the study of surface colonization and biofilm development.

MICROBIAL SENSING AND SIGNALING IN SURFACE COLONIZATION AND BIOFILM DEVELOPMENT

Environmental factors play important roles in determining microbial surface colonization events (47, 60, 322–324). In general, the interaction of microbial cells with the substratum surface under specific physicochemical and nutritional conditions at the seawater-surface interface likely contributes substantially to the initiation and success of microbial surface colonization in marine environments. Substratum physicochemical properties such as surface free energy, electrostatic charge, hydrophobicity, wettability, roughness, microtopography, and vulnerability to wear (such as corrosibility of a metal surface) and surface chemodynamic properties such as surface conditioning, nutrient enrichment, and charge accumulation or alternation may influence the ability of microorganisms to adhere to a particular abiotic surface (47, 325). For example, environmental pH and ionic strength may alter the surface charge of both the microorganism and the substratum surface when they are exposed to the aquatic environment, influencing microbial surface adhesion in various ways (325–327). Nutrient limitation caused by N, P, or Fe scarcity in marine environments may induce certain microorganisms to adapt to a surface-associated lifestyle or to disperse from a biofilm to find more favorable surfaces (2, 60, 328–332). Biofilm formation in the marine environment may play an important role in microbial selection of the optimal habitat (333, 334). In marine vibrios, certain components of the pathways of catabolite repression (modulating cellular responses to high-energy-carbohydrate availability), the stringent response (modulating the use of available resources in response to low-nutrient stress such as amino acid, fatty acid, or iron starvation), and nucleoside scavenging (modulating nucleoside uptake and catabolism in response to environmental nucleoside scarcity) exert regulatory effects on surface colonization and/or biofilm formation (335–340). The adaptations required for successful surface colonization certainly include the ability to detect and respond to surface-related cues.

Microorganisms utilize a variety of sensing mechanisms to adapt to and exploit changing (micro)environments (341). The environmental cues may be physical (the surface as a diffusion barrier or potential energy barrier), chemical (redox potential, conditioning film composition, adsorbed nutrients, metabolizable substrates, and electron donors and acceptors), or physicochemical (microviscosity and water activity) (47). Known environmental cues that attract individual microorganisms to surfaces are diverse, particularly including high inorganic and organic nutrient levels, the availability of electron donors and acceptors, and hydrodynamic conditions (342). Sensing may be the necessary first step for marine microorganisms to establish a surface-associated lifestyle, and thus, microbial surface sensoritomes play a critical role in the primary interactions between the microbial cell and the surface that is colonized (343, 344).

Microbial Two-Component Signal Transduction Systems

Two-component signal transduction systems (TCSs) are very common in both *Bacteria* and *Archaea* (284, 345, 346). These systems enable microorganisms to constantly sense and respond to environmental changes and stresses, such as those caused by the availability of inorganic nutrients and metabolizable organic substrates, temperature, pH, O_2, redox potential, light intensity, osmolarity, and toxins, including reactive oxygen and nitrogen species as well as other substances (347). Upon activation by an environmental stimulus via a specific TCS sensor histidine kinase (HK) component, the cognate TCS response regulator (RR) component may induce the binding of a regulatory molecule to DNA, RNA, or protein or cause an increase in enzymatic activity (348). These responses lead to changes in cellular transcriptional, enzymatic, or mechanistic properties and alterations in microbial physiology and/or behavior (346, 349). For example, the genome of *Vibrio cholerae* O1, frequently isolated from estuarine and coastal environments and a causative agent of Asiatic cholera, harbors 43 HK and 52 RR genes (350). Twelve of these RRs were found to have a role in host colonization (350). In addition, *V. cholerae* O1 employs the VpsS hybrid HK and the VpsR and VpsT RRs to regulate the production of the exopolysaccharide VPS (*Vibrio* polysaccharide) that enables the formation of biofilms and consequent resistance to oxidative stress and chlorine biocidal activity (9, 351–354). In *Vibrio fischeri*, the RscS and SypF HKs were found to play an important role in inducing symbiotic biofilm formation and squid colonization via the SypE and SypG RRs that modulate the transcription of the symbiosis polysaccharide (*syp*) locus (355). A *V. cholerae* VpsR homologue also modulates *V. fischeri* polysaccharide production and biofilm formation via a putative cellulose biosynthesis locus found only in this vibrio species (9). TCSs are also employed by other vibrio species to regulate extracellular polysaccharide production and biofilm formation, although the exact mechanisms may be slightly or even substantially different in different organisms (9). Systematic studies of the TCSs in *Pseudomonas aeruginosa*, an opportunistic pathogen and an environmental bacterium found frequently in coastal waters and sometimes even in open oceans (356–358), have confirmed that biofilm formation is a highly regulated process that proceeds through a number of distinct stages (347). An array of TCSs play a key role in the regulation of the production of extracellular ap-

pendages, such as flagella, type IV pili, and Cup fimbriae, that are often involved in *P. aeruginosa* initial surface attachment as well as the production of extracellular exopolysaccharides, such as Pel and Psl, that are required for subsequent *P. aeruginosa* biofilm formation (347).

The *Escherichia coli* osmosensing EnvZ/OmpR system and the cell envelope disturbance-sensing CpxA/CpxR system were among the first TCSs indentified as important sensing, signaling, and regulatory mechanisms for bacterial surface colonization and biofilm formation (359). The nutritional and ionic enrichment that is generally observed on submerged surfaces creates a microhabitat that has higher osmolarity than that of the surrounding aquatic environment (6, 144, 347). The EnvZ/OmpR and CpxA/CpxR systems provide a mechanism to promote the microbial response to such an osmolarity gradient (i.e., a nutrient gradient) and to promote microbial surface attachment (360). Homologues of the EnvZ/OmpR and CpxA/CpxR TCSs have been identified in marine bacteria, including *V. cholerae* (361, 362). However, these TCSs have been found to play a minimal role in the regulation of *V. cholerae* surface colonization and biofilm formation (15, 362). Instead, the OscR and CosR osmolarity-responsive regulators were found to play a major role in regulating osmolarity- and salinity-induced *V. cholerae* biofilm physiology (362–364). Therefore, marine and nonmarine bacteria may employ different mechanisms to regulate osmolarity-responsive surface colonization and biofilm formation due to environmental and evolutionary differences.

Many TCSs in environmental microorganisms are related to sensing and adaptive responses to inorganic nutrients and metabolizable organic substrates, such as organic acids, sugars, and amino acids (365–367). For example, the extracellular sensors of the TCS PhoQ, DcuS, CitA, and AbfS, involved in monitoring environmental divalent ions such as Ca^{2+} and Mg^{2+}, C_4-dicarboxylic acids, citrate, and oligosaccharides, respectively (366), may help the microorganisms to detect a favorable surface based on nutrient enrichment. The phosphate-responsive PhoR/PhoB system involved in high-affinity phosphate-specific transport regulation under P starvation conditions is a common TCS in bacteria (368). This TCS is also involved in surface colonization, biofilm formation, or microbial dispersion from biofilms in some marine bacteria (330, 331, 369). In marine *Pseudoalteromonas piscicida* isolates, the CdsS/CdsR TCS regulates the expression of genes involved in chitin degradation (370), which is facilitated by bacterial surface colonization. In *V. cholerae*, the expression of chitin-inducible genes, including those involved in chitin degradation and utilization, chemotaxis, surface colonization, and natural competence, is modulated by the orphan TCS sensor kinase ChiS (371, 372). Chitin is the most abundant nitrogenous polysaccharide in the ocean and can be degraded and utilized by many marine bacteria (373). N and P are inarguably the most important macronutrients in the ocean, controlling the ocean's primary and secondary productivity, carbon sequestration, and many other biogeochemical functions and ecosystem services (297, 374–379). How surface-associated microorganisms, using putatively diverse regulatory pathways, respond to and influence the ocean's changing N and P regimes warrants in-depth investigation.

TCSs exist in >95% of *Bacteria* and ~50% of *Archaea*. Microbial genome sequencing has identified a great number of TCSs, yet the functions and environmental stimuli of most of these systems have not been determined. The MiST2.2 Microbial Signal Transduction Database (last accessed 10 October 2014) predicted 421,394 gene sequences that encode TCS proteins (not including chemotactic proteins) from a total of 7,937 (complete and draft) bacterial and archaeal genomes (380). The P2CS (Prokaryotic 2-Component Systems) database (last accessed 10 October 2014) predicted 164,651 gene sequences that encode TCS proteins, including 74,029 HKs and 81,882 RRs (381). On average, a single microbial species usually possesses >50 TCSs (382), and some bacteria possess hundreds of TCSs operating in parallel for the adaptive response to diverse environmental conditions (365). For example, *Vibrio parahaemolyticus* O1:Kuk strain FDA_R31 alone may harbor 497 TCS proteins, based on predictions of the MiST2.2 database. Microorganisms that live in rapidly changing environments typically possess a large number of TCSs, and the number of TCSs that a microorganism can possess appears to correlate with its habitat's environmental complexity and niche diversity (346). It is reasonable to hypothesize that the marine microorganisms that are capable of major changes in lifestyle (such as the transition from the motile to the sessile lifestyle and vice versa) may harbor large numbers of TCSs functional in both free-living and surface-associated activities and in the transitions between these two lifestyles.

Microbial Chemotaxis

Chemotaxis systems coordinate the sensing, signaling, and responsive motility of a bacterium or archaeon in response to chemical attractants or repellents (383) and are among the most thoroughly studied TCSs (384–386). Many marine microorganisms (up to 80%) are motile, especially in highly productive circumstances, such as the organic particle- and nutrient-enriched conditions that occur during algal bloom crashes (387–389). Motility is a physiological and behavioral trait usually linked to the response to environmental gradients (341). It is reasonable to hypothesize that a large fraction of aquatic microorganisms are chemotactic, although they tend to attach if a suitable surface exists (390). The MiST2.2 database (last accessed 10 October 2014) predicted 90,807 chemotaxis protein-encoding gene sequences from a total of 7,937 (complete and draft) bacterial and archaeal genomes (380).

The microbial chemotactic apparatus is highly sensitive, sensing and responding to as little as a 3 nM change in the concentration of an environmental chemical stimulus (391). Chemotaxis is used by environmental bacteria not only for increased acquisition of organic substrates but also for enhanced uptake of inorganic nutrients (392). *Thalassospira* sp. was found to be chemotactic toward inorganic phosphate during starvation, a behavior consistent with its natural habitat of the ultraoligotrophic eastern Mediterranean Sea (393). A recent study showed that coral surface-associated bacteria exhibited significantly higher levels of chemotaxis than free-living bacteria in nearby non-coral-associated waters (394). Numerous processes, such as cell lysis, phytoplankton exudation, animal excretion, food vacuole egestion, and particle degradation and dissolution, provide point sources rich in organic substrates and inorganic nutrients in marine waters (186, 392, 395). Chemotaxis toward marine particles or their nutrient plumes may facilitate carbon and nutrient cycling and the microbial loop (393).

Chemotactic responses driven by environment sensing and directed motility have frequently been proposed to facilitate microbial surface attachment (3, 6, 8, 47, 338, 392, 396–398). Results to

date show that chemotaxis can be important (399–405), advantageous (406), or dispensable (407) for initial surface colonization, indicating possible species- or strain-specific differences in the role of chemotaxis in microbial surface interactions or surface- or environment-specific differences in microbial chemotactic responses. Energy taxis can also be important to surface colonization by certain bacteria (408–411). The microenvironment near a submerged surface is highly heterogeneous in that multiple gradients exist, including gradients of oxygen, pH, osmolarity, electron donors, electron acceptors, metabolizable substrates, redox potential, and chemical cues, including chemotactic attractants or repellents (34). Most studies showing a positive effect of taxis on bacterial surface colonization employed biotic surfaces, with only a few cases in which abiotic surfaces were also tested (402, 404). Thus, we hypothesize that there are threshold concentrations of taxis signals, which dictate the initiation of the microbial attachment response driven by the chemotactic or energy taxis mechanisms. A submerged abiotic, inert surface likely does not satisfy this requirement, as the taxis signals in the environment near such a surface may not achieve high enough concentrations to induce the tactic response, even considering the accumulation of the conditioning film on the surface.

Microbial Quorum Sensing

Many *Bacteria* and *Archaea* employ QS as a specialized intraspecies and interspecies communication mechanism for population density-dependent sensing, signaling, and responsive adaptation (412–417). A typical QS pathway is characterized by the production, release, and detection of small signal molecules collectively called autoinducers, resulting in coordinated behavior once a sufficient signal concentration, reflecting a sufficient quorum size, is reached. QS is a common strategy to achieve a group benefit and coordinated behavior in the prokaryotic world and is particularly important for surface- and biofilm-living microorganisms that often reach high densities (417).

QS plays important roles in regulating initial microorganism-surface interactions, microbial surface attachment, initiation of biofilm formation, and biofilm development (33). *V. fischeri* harbors three distinct QS systems (i.e., AinS/AinR, LuxI/LuxR, and LuxS/LuxPQ); however, only the AinS/AinR system is involved in the modulation of the initial steps of surface colonization, and only the AinS/AinR and LuxS/LuxPQ systems are involved in the modulation of subsequent biofilm development (418, 419). *V. cholerae* harbors four distinct QS systems (i.e., CqsA/CqsS, LuxS/LuxPQ, CqsR, and VpsS), and they all participate in the modulation of surface colonization and biofilm formation (420). Functional redundancy of the four QS receptors is employed by *V. cholerae* to prevent premature induction of a QS response that may be caused by signal perturbations (420). The QS systems in *V. fischeri* assist in establishing a symbiotic relationship between the bacterium and its host, *Euprymna scolopes*, while the QS systems in *V. cholerae* contribute to making this bacterium a deadly pathogen to humans.

QS autoinducers were found to enhance cell adhesion to sulfur and pyrite surfaces by *Acidithiobacillus ferrooxidans* (421), a chemolithoautotrophic bacterium that carries out CO_2 fixation coupled to ferrous iron and sulfur oxidation (422, 423). Extracellular polymeric substances (EPSs) identified as lipopolysaccharides appear to be a prerequisite for *A. ferrooxidans* attachment to pyrite and sulfur (424), and their biosynthesis is likely controlled by the cellular QS mechanism (425). Interestingly, *A. ferrooxidans* harbors two QS systems (426). A Lux-like system is upregulated when *A. ferrooxidans* is grown in sulfur medium (427, 428), while an Act-based system is upregulated when *A. ferrooxidans* is grown in medium containing iron instead of sulfur (426). Thus, it has been suggested that the two QS systems respond to different environmental signals that may be related to the abilities of *A. ferrooxidans* to colonize and use different solid sulfur- and iron-containing minerals (426).

FeOB and SOB are important participants in the biogeochemical cycling of iron and sulfur, bioleaching of metal ores, and biocorrosion of metals (18, 78, 99, 178, 429–431). Most of the FeOB and SOB are microaerophiles that prefer low-oxygen conditions for chemolithoautotrophic CO_2 fixation, and some of them are facultative anaerobes that can carry out iron and sulfur oxidation by using alternative terminal electron acceptors such as nitrate and nitrite instead of oxygen (99, 133, 178, 429, 430, 432, 433). QS-related genes have recently been identified in sulfur-oxidizing *Gammaproteobacteria* and *Epsilonproteobacteria* and in *in situ* biofilms of deep-sea hydrothermal vents (434, 435). QS may help FeOB and SOB colonize surfaces to obtain inorganic Fe and S substrates and establish optimal niches within biofilms (436, 437). In seawater, particles may be a rich source of reduced iron (147, 177, 181, 186, 301, 438, 439) and reduced sulfur (133, 140, 141, 147). QS-mediated microbial surface colonization and biofilm formation may play an important role in the biogeochemical cycling of Fe and S in marine environments.

QS autoinducers and/or their synthetic genes have been found in marine microbial mats, subtidal biofilms, deep-sea hydrothermal vent biofilms, and marine organic particles (239–241, 435, 440, 441), indicating that QS may be common in marine surface-associated microbial communities. QS autoinducers modulate the production and activity of extracellular hydrolytic enzymes (e.g., lipases, aminopeptidases, and phosphatases) in marine snow- or *Trichodesmium* colony-associated microbial communities (240, 241, 442). The liberation of dissolved nutrients and organic substrates may benefit surface-associated microorganisms, as well as *Trichodesmium* bacteria themselves for CO_2 and N_2 fixation, especially in oligotrophic environments. Diverse and novel autoinducer synthase genes have been identified in the Global Ocean Sampling metagenomic database, which covers 68 stations across three oceans (443). Many environmentally important microorganisms, including ammonia-oxidizing, nitrite-oxidizing, anammox, denitrifying, nitrogen-fixing, and sulfur-oxidizing bacteria as well as methanogenic *Archaea*, employ QS systems (416, 435, 444–448). The *Proteobacteria* are the predominant QS autoinducer producers in natural environments (449). More than 80% of MRC bacteria harbor QS regulatory systems (8, 173, 272, 450, 451). It has been hypothesized that QS contributes to the surface colonization success of MRC bacteria (8), likely because submerged surfaces in seawater may serve as a source of organic nutrients that attract MRC bacteria and support growth to levels sufficient to support density-dependent QS regulation (450). In addition to its role as an important regulatory mechanism for initial microbial surface colonization, QS may also participate in mediating the interactions of surface colonizers. Autoinducer-2 molecules, an important family of QS signal compounds, are synthesized by many bacteria and appear to facilitate interspecies communications (452). These QS signals may be employed by certain pioneer surface-colonizing bacteria to alter the composi-

tion and structure of the primary colonizer community and influence the subsequent succession of other microbial species on surfaces (452). A recent study has shown that a MRC bacterium promotes initial colonization and biofilm formation by other marine bacterial species via extracellular factor secretion (453). However, whether this extracellular factor is a QS autoinducer and whether the MRC QS systems are involved in the sequential succession of surface- and biofilm-associated microbial communities in marine environments remain to be determined.

Posttranscriptional Regulation by Small RNAs

Small RNAs (sRNAs), a group of noncoding regulatory RNAs, usually with lengths of 25 to 500 nucleotides, are an important type of regulator that binds to mRNA or proteins to modulate translation in diverse microbial physiological processes (454). sRNAs interact with TCSs, the primary mechanism for effective sensing of environmental cues in microorganisms, to form extensive regulatory networks (455). Many TCSs, via the regulation of sRNAs, control target gene expression with enhanced signaling flexibility, dynamics, and timing; conversely, via sRNA regulation, certain TCS regulons can be recruited into other regulatory networks, such as the QS systems, forming a sRNA-mediated feedback loop to achieve fine-tuning of gene regulation and homeostatic control of the involved regulators (455). The intrinsic interconnection of the sRNA, TCS, and QS regulatory systems implicates the sRNAs in microbial surface interaction and biofilm formation.

Experiments have shown that members of the CsrB family of sRNAs, coordinating with the global regulator CsrA (or its homologue proteins) and certain related TCS and QS regulators, play central roles in modulating the switch between motile and sessile bacterial lifestyles, although the precise roles may vary in different bacterial species (454). In *V. cholerae*, the VarS/VarA TCS; CsrA; and the CsrB, CsrC, and CsrD sRNAs regulate the activity of the QS response regulator LuxO (456), which can also be activated (phosphorylated) by the QS autoinducer-free sensor kinase proteins CqsS and LuxQ via the phosphotransfer protein LuxU (457). At a low cell density, phosphorylated LuxO activates the expression of four *qrr* (quorum-regulatory sRNA) genes that encode the sRNAs Qrr1 to Qrr4, which redundantly promote the translation of AphA (the low-cell-density QS master regulator), inhibit the translation of HapR (the high-cell-density QS master regulator), and activate the translation of Vca0939, stimulating biofilm formation (49, 458–460). In *Vibrio harveyi*, phosphorylated LuxO activates the expression of five *qrr* genes encoding the sRNAs Qrr1 to Qrr5, which additively promote the translation of AphA and inhibit the translation of LuxR (homologue of HapR), likely resulting in reduced biofilm formation, however (49, 460). Although the Qrr sRNAs seemingly participate in similar regulatory pathways in *V. cholerae* and *V. harveyi* (460), the collective actions (redundant versus additive) of the involved Qrr sRNAs and their ultimate effects (stimulation versus inhibition) on biofilm formation are different (49, 457, 461–463). In addition, some *Vibrionaceae*, such as *V. fischeri* and *Photobacterium angustum*, have only Qrr1, likely adding more variation to sRNA regulatory outcomes (460).

Recently, the sRNA VqmR has been identified as another regulator of biofilm formation in *V. cholerae* (464). The transcription of the *vqmR* gene is activated by the VqmA DNA-binding transcription factor, and VqmR directly modulates at least eight mRNA targets, including the *vpsT* transcriptional regulator of biofilm production (464). The *vpsT* regulator is also targeted by the histone-like nucleoid structuring protein H-NS, providing another layer of regulation of biofilm production by *V. cholerae* (15, 465). Besides the exopolysaccharide VPS, the expression of three biofilm matrix proteins, RbmA, RbmC, and Bap1, is also required for biofilm formation and structure in *V. cholerae* (15, 402, 466). These proteins facilitate biofilm formation at particular steps: RbmA is capable of binding the exopolysaccharide VPS and strengthening early cell-cell adhesion, Bap1 facilitates biofilm adhesion and recruits planktonic cells to the surface, and Bap1 and RbmC encase cell clusters that are attached to the surface (467–469). The type II secretion system (T2SS) delivers these biofilm matrix proteins for biofilm formation in *V. cholerae* (470). The expression of these biofilm matrix proteins involves regulation by the cyclic AMP (cAMP)-cAMP receptor protein (CRP) complex and the transcriptional regulator VpsR (471, 472). However, the expression of RbmC can bypass the global master regulators, virtually through direct regulation by the sRNA VrrA, the expression of which is in turn modulated by the alternative RNA polymerase sigma factor σ^E (473). Biofilm formation, as well as motility and chemotaxis in *V. cholerae*, also involves the sRNA RyhB that is negatively regulated by iron and the ferric uptake regulator Fur (474). Multiple sRNAs, as well as other regulatory pathways, provide *V. cholerae* with both specific and adaptable control over biofilm formation, a mechanism that is important for a versatile and error-proof response to the diverse environmental cues that can induce surface-associated living. sRNAs in other marine bacteria have received little attention, and many new mechanisms and pathways may await discovery (344, 475).

Centralized Regulation by Second Messengers

Second messenger molecules are employed in many microbial environmental signaling pathways to relay external signals from membrane receptors to intracellular effectors (476). cAMP, the first second messenger described, participates in the cAMP-CRP regulatory network, which exerts global control over key cellular physiology processes, including the production of flagella, microbial motility, cell surface hydrophobicity, quorum sensing, type IV pilus expression, surface attachment, and biofilm formation (27, 338, 476–479). Cyclic di-GMP (c-di-GMP) is another key and ubiquitous second messenger molecule in prokaryotes, playing central roles in microbial signaling and adaptability (480). Despite the tremendous diversity of microbial components and processes and mechanisms that are involved in the switch from the planktonic to the sessile lifestyle, most bacteria examined to date employ c-di-GMP as the central regulator to control surface colonization and biofilm formation (480–482). For example, *Ruegeria mobilis*, a member of the MRC, employs the c-di-GMP regulatory pathway to modulate biofilm formation and antibiotic production (483). In *Agrobacterium tumefaciens*, c-di-GMP activates, in a surface contact-dependent manner, enhanced production of the unipolar polysaccharide adhesin, which is functionally equivalent to a holdfast, for integrated control of the switch from a motile to a sessile lifestyle (484, 485). The environmental bacterium *Shewanella oneidensis* MR-1, which harbors a number of respiratory pathways, including the anaerobic reduction of iron(III), manganese(IV), and uranium(VI), forms biofilms on mineral surfaces through a process controlled by c-di-GMP (486). The marine bacterium *Shewanella woodyi* also employs the c-di-GMP signaling

pathway for controlling biofilm physiology (487). The c-di-GMP signaling pathway may play a key role in *A. ferrooxidans* biofilm formation and bioleaching of minerals (488), whereas diverse c-di-GMP signaling pathways control the switch between predatory and nonpredatory lifestyles of *Bdellovibrio bacteriovorus*, which preys upon other Gram-negative bacteria on surfaces and within biofilms (489). The intracellular c-di-GMP concentration is regulated by GGDEF domain-containing diguanylate cyclases (DGCs) that catalyze c-di-GMP synthesis from two molecules of GTP and by c-di-GMP-specific EAL or HD-GYP domain-containing phosphodiesterases (PDEs) that catalyze c-di-GMP hydrolysis (480). Bacteria usually contain multiple DGCs and PDEs. For example, the *V. cholerae* genome contains >60 genes predicted to encode distinct c-di-GMP-modulating DGCs and PDEs for a flexible environmental response and high-fidelity signaling (490). The c-di-GMP regulatory pathways are involved in modulating the expression of type IV pili, the exopolysaccharide VPS, and T2SS-facilitated secretion of biofilm matrix proteins, playing important roles in surface colonization and biofilm formation by *V. cholerae* (470, 491). Surface-associated bacteria usually harbor more c-di-GMP regulators than free-living bacteria, presumably as an adaptive strategy (120). O_2, H_2O_2, NO, redox potential, light, sucrose, amino acids, polyamines (such as norspermidine and spermidine), Zn^{2+}, bile acids, bicarbonate, indole, QS autoinducers, *cis*-2-dodecenoic acid and *cis*-11-methyl-dodecenoic acid (unsaturated fatty acids that serve as bacterial diffusible signal factors), and nutritional conditions that cause starvation (or depletion of a specific carbon source such as glucose or glycerol) have been identified as environmental cues that induce the bacterial response via altering the intracellular c-di-GMP concentration (480, 492–508). However, the vast majority of the environmental signals that modulate the activity of the DGCs and PDEs remain unidentified.

Multiple sensory transduction pathways, including mainly QS (as well as TCSs and chemotaxis), that sense a vast array of extracellular signals have been found to interact with the c-di-GMP intracellular regulatory networks to influence microbial biofilm formation (330, 480, 509–511). The second messenger- and sRNA-mediated signaling pathways are also interconnected. A recent study indicates that the *V. cholerae* Vca0939 protein is a diguanylate cyclase, and its translation is activated at low cell density by the Qrr sRNAs, leading to c-di-GMP accumulation and thus enhanced VPS-dependent biofilm formation (512, 513). The cAMP signaling pathway also interacts with the c-di-GMP pathway, playing a role in regulating *V. cholerae* biofilm formation (472). The c-di-GMP signaling mechanism represents a unifying principle governing the microbial switch from a planktonic to a sessile lifestyle (514, 515).

An Example of Microbial Interaction with Surfaces: *Vibrio* Chitin Utilization and Its Implications

Chitin is the most abundant biopolymer in aquatic environments and a major component of marine snow (166, 193, 516). About 10^{11} metric tons are produced annually as marine detritus (120, 164). Chitin is highly insoluble, but its degradation products represent an abundant source of carbon, nitrogen, and metabolic energy for microbial communities. Chitin utilization constitutes a key pathway in global carbon and nitrogen cycling (186, 193), and this polymer also provides a surface for vibrios to colonize, particularly under adverse environmental conditions (516–520).

The utilization of chitin by vibrios involves multiple levels of gene regulation that govern motility, chemotaxis, extracellular polysaccharide and biofilm matrix protein synthesis and secretion, type IV pilus production, chitin-binding protein secretion, chitin surface attachment, biofilm formation, extracellular chitinase secretion, chitoporin expression, and competence (166, 338, 470, 520–523). Association with insoluble materials may be the preferred lifestyle of vibrios, including deep-sea hydrothermal vent species (15, 403, 524), and regulatory systems involving TCSs, chemotaxis, QS, sRNAs, cAMP, c-di-GMP, alternative sigma factors, and the stringent response enable vibrios to optimize resource utilization and survival (Fig. 2) (49, 339, 472, 475, 511, 518, 525–529).

Vibrio chitin utilization and biofilm formation are also regulated by the phosphoenolpyruvate:sugar phosphotransferase system (PTS) (337, 530), which catalyzes the transport and phosphorylation of numerous monosaccharides, disaccharides, amino sugars, polyols, and other sugar derivatives and possesses diverse regulatory functions related to processes such as chemotaxis, detection of QS molecules, virulence, potassium transport, and metabolism of carbon, nitrogen, and phosphorus (531, 532). Vibrios are strongly chemotactic toward several PTS substrates, including *N*-acetylglucosamine, trehalose, glucose, sucrose, mannose, and mannitol (164, 166, 533). Mannitol is of particular interest, as it enhances *V. cholerae* biofilm formation by activating, via the PTS, the transcription of the VPS exopolysaccharide synthesis genes (333). Mannitol is a common compatible solute and osmoprotectant and a primary photosynthetic product and carbon reserve compound of brown algae (534). Mannitol and its induction of biofilm formation provide *V. cholerae* additional fitness advantages in the highly variable marine environment. This also implies that biofilm formation induced by chitin or its degradation products may proceed through the PTS regulation pathway in other chitin-utilizing marine bacteria.

In addition to chitinous detritus and live zooplankton and their carcasses and molts, vibrios are frequently enriched on other marine particles or surfaces, such as marine snow, fecal pellets of zooplankton, and detritus from the demise of phytoplankton and jellyfish blooms (70, 172, 518, 535–538). It has also been estimated that there are 5.25 trillion plastic particles weighing 268,940 tons afloat at sea (539, 540). Some of the "plastisphere" components, such as polypropylene, are preferentially colonized by vibrios (541).

Although vibrios are usually detectable and sometimes abundant in coastal and brackish waters, especially in eutrophic environments, they are usually subdominant and opportunistic bacteria (247, 535, 542). Marine vibrios in natural biofilms may contribute to inducing the settlement of invertebrate larvae (543). In addition, vibrios are common producers of auxins such as indole-3-acetic acid (544), likely playing a role in stimulating the activity (such as mucus exudation) of marine algae and the formation of vibrio-alga associations (545). Surface association not only increases vibrio survival and fitness but also increases opportunities for vibrio intraspecies and interspecies exchanges of genes, including those for the utilization of unusual substrates and for virulence (15, 546–549). Such exchanges are supported by surface-induced natural competence and likely involve plasmids, phages, transposons, integrons/gene cassettes, and perhaps other horizontal gene transfer mechanisms (550–552). QS-mediated biofilm formation can include large numbers of toxigenic *V. chol-*

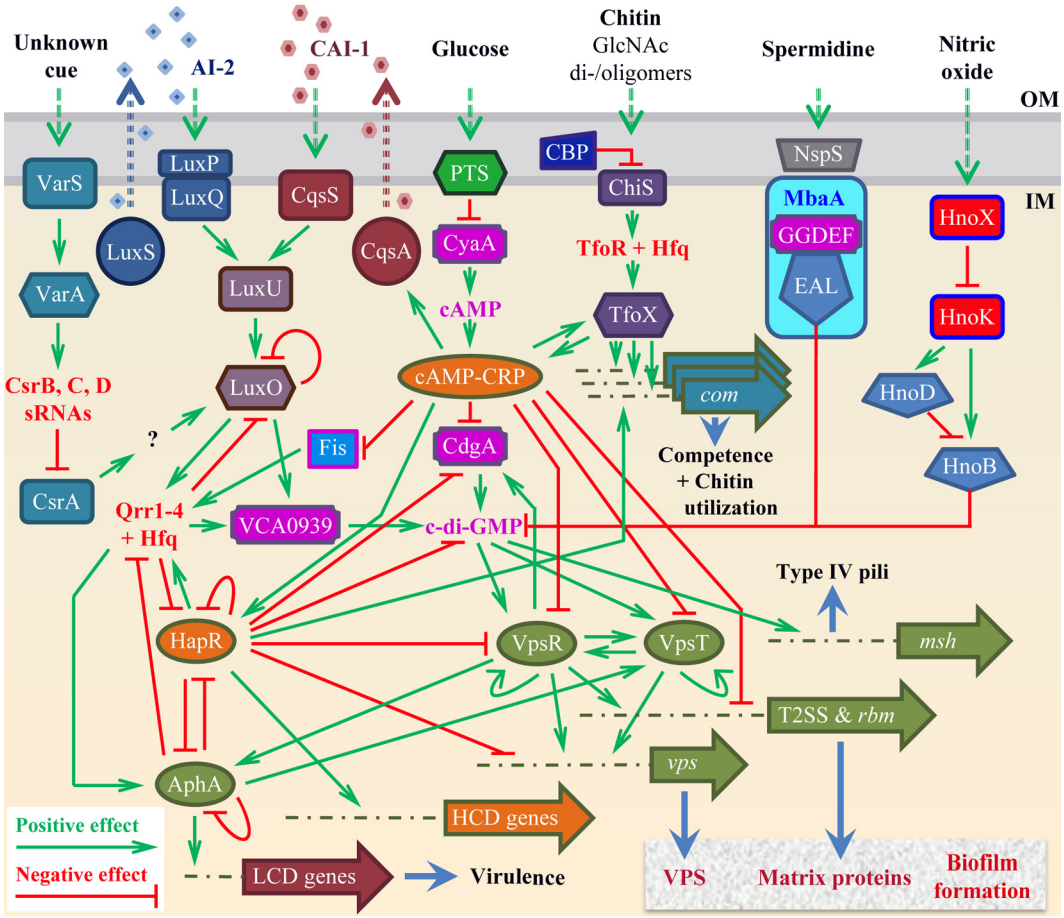

FIG 2 Interacting sensing, signaling, and regulatory pathways important for the *Vibrio cholerae* sessile lifestyle. Diverse environmental cues such as chitin disaccharide and oligosaccharides, bile acids (not shown), nitric oxide, norspermidine (not shown), spermidine, carbon source depletion, and population size signals (such as the autoinducers cholerae autoinducer 1 [CAI-1] and autoinducer 2 [AI-2]) are sensed and processed by *V. cholerae*, which employs signal transduction sensor kinases (such as ChiS, VarS, LuxQ, CqsS, CqsR, VpsS, and HnoK) and response regulators (such as LuxO, VarA, HnoB, HnoD, TfoX, VpsR, and VpsT); the quorum-sensing master transcriptional regulators AphA and HapR; small RNAs (such as CsrB, CsrC, CsrD, Qrr1 to -4, and TfoR); and the RNA chaperone Hfq, cAMP, and c-di-GMP for signal relay and response regulation. The type IV pili are involved in initial surface attachment. The activated production of VPS (*Vibrio* polysaccharide) (the major component of the *V. cholerae* biofilm matrix) and biofilm matrix proteins contributes to biofilm formation. It is evident that most regulatory pathways converge on c-di-GMP, which plays a central role governing the microbial switch from the planktonic to the sessile lifestyle. There are some other surface- and biofilm-related sensing, signaling, and regulatory pathways, such as the CqsR and VpsS QS pathways that are functionally redundant to the CqsA/CqsS and LuxS/LuxPQ QS pathways, the chemotactic pathway that senses extracellular chitin disaccharide and oligosaccharides and modulates bacterial tactic movement toward chitin surfaces for efficient colonization and chitin utilization, the stringent response regulatory pathway that maximizes the use of available resources in response to various low-nutrient stresses, the nucleoside scavenging-and-signaling pathway for regulating natural competence, and the pathways mediated by H-NS and alternative sigma factors, which are not shown in order to avoid cluttering. LCD, low cell population density; HCD, high cell population density; LuxS, autoinducer-2 synthase; LuxP, autoinducer-2 periplasmic binding protein; LuxQ, autoinducer-2 membrane-bound sensor histidine kinase; CqsS, CAI-1 membrane-bound sensor histidine kinase; LuxU, autoinducer phosphorelay protein; LuxO, LuxU cognate response regulator; CBP, chitin-binding protein; NspS, periplasmic spermidine-binding protein; HnoX, NO sensor protein; OM, outer membrane; IM, inner membrane; CsrA, global posttranscriptional regulatory protein that activates LuxO via an unidentified regulatory factor (denoted "?"); Qrr, quorum regulatory small RNA; Hfq, RNA-binding and chaperone protein; cAMP-CRP, cAMP-cAMP receptor protein complex; Fis, factor for inversion stimulation, a small nucleoid protein; PTS, phosphoenolpyruvate phosphotransferase system; CyaA, adenylate cyclase that synthesizes cellular cAMP; VCA0939, CdgA, and the GGDEF domain of MbaA, diguanylate cyclases that synthesize cellular c-di-GMP; HnoB and the EAL domain of MbaA, phosphodiesterases that degrade c-di-GMP; HnoD, protein containing a degenerate phosphodiesterase functioning as an HnoB allosteric inhibitor; VpsR and VpsT, transcriptional regulators that modulate VPS synthesis, with VpsR also being a regulator of *V. cholerae* biofilm matrix protein synthesis; T2SS, type II secretion system; *com*, *msh*, *rbm*, and *vps*, gene operons for chitin-induced natural competence, type IV pilus production, biofilm matrix protein production, and VPS production, respectively. This figure is drawn based on information reported previously (15, 49, 51, 338, 414, 420, 470–472, 475, 491, 500, 505, 511, 512, 527).

erae bacteria, usually in the viable-but-nonculturable (VBNC) state (33, 553, 554). Such biofilm-associated *V. cholerae* bacteria are more virulent than their free-living counterparts (512, 553, 555, 556), and VBNC *V. cholerae* can be resuscitated by QS autoinducers (557), which also promote horizontal gene transfer to *V. cholerae* in multispecies biofilms (558). QS-regulated chitin metabolism also enhances the resistance of *V. cholerae* biofilms against heterotrophic protist grazing (559). These properties of biofilm vibrios exacerbate the impacts of vibrios on human health and greatly increase difficulties in monitoring pathogenic vibrios in marine environments. Furthermore, the increasing persistence and dissemination of vibrios in aquatic environments and the in-

creasing incidence of human vibrio illnesses worldwide are linked to phytoplankton blooms, ocean warming, and the capacity of vibrios to colonize surfaces (15, 265, 560–564). Higher temperature also significantly increases population abundance and upregulates virulence determinants such as motility, resistance to antimicrobial compounds, hemolysis, and cytotoxicity in coral pathogens (565, 566). Surface-living vibrios are thus important not only in global carbon and nitrogen cycling but also in human and marine animal health. How vibrio ecophysiology, biogeochemical function, and pathogenicity may respond to, react with, and evolve in response to the impact of global climate change, ocean acidification, and ocean deoxygenation warrants further investigation.

MICROORGANISM-SURFACE INTERACTIONS IN SURFACE COLONIZATION

Surfaces once submerged in marine waters are rapidly colonized, and subsequent biofilm formation follows a sequence of chemical and biological events. These events may include the rapid formation of an initial "conditioning film," colonization by pioneer microorganisms (usually bacteria), recruitment of secondary colonizers and growth of microcolonies, and development and maturation of biofilm architecture and the biofilm microbial community (17, 22, 397, 567–569). Chemical interactions of solutes with substratum surfaces, biological interactions of microbial cells with surfaces and other microbial cells, and specific gene regulation events at the individual, population, and community levels may play important roles in microbial surface colonization, modification of surface physicochemical properties, structured biofilm development, and establishment and maturation of functional communities.

Surface Conditioning Film Formation and the "Masking Effect"

Almost any kind of solid substratum, once submerged in seawater, is quickly (in seconds) and inevitably covered with a layer of adsorbed molecules that form a conditioning film prior to the attachment of microbial cells (47, 342, 570). Proteins and glycoproteins are usually the major constituents of conditioning films (571, 572), although lipids, polysaccharides, nucleic acids, aromatic amino acids, uronic acids, humic acids, and some other biomolecules may also be present (573). The conditioning film affects the surface nutritional conditions and physicochemical properties, usually causing a convergence of surfaces that initially vary strongly in hydrophobicity and roughness (6, 7, 572). The initial surface-colonizing microbial communities thus may be similar due to the masking effect of the conditioning film on the surface chemistry of different substrata (17, 574). However, the net effect of the conditioning film on microbial surface adhesion remains controversial. Different surface components, such as proteins, nucleic acids, and lipids, may facilitate the attachment of different bacteria (575). Thus, the formation of the conditioning film may either stimulate or inhibit adhesion by specific organisms (325). Furthermore, surfaces with different substratum physicochemical properties may select different primary surface-colonizing microbial communities in spite of the masking effect of conditioning film (20, 576). The composition of the primary colonizing microbial community is likely to be determined by the relative contributions of the masking effect of the conditioning film and the native surface physicochemistry of the substratum. For example, reactive or energetic surfaces may change or modify the chemical properties of the common conditioning film and thus may select for surface-colonizing microbial communities that differ from those on inert surfaces (18, 396). It is reasonable to hypothesize that the constituents of either the conditioning film or the surface substratum that exert the strongest biological effect may be the most influential factors controlling the composition and structure of the primary surface-colonizing microbial community. In addition, seawater TEPs may rapidly adhere to a newly submerged surface to form scattered organic film patches, participating in surface conditioning (though only in small and localized areas) and bringing preexisting TEP-colonizing microorganisms to the growing surface-associated microbial community (577). This adds another dimension of complexity to microorganism-surface interactions and surface-associated microbial community composition and dynamics in marine environments.

Key Microbial Surface Components for Colonization

The initial microbial association with a surface in natural seawater starts with the transport of the microorganism to the surface, likely facilitated by diffusive or convective transport and active swimming (6). Passive and active motion may play a critical role in helping to overcome the diffusion barrier and the potential energy barrier produced by electrostatic repulsive forces (6, 578). Microorganisms are able to sense and respond to surface environmental signals and actively initiate surface adhesion by altering gene expression with consequent changes in cell surface chemistry, physiology, and behavior (56, 359). Different microorganisms may respond to distinct environmental signals, allowing each microbial species to efficiently colonize its preferred surface (micro)environment and to avoid direct competition (360). Different microorganisms may also employ different surface adhesion mechanisms, which are usually associated with different secretion systems (343). Different cell surface components may have distinct functional roles in microbial surface colonization. In particular, some components may mediate specific interactions, and others may mediate nonspecific interactions with surfaces. The "secretome" of a microorganism thus defines its colonization potential on various substrata (343). Microbial attachment to abiotic surfaces is generally thought to be mediated by nonspecific processes, while attachment to biotic surfaces is usually mediated by specific processes (62). Cell surface components involved in specific substratum attachment may recognize distinct surface physicochemical or biotic properties, which may also play a role in regulating the expression and effectiveness of these surface-adhering components (579).

Specific ligand-receptor interactions have been found to play an important role in bacterial attachment to biological surfaces and biofilm formation (48). For nonspecific interactions, certain microbial outer surface structures, such as flagella, fimbriae, pili, and curli, as well as proteinaceous, polysaccharide, and eDNA components (other than adhesion-specific ligands and receptors), collectively known as adhesins, may be essential in the attachment process, particularly during the transition from the initial reversible interaction mediated by surface physicochemical properties to irreversible adhesion (48, 343, 580–584). In addition to these seemingly common mechanisms, some other and potentially unique mechanisms may exist in marine bacteria to facilitate surface colonization and biofilm development. For example, in the marine bacterium *Pseudoalteromonas* sp. strain D41, four outer mem-

brane proteins, homologous to a TonB-dependent receptor (TBDR), the OmpA and OmpW porins, and a type IV pilus biogenesis protein, respectively, were identified to be important for the biofilm formation process on hydrophobic and hydrophilic surfaces (585). So far, the involvement of the TBDR in biofilm formation has been found only in marine bacteria (585).

The Holdfast, a Specialized Colonizing Apparatus in Primary Surface Colonizers

Numerous marine bacteria, especially those in the MRC group (8, 272), the iron-oxidizing *Betaproteobacteria* and *Zetaproteobacteria* classes (586), the sulfur-oxidizing *Beggiatoaceae* and *Leucotrichaceae* families (587, 588), morphotype IV of the *Blastocaulis-Planctomyces* group (14, 589), and budding and prosthecate/stalked bacteria such as the *Hyphomonadaceae* and *Caulobacteraceae* (590–592), produce a polar holdfast structure to facilitate surface colonization. Some other marine bacteria may also produce a holdfast, as indicated by their ability to form rosette-like aggregates, a characteristic associated with (though not shown to date to be directly connected to) holdfast production (593–595). The expression of the holdfast seems to be inducible, by direct contact with a surface or other bacteria or by specific microbial physiological status or environmental conditions (591–593, 596–598). In *Caulobacter crescentus*, a sequence of specific steps is involved in surface colonization, with initial reversible adhesion mediated by pili, followed by an arrest of flagellar rotation and subsequent induction of a holdfast for irreversible adhesion (599). *C. crescentus* produces its holdfast only at the appropriate time for surface attachment, and the flagellum serves as the mechanosensor for the induction of holdfast expression and adhesion (481, 600). Some other marine bacteria, such as *Hyphomonas* sp. strain VP-6, may use a similar mechanism for surface colonization (591), and surface mechanosensing mechanisms employing flagella were found in several other bacteria, including marine vibrios (15, 481, 601, 602).

MRC bacteria have been identified as the key pioneer colonizers on both abiotic and biotic surfaces in marine environments (8, 13, 20, 136, 173, 272, 450, 574, 603, 604). Recently, the iron-oxidizing *Zetaproteobacteria* were identified as a group of pioneer colonizers contributing to early-stage carbon steel biocorrosion in marine environments (18, 81). Other putative holdfast-producing bacteria are also frequently detected in marine surface-associated environments. For example, *Planctomycetales* colonize marine particles and algal or abiotic surfaces (12, 14, 605–607), and sulfur-oxidizing, iron-corroding *Leucotrichaceae* colonize algal and submerged carbon steel surfaces (18, 608). Stalked or prosthecate *Caulobacter* and *Hyphomonas* bacteria are primary colonizers of algal or submerged surfaces (246, 266, 607). It is reasonable to hypothesize that holdfast-mediated irreversible attachment may be a key step in surface colonization by most of these pioneer bacteria.

Flagellum-mediated motility and surface mechanosensing may play critical roles in holdfast-mediated surface attachment by flagellated bacteria (593). *Ruegeria* sp. strain TM1040 (previously *Silicibacter* sp. strain TM1040) mutants defective in wild-type swimming motility, due to a loss of flagella or to increased cell length, are also defective in attachment to dinoflagellates (609). Although most holdfast-producing (or rosette-forming) bacteria possess a polar monotrichous flagellum (590–592), not all of the holdfast-producing bacteria have a polar flagellum or flagella. Some bacteria use polar fimbriae for initial surface contact, followed by the use of the holdfast for subsequent irreversible attachment, which is likely induced by fimbria-surface interactions (596, 597). Genes encoding the *Aggregatibacter actinomycetemcomitans* (previously *Actinobacillus actinomycetemcomitans*) homologue Tad and Flp fimbrial proteins are present in select MRC bacteria (610), likely playing a role in surface colonization (595). Some other bacteria may induce holdfast expression and attachment in response to direct cell surface-substratum contact. It is likely that the flagellum is the major, but not the sole, mechanism of surface mechanosensing and holdfast induction for surface colonization in marine microorganisms.

COOPERATION AND COMPETITION IN SHAPING THE COMPOSITION, DYNAMICS, AND FUNCTION OF MULTISPECIES MICROBIAL BIOFILMS

Marine surface-associated communities are composed of diverse microbial species (17, 108, 151, 153, 574, 611, 612), which usually form biofilms with specific structures and functions (13). Biofilms are composed mainly of a highly hydrated EPS matrix that encases both surface-associated microorganisms and their extracellular products (29, 613). In addition to structural components such as extracellular polysaccharides, proteins, nucleic acids, lipids, and other biopolymers, such as humic substances, which collectively determine key biofilm microenvironmental physicochemical properties, including matrix density, porosity, water content, hydrophilicity, charge, sorption capacity, mechanical stability, fluid dynamics, and mass transport (29, 59, 584), the biofilm matrix also contains microbial functional components such as extracellular enzymes, intraspecies and interspecies signaling molecules, toxins, and extracellular membrane vesicles (EMVs) that facilitate microbial interactions (29, 53, 61, 62). Besides playing important structural and functional roles in mature biofilms, microbial interactions also occur during early surface colonization and biofilm development stages, contributing to the diversity and succession of surface-associated microbial communities (62, 567).

Coaggregation, a Common Mechanism for Microorganism Recruitment to Surfaces

Besides initial surface attachment, microorganisms can also be recruited to the surface-associated community by secondary microorganism-microorganism and microorganism-surface matrix interactions (397). Coaggregation has been proposed as a central mechanism, likely mediated by specific cell surface adhesin-receptor interactions between participating microorganisms (614), for the formation and development of multispecies biofilm communities (567, 615, 616). Some surface-colonizing microorganisms performing this bridging function recruit different microorganisms to join in the development of the surface microbiota (616).

It has long been recognized that coaggregation may be a key driver shaping biofilm community composition and function in diverse environments (616). Primary surface-colonizing bacteria commonly employ coaggregation as a mechanism to recruit secondary surface colonizers to establish sequential successional dynamics and the ordered spatial structure of the biofilm community. This has been most thoroughly studied in freshwater and wastewater systems and in human oral biofilms to date, although the implications for marine biofilms are clear. Freshwater and wastewater bacteria coaggregate (567, 617–619), and some freshwater bacteria that can serve as bridging mediators for recruiting

different microorganisms to the surface-colonizing microbial community have also been identified (567, 620–622). Coaggregation of both early and later surface colonizers with the bridging microorganisms contributes to the dynamic changes of species composition and diversity observed in surface-associated microbial communities (567, 616, 623). Chemotaxis is normally required for effective microbial coaggregation (624), and freshwater bacterial coaggregation is strongly influenced by the metabolic status of the microorganisms involved and environmental conditions such as nutrient availability, pH, and ionic strength of the aquatic system (625, 626). Environment-regulated and/or cell physiology-controlled expression of the microbial coaggregation adhesins or receptors may be the reason for the observed phenomena (61). Interspecies coaggregation mediated by the specificity of adhesin-receptor interactions may be driven by the evolution of the microbial partners (627), which may also lead to the establishment of broader cooperative traits (628, 629). For example, ammonia-oxidizing bacteria (AOB) and nitrite-oxidizing bacteria (NOB) form symbiotic partnerships via coaggregation to carry out nitrification in activated sludge flocs and biofilms (619, 630, 631). This cooperation is essentially facilitated by the spatial juxtaposition of these two groups of bacteria and by the effective transfer of nitrite from AOB as a product of energy metabolism to NOB as a substrate for energy metabolism. In similar ways, coaggregation likely facilitates other metabolic cooperation processes via the transfer of other metabolites or energy in surface-associated microbial communities (632–634).

Coaggregation draws different microorganisms into close spatial juxtaposition within multispecies biofilms, which not only may increase the diversity of species composition and metabolic pathways of the community but also may enhance the opportunity for and efficiency of cell-cell signaling, metabolite transfer/exchange, cross-species protection, genetic exchange, and contact-dependent gene expression (61, 567, 628). Although investigations of coaggregation partnerships and their consequences have scarcely been undertaken with marine bacteria (635, 636), it is reasonable to hypothesize that coaggregation-based cell-cell interactions may play as important a role in marine biofilm formation as in freshwater environments (616, 628). According to McCormick et al. (628), microbial coaggregation associated with marine particles may help to establish a parsimonious food chain, increasing the energetic potential of metabolites of these resource islands in generally oligotrophic surroundings.

Cheating: It Happens in the Microbial World, Too

Surface-colonizing microorganisms also possess diverse mechanisms of competition. Competition sensing is a recently proposed bacterial strategy for the direct detection of and response to, via stress responses such as those caused by nutrient limitation, ecological competition, which is particularly intense in surface- and biofilm-associated communities (637). Some primary surface colonizers may inhibit colonization by other and/or later-arriving taxa (638), and this competition may be quite subtle. *P. aeruginosa* in multispecies microbial biofilms increases the production of organic iron chelators, siderophores, in response to increasing Fe scarcity, thus enjoying a competitive advantage over other microorganisms (639–641). Although this strategy may increase the ability of *P. aeruginosa* to sequester iron and thus outperform other microorganisms, it also produces the opportunity for siderophore nonproducers to benefit. Siderophore nonproducers, "cheaters," may be able to harvest more iron via *P. aeruginosa*-produced siderophores without paying any cost of siderophore production (639). Such cheating microorganisms may actively colonize or be recruited as secondary colonizers of submerged surfaces.

Iron is an essential trace element, existing mainly as solid, very-low-solubility, Fe^{3+}-bearing mineral phases in oxic and pH-neutral environments (433, 642). Due to its very low concentration (643), dissolved iron constitutes a limiting micronutrient for primary productivity in large areas of the world's oceans, particularly in high-nutrient (nitrate, phosphate, and silicate) but relatively low-phytoplankton-biomass areas (644, 645). Furthermore, marine bacteria contain more iron per unit biomass than phytoplankton, and thus, bacterial iron assimilation may constitute another constraint on iron availability to phytoplankton (646). Iron is also a key resource limiting microbial N_2 fixation, phosphate acquisition, and, thus, productivity in the ocean (181, 647–649). It has been proposed that iron may control productivity in half of the world's oceans (650, 651) and may have accounted for one-quarter of the decrease in the atmospheric CO_2 concentration during the Earth's historical glacial maxima (652). Besides being a limiting resource for photosynthesis and N_2 fixation, iron is also an essential functional component of key enzymes in respiration, DNA replication, fatty acid metabolism, and other vital cellular and physiological processes (653). In the global ocean, the iron cycle affects, directly and indirectly, the biogeochemical cycling of C, N, P, Si, and S and thus exerts a strong influence on the regulation of the Earth's climate (654). Although the bulk concentration of particulate iron (~0.4 nM) is similar to the bulk concentration of free dissolved iron (0.03 to 1.0 nM) in the surface ocean (642), marine particle-associated iron is highly localized and concentrated. Thus, marine particles may provide a rich source of iron for particle-associated microbial processes (53, 177, 181, 227, 301, 642, 655). This feature is exploited by many marine microorganisms, especially in environments with strong iron limitation, for CO_2 fixation, N_2 fixation, and other key biogeochemical processes (155, 656). Under iron stress conditions, many marine particle- and surface-associated microorganisms produce and secrete siderophores to facilitate iron dissolution and uptake (657, 658), and this physiological process is usually coregulated with the microbial surface- and biofilm-associated physiology and modulated by the TCS, QS, sRNA, and c-di-GMP regulatory systems (179, 659–663). Interestingly, some surface- or biofilm-associated bacteria possess the genes for siderophore-specific transport systems such as the TonB-dependent outer membrane transporters or ABC-type siderophore transport systems (664, 665) while lacking the genes for siderophore production (666, 667). These siderophore-nonproducing cheaters may gain the benefit of taking up siderophore-bound iron if they can recruit as surface colonizers localized near siderophore-producing microorganisms (35, 668). Cheating as a special form of competition may be important in surface- and biofilm-associated marine microbial communities.

Quorum sensing provides a fundamental means of microbial cooperation (39, 441). In natural environments, this cooperative behavior benefits the biofilm population and community, for example, by synchronizing the production and secretion of extracellular enzymes for efficient degradation and utilization of biopolymeric substrates (669, 670). However, QS-based cooperation may suffer from and even be compromised by cheating. For example, in natural environments, 50% of *V. cholerae* strains may be QS

deficient, and interestingly, some of these strains may actively cheat by false signaling to lure the QS-capable strains to produce QS-dependent "public goods" (670). These cheating bacteria behave very much like "swindlers," whereas the above-mentioned siderophore-nonproducing bacteria behave very much like "thieves." However, both strategies of cheating seem to be effective for competition in surface-associated microbial communities.

Although cheating may lead to a disruption or breakdown of cooperation (671), cheaters are very common in the microbial world, especially within high-density populations or communities such as those on surfaces and in biofilms (672). Lee et al. (673) proposed that the existence of cheaters in a cooperative microbial community may provide a general mechanism for the evolution of diversity that is involved in providing public goods, such as siderophores for iron scavenging, extracellular enzymes for metabolizable substrate acquisition, quorum sensing autoinducers for population or community adaptivity, extracellular matrix biopolymers for biofilm formation and structure, surfactants for motility on surfaces, and exotoxins for host invasion (668, 671, 672, 674–676). The functionality and sustainability of a biofilm microbial community may depend upon the balance between cooperative and competitive interactions (677), likely driven by the coevolution of cooperators and cheaters and maintained by the compositional and metabolic diversity in the microbial system (678).

Deadly Competition: Chemical Agents, Predation, and Specialized Weapons

There are various competition strategies that are more directly antagonistic than cheating among microorganisms (62, 679), especially on surfaces or in biofilms, where high microbial densities and close spatial proximities are achieved. More than 50% of marine bacterial isolates were found to be antagonistic toward other bacteria, and this trait was more common in particle-associated bacteria than in free-living bacteria (680, 681). For example, many MRC bacteria produce antimicrobial substances such as tropodithietic acid (TDA), indigoidine, tryptanthrin, and peptide antibiotics (8, 173, 272, 450, 594, 682). TDA biosynthesis is modulated by the QS and c-di-GMP regulatory systems in MRC bacteria, and TDA also induces its own synthesis as well as bacterial surface attachment, indicating its roles in the bacterial motile-to-sessile lifestyle switch and interspecies competition (483, 683, 684). Indigoidine synthesis is also regulated by QS and provides a competitive advantage that contributes to the surface colonization success of its producers (450, 685). Surface-associated MRC bacteria are over 10 times as likely as their free-living counterparts to produce antibiotics in marine environments (680), and this difference may be related to the differences in bacterial gene repertoires (8, 173, 594). Antibiotic production may play a role in the success and prevalence of MRC bacteria as pioneer surface colonizers in the ocean (8, 17, 173, 272, 450).

Some other marine bacteria, such as *Bdellovibrio* and like organisms (BALOs), which are affiliated with the *Bacteriovoracaceae* and *Bdellovibrionaceae* in the *Deltaproteobacteria* lineage and *Micavibrio* in the *Alphaproteobacteria* lineage, are obligate predators that prey on other environmental microorganisms (686). BALOs have evolved host interaction predatory-specific genomic islands (687). As surface-associated microbiota have much higher densities than free-living communities, BALOs are more abundant on surfaces, exploiting a rich resource of prey microorganisms in marine environments (688, 689). Living in biofilms also provides protection against extreme or hostile environmental conditions for BALOs, enhancing their survival in nature (690). BALOs may employ chemotaxis to respond to chemoattractants and to track prey bacteria (691) and employ gliding motility to "scout" for prey on surfaces (692). *Bdellovibrio bacteriovorus* predation requires the type IV pili (693), which may play an important role in initial attachment to a prey bacterium in aquatic environments and possibly in movement for locating prey bacteria within the matrix of biofilms (694). BALOs are phylogenetically and environmentally diverse in the ocean (695–697), and they display niche separation, different predation strategies, and prey selectivity such that some BALOs are more specific for particular prey organisms, while others are more prey generic (696, 698–700). Some other bacteria of the *Proteobacteria* (including *Alpha-*, *Beta-*, *Gamma-*, and *Deltaproteobacteria*), *Actinobacteria*, *Bacteroidetes*, and *Chloroflexi* lineages are also predatory (701). Marine predatory bacteria may play a role in shaping the composition, abundance, and biogeochemical functions of the affected surface-associated microbiota (62, 699, 702). However, this hypothesis has not yet been systematically tested.

Some surface-associated bacteria use contact-dependent growth inhibition (CDI) systems that constitute cognate toxin-immunity protein pairs for interbacterial competition (703, 704). The CDI systems are mainly type V secretion systems, and the secreted toxins display RNase, DNase, or membrane pore-forming activities toward target cells of the same species, suggesting the involvement of these systems in competition between closely related bacterial strains (703, 705, 706). Thus, CDI systems may enforce cooperation among surface-associated bacteria by inhibiting the growth of cheaters that lack cognate immunity proteins (703). Genomes of many *Alpha-*, *Beta-*, and *Gammaproteobacteria*, including marine species, harbor the genes that encode CDI systems (707–709), which may be prevalent in marine surface-associated microbial communities.

Recently, it was found that more than a quarter of Gram-negative bacteria harbor a type VI secretion system (T6SS), which is involved in bacterial predation on neighboring bacterial cells via a contact-dependent mechanism as well (705, 710). Furthermore, some bacteria have evolved a "tit-for-tat" counterattack strategy, also using the T6SS mechanism (711, 712). Surface association may be favorable to T6SS effector delivery (713), in which the threonine phosphorylation signal transduction pathway (TPP) may play an important role in surface-dependent T6SS activation (714). Nearly one-third of the identified T6SS gene clusters harbor TPP-related components; thus, surface activation of the T6SS by signal transduction may be very common in bacteria (715).

It has been found that the expression and secretion of the antimicrobial T6SS, such as T6SS1 in *V. parahaemolyticus*, are upregulated upon surface sensing (716). The effect of T6SS-mediated intraspecific and interspecific competition may be maximized particularly in high-density populations or multispecies communities such as microbial biofilms and aggregates (717–719). Bacterial T6SS mutants have severe impacts on biofilm formation (718, 720). In *V. cholerae*, the T6SS is required for host intestinal colonization (350, 721). The expression of T6SSs is usually induced by specific environmental signals such as temperature, salinity, cell density, and surface sensing and regulated by mainly the TCSs and by the QS, sRNA, c-di-GMP, cAMP-CRP, and alternative sigma factor systems (350, 713, 716, 722–727), all of which are

involved in the modulation of microbial surface colonization and in the regulation of gene expression in biofilms (414, 728). The coordination of the TCS or the QS, sRNA, or c-di-GMP regulatory system with the expression of T6SSs may potentially aid in microbial surface colonization fitness via the displacement of competing bacteria at locations having growth-supportive conditions and via the promotion of horizontal gene transfer (718, 729). For example, in *V. cholerae*, the expression of the T6SS is regulated by quorum-regulatory Qrr sRNAs, which repress the T6SS genes at low cell density (727). This process may help *V. cholerae* to conserve resources and gain benefit in a multisubpopulation or multispecies biofilm, as assembly of the T6SS requires the synthesis and secretion of a cluster of protein components and would not be advantageous when there are few targets available (713, 730, 731). Although there is no direct evidence showing a QS regulatory effect on bacterial T6SS functioning in natural marine environments, QS signal compounds have been identified in marine surface-associated microbial communities (440, 441), indicating that it is possible that both mechanisms may be functional and coordinated in bacterial ecophysiology in marine surface-associated microbiota.

Alphaproteobacteria (especially MRC bacteria) have been demonstrated to be the key primary surface colonizers in marine environments (8, 13, 20, 173, 272, 450, 604). However, the T6SSs are found primarily in *Gammaproteobacteria* among the marine bacteria (732). Recently, T6SSs have also been identified in some bacterial strains, genomes, and marine metagenomes of *Bacteroidetes* (733–736), an important group of secondary surface colonizers in marine environments (13, 17, 108, 130, 272, 574). Therefore, it is reasonable to hypothesize that T6SS-mediated microbial competition may contribute to the successional change and spatial variation of the composition and structure of surface-associated marine microbial communities, in which certain T6SS-harboring bacteria may constitute important groups of secondary colonizers.

Extracellular Membrane Vesicles as Mechanisms for Both Cooperation and Competition

Cooperation and competition as important ecological characteristics are not just for surface-associated microorganisms. Free-living marine microorganisms, including the ocean ecosystem-dominant cyanobacterial genera *Prochlorococcus* and *Synechococcus*, many heterotrophic bacteria, and seawater microbial communities in both coastal and oligotrophic open-ocean environments, have recently been found to produce and secrete EMVs that contain proteins, lipids, DNA, and RNA (737). The proposed benefits of this ecological phenomenon include (i) enhancing microbial nutrient sensing and uptake via EMV-contained transport receptors, substrate-binding proteins, and degradative enzymes that target environmental HMW molecules; (ii) stimulating neighboring helper microorganisms to grow, produce, and share beneficial products such as enzymes, vitamins, siderophores, and other materials that the EMV-secreting microorganism cannot produce; (iii) facilitating microbial communication and horizontal gene transfer via mediating cell-to-cell exchange of signal molecules and DNA at the ecosystem level; and (iv) preventing phage attack by using the secreted EMVs as decoys (737–741). For example, the EMVs of the psychrotolerant bacterium *Pseudoalteromonas antarctica* NF3 contain proteases, peptidases, glycosyl hydrolases, lytic transglycosylases, glycosyltransferases, TBDRs, and sulfate-binding proteins (738). The EMVs of another Antarctic bacterium, *Shewanella livingstonensis* NF22, also contain TonB-dependent siderophore receptors, phosphate-binding periplasmic protein precursors, and proteins involved in aromatic hydrocarbon degradation (739). Most of these proteins are likely involved in organic matter degradation and nutrient uptake, potentially important to bacterial survival in the nutrient-limited Antarctic environment. EMVs can also be employed to attack competing microorganisms (19, 29, 741, 742). For example, the EMVs of *P. antarctica* NF3 also contain enzymes that hydrolyze bacterial cell wall polymers (738). However, the benefits provided by EMVs may come at a very high cost for free-living microorganisms, especially for those living in oligotrophic marine environments (740). It has been estimated that $\sim 10^4$ to 10^5 tons of fixed carbon are released into the ocean daily via EMVs by *Prochlorococcus* alone (737), without taking into account other EMV-secreting microorganisms and other limiting resources such as N, P, and Fe contained in the EMVs. In addition, the benefits are not very reliable for free-living microorganisms because there is little or no control of the fates and effects of the EMVs once they are released into the surrounding aquatic environment. Physical, chemical, and biotic (from nontarget organisms) factors may all exert impacts on the fates and effects of the secreted EMVs in marine waters.

EMV secretion is common in all three domains of life (743), and EMVs are an important component of the biofilm matrix (15, 19, 29). The secretion of EMVs is regarded as a bacterial stress response and may be regulated by environmental cues (744, 745). EMVs are beneficial for planktonic microbial cells in forming aggregates and contributing to adherence to surfaces and thus facilitate microbial surface colonization and early-stage biofilm development (744, 746, 747). For example, the EMVs of *P. antarctica* NF3 contain several types of adhesins (738). Adhesins in EMVs may promote microbial coaggregation and assist in the recruitment of secondary surface colonizers (748, 749). EMVs may also contain signaling molecules that facilitate intraspecific and interspecific communication and cooperation at the microbial population and community levels (741, 742). *V. cholerae* EMVs contain the major biofilm matrix proteins RbmA, Bap1, and RbmC (750) as well as chitinases (750), indicating once again that chitin is an important resource for vibrios in marine environments and highlighting the importance of surface colonization for chitin utilization. In *V. fischeri*, biofilm formation is correlated with EMV production, which is induced by the sensor kinase RscS (751). How is the production of EMVs regulated in other marine bacteria? Is there any environmental cue or physiological control for the production of EMVs? The answers to these questions will advance our understanding of the processes and mechanisms of microbial EMV production and their contributions to biofilm formation and development.

In biofilms, the EMVs and their contents are confined, at least partially, to the EPS matrix, and they should be both more chemically stable and physically closer to the target microbes (either as cooperators or competitors of the EMV-secreting microorganism). The cost of producing and secreting EMVs in biofilms may be better justified than in planktonic environments. Therefore, a free-living cyanobacterium living in the open ocean may have a harsher life than a cyanobacterium living in a microbial mat (752, 753). Living in a crowded "city," called biofilm, may be a preferred lifestyle for most aquatic microorganisms if conditions permit

(22). Furthermore, no matter which mode of life is undertaken, either free-living or surface associated, the microorganisms in nature need to benefit their cooperators, oppose their competitors, and maintain a benign or at least neutral interaction with other not-so-friendly and not-so-hostile neighbors. All of these activities require the expenditure of metabolic energy and precious resources, which may not be easy to obtain in many marine environments. Due to the close positioning of microorganisms, the protective nature of the EPS matrix, and the development of sensing, signaling, and regulatory mechanisms and social behaviors among different microorganisms in biofilms (21, 35), the functional efficiency of biofilm microbial communities should be higher and more stable than those of planktonic microbial communities. In future research, investigations of the ecological functions of the surface-associated and biofilm microbiota that take into account the molecular mechanisms, community processes, material and genetic fluxes, ecosystem metabolism efficiency, and other systems biology perspectives may be highly productive.

KEY MICROBIAL SURFACE COLONIZERS IN MARINE ENVIRONMENTS

As is highlighted throughout this review, there are two major lifestyles in marine microorganisms, free-living and surface associated. Most marine microorganisms appear to prefer one lifestyle or the other, although some may switch their preference under certain environmental conditions or during certain life stages. For example, some marine bacteria, such as those affiliated with the SAR11 and SAR86 lineages, are mainly free-living (754, 755), while the marine *Rhodobacteraceae* group of the *Alphaproteobacteria* (i.e., the MRC), the *Alteromonadaceae* and *Vibrionaceae* groups of the *Gammaproteobacteria*, and *Bacteroidetes* (mainly the *Flavobacteria* group) are frequently surface associated (13, 272). The separation of the free-living and surface-associated lifestyles is likely a result of long-term evolution, and these distinct capabilities are deeply rooted in microbial genetics (756–758). The ecophysiology of surface-associated marine *Alteromonas* and *Vibrio* is discussed above, so the foci of this section are the MRC and *Bacteroidetes*.

The Marine *Roseobacter* Clade

MRC bacteria are ubiquitous in the world's oceans and abundant as both free-living and sessile organisms. When sessile, they are usually associated with the phycospheres of diatoms, dinoflagellates, and other algae and with zooplankton fecal pellets, marine particles, and submerged surfaces (8, 13, 173, 272, 450, 594, 756, 759–761). These bacteria are generally heterotrophs, able to metabolize a variety of labile and recalcitrant organic substrates, including monocyclic and polycyclic aromatic hydrocarbons as well as various algal osmolytes and other metabolites (173, 175, 272, 594, 762–767). They usually react to and grow quickly after small increases in levels of labile organic substrates, such as amino acids, simple sugars, and DMSP, especially during the initial phase of algal blooms (8, 13, 252, 265, 272, 768–772).

Some of the MRC bacteria produce auxins (such as indoleacetic acid), essential vitamins, and siderophores, entering into mutualistic relationships with algae (272, 595, 603, 610, 758, 762, 765, 773, 774). All MRC bacterial genomes harbor the genes that encode c-di-GMP signaling systems, and more than half of the MRC genomes harbor the genes that encode motility, chemotaxis, and diverse chemoreceptor proteins (8, 595, 609, 682, 762, 775), likely important in locating algae and establishing tight interactions and associations (8, 595, 776). Many MRC bacteria have holdfasts, type I and type IV secretion systems, QS regulatory systems, and versatile physiological capabilities for living in suboxic and anoxic (micro)environments (employing denitrification, for example), which are important for living on surfaces and in biofilms (8, 173, 272, 450, 603, 758, 762, 777).

In addition to the physiological and genetic traits that are directly related to surface living, many MRC bacteria have other properties that are advantageous to living on surfaces or in biofilms. Some MRC bacteria conduct aerobic anoxygenic photosynthesis. This process seems to be enhanced by surface association (150, 151, 173, 762, 778–780) and may enhance ATP production, active transport, motility, and cell growth yield on available organic matter (272, 779). Some MRC bacteria synthesize and store poly-β-hydroxyalkanoates when carbon and energy resources are available but inorganic nutrients are limiting (781, 782), which may enhance bacterial viability via poly-β-hydroxyalkanoate catabolism when other sources of organic substrates are scarce (594). Some MRC bacteria also carry out lithotrophic sulfur oxidation to conserve additional energy (783, 784), which may be explored to enhance anaplerotic CO_2 fixation, growth, and survival (761, 785). These traits provide MRC bacteria with additional competitive advantages for energy acquisition, energy conservation, and stabilization of bacterium-alga and bacterium-surface associations.

Many MRC bacteria can produce antibiotics that may enhance their competitiveness against other surface-colonizing bacteria, especially in the phycosphere, where antibiotic production is probably not limited by the availability of energy and organic substrates (8, 272, 450). Furthermore, plasmids, chromids, and other extrachromosomal mobile genetic elements, such as the phage-like gene transfer agents (GTAs), are common in MRC bacteria, contributing to gene transfer, metabolic versatility, and fitness, especially in microhabitats such as those on surfaces and in biofilms (762, 786–789). In some MRC bacteria, the genes encoding the biosynthesis of TDA, siderophores, and extracellular polysaccharides are located on plasmids or chromids, indicating the direct involvement of extrachromosomal genetic material in bacterial surface associations (603, 789). For example, *Marinovum algicola* DG898 harbors three plasmids and eight chromids, and one of the chromids harbors the 52-kb biofilm functional gene cluster that is essential for surface attachment and adaptation to the phycosphere (790). MRC bacteria are well adapted to surface living, and this trait has been suggested to originate from the coevolution of MRC bacteria with marine algae (757). Furthermore, MRC bacteria may promote surface colonization and biofilm formation of other marine bacteria (453), likely playing a role in shaping the composition and succession of surface-associated microbial communities (17). All the available evidence indicates that MRC bacteria are important primary surface colonizers in marine environments.

Marine *Bacteroidetes*

Diverse genomic and ecophysiological evidence indicates that marine *Bacteroidetes* are highly adapted to surface living and POM unitization. Studies have shown that *Bacteroidetes* bacteria are common in marine environments (791), abundant in organic particle-rich coastal waters (108, 113, 130, 611, 791), responsive to algal and jellyfish blooms (272, 537, 756, 791–793), copiotrophic

(252), and prone to leading a surface-associated life (12, 17, 246, 272, 574, 607) supported by the extracellular degradation of complex biopolymers such as polysaccharides and proteins (194, 791, 794–797). These bacteria harbor a large number of genes for adhesive exopolysaccharides, adhesion proteins, proteases, peptidases, glycoside hydrolases, and lipases, and several genes for biopolymer degradation are coregulated with the genes for TonB-dependent transport systems (794, 795, 798–802). These properties indicate that the marine *Bacteroidetes* are specialists in surface colonization and play a key role in the degradation and utilization of HMW DOM and POM (272, 791). A recent metagenomic study showed that submerged insoluble polysaccharides such as cellulose are colonized by biofilm-forming marine bacterial communities, of which the *Bacteroidetes* are a major group that harbors an extensive repertoire of genes encoding glycoside hydrolases (803). Marine *Bacteroidetes* may also harbor TonB-dependent transport systems that can be used for the uptake of polysaccharides (804).

Marine *Bacteroidetes* commonly possess gliding motility, which is important for surface living, chitin utilization, and other ecophysiological activities (805), but these bacteria generally do not produce flagella. So how do they locate and colonize surfaces such as marine particles? Azam and Malfatti (186) proposed that nonswimming particle colonizers, such as *Bacteroidetes*, first attach to the highly abundant small gel particles in seawater. Aggregation of small gel particles with larger particles and agglomeration with other materials, such as phytoplankton or detritus, bring attached bacteria to the large marine particles and aggregates such as marine snow (186). Recently, Bar-Zeev et al. (577) verified that microgel TEPs indeed facilitated biofilm formation in test aquatic systems. The *Bacteroidetes* were also the dominant group of bacteria attached to TEPs in mesocosm experimental systems, especially under intermediate- and high-turbulence conditions (806).

Some other mechanisms may also contribute to the success of surface living by *Bacteroidetes*. Certain marine *Bacteroidetes* harbor rhodopsin pigments for light energy harvesting (807–809), with proteorhodopsins functioning as light-driven H^+ pumps (810, 811), KR2-type rhodopsins functioning as light-driven Na^+ pumps (812), and NM-R3-type rhodopsins functioning as light-driven Cl^- pumps (813). In all three cases, membrane polarity can be produced and used to drive active transport. Proteorhodopsins are likely the most prevalent rhodopsins in *Bacteroidetes* and other marine bacteria, and genes encoding their synthesis are extremely abundant and highly expressed. These pigments likely play an important role in energy metabolism in the surface oceans, especially under oligotrophic or other stressful conditions (779, 814–817). Proteorhodopsin-mediated energy conservation of *Bacteroidetes* may promote growth and survival, facilitate the degradation of complex or recalcitrant biopolymers, and enhance the uptake of organic substrates at low concentrations (818). The phototrophic potential of proteorhodopsin-containing *Bacteroidetes* was found to be correlated with the quality and dynamics of environmental DOM (819). Furthermore, proteorhodopsin-mediated light energy harvesting significantly enhances *Bacteroidetes* anaplerotic CO_2 fixation when suitable organic substrates are available (819). *Bacteroidetes* may also possess sensory-like rhodopsins, which function in phototaxis to direct a bacterium toward desirable light conditions (820, 821). For example, the genome of *Polaribacter* sp. strain MED152 harbors a suite of genes for light sensing and responses (822). It has been suggested that the proteorhodopsins and the light-sensing proteins may play a role in the dispersion of *Bacteroidetes* from particles (822, 823). This mechanism likely involves inducing the secretion of EPS-degrading enzymes that disrupt biofilm and release bacteria from the biofilm matrix, preventing particle-associated bacteria from sinking with the colonized particles into the dark deep water, which usually lacks metabolizable organic substrates. This mechanism may help *Bacteroidetes* maintain themselves in the relatively productive and labile particle-rich sunlit surface water, contributing to the success of *Bacteroidetes* on surfaces.

Gliding is a unique movement used by bacteria to explore surfaces (824). The gliding capability of many marine *Bacteroidetes* undoubtedly contributes to the success and fitness of this group of bacteria for life on surfaces (272). Some marine *Bacteroidetes* are gliding predators that can prey on other surface-associated bacteria (825) as well as diatoms and cyanobacteria (826). The gliding motility of *Bacteroidetes* is powered by proton motive force (824), and proteorhodopsin-harboring predatory *Bacteroidetes* may gain an extra advantage in surface life via light energy-powered gliding motility and microbial predation, although this is speculative. Predatory *Bacteroidetes* may contribute to the control over surface-associated microbial composition and abundance, algal associations and interactions, and marine carbon and nutrient cycling in photic seawater. However, it is still not clear if predatory capability is common among marine *Bacteroidetes*. Further investigations are necessary to better understand the diverse ecophysiological processes and biogeochemical roles of this group of bacteria in particles and in biofilms in the ocean.

Marine *Roseobacter* Clade Bacteria and *Bacteroidetes* in Surface-Associated Community Dynamics

Although both MRC bacteria and *Bacteroidetes* lead a motile-sessile (or floating-sessile) biphasic lifestyle and are frequently found to colonize algal surfaces (595), they may respond to algal blooms differently. At the start of an algal bloom, when the algal population is small and growing, the algae are healthy and active in synthesizing labile DOM such as simple sugars, sugar alcohols, organic acids, amino acids, and DMSP, some of which may be released into the environment as algal exudates (209, 272, 758, 827). In this phase, algal cells provide localized and concentrated labile organic substrate sources, so surface colonization is advantageous to certain marine microorganisms, such as many MRC bacteria (758), and allows rapid responses to the labile DOM substrates. The capability for quick responses to algal exudates makes the MRC bacteria a major group of pioneer surface colonizers (136, 272). With bloom development and the buildup of environmental stresses such as increasing scarcity of inorganic nutrients and accumulation of waste products, the physiological status of the blooming algae changes (828). Usually, unhealthy and senescent algal cells produce and secrete more protective or stress-related extracellular substances, such as polysaccharides (227, 272, 828–830). For example, the secretion of extracellular polysaccharides and the production of TEPs by most marine algae increase significantly under nutrient-limiting conditions that are commonly experienced during the declining bloom phase (831–833). In the demise phase of an algal bloom, dying and broken algal cells release polymeric cellular contents, and some algae may enter the autocatalytic programmed cell death phase of the growth cycle and release huge amounts of TEPs into seawater (834). Furthermore, cellular organic matter can also be released from algal cells by cell lysis due to viral infections, grazing, and sloppy feeding,

especially during blooms, when very high algal population densities are reached (272, 835, 836). The organic algal exudates, secreted TEPs, and lysed cellular contents may facilitate the formation of marine snow and sometimes the massive formation of mucilages in seawater (830, 837, 838). In these late and decaying bloom phases, marine *Bacteroidetes* may gain dominance in the microbial communities and become the predominant surface colonizers on senescent algae, algal aggregates, and detrital particles (109, 272, 839, 840), attacking and utilizing various kinds of biopolymers (841). Various studies, including recent genomic and environmental genomic investigations, have suggested that certain *Bacteroidetes* bacteria may prefer to utilize complex, biopolymeric substrates over simple, monomeric organic compounds as primary carbon and energy sources (272, 791, 822), indicating their major roles in cycling algal polymeric DOM and POM.

MRC bacteria and *Bacteroidetes* likely employ distinct physiological and metabolic strategies during algal blooms (272). Thus, it is reasonable to hypothesize that MRC bacteria and *Bacteroidetes* may adopt different strategies for exploiting resources from algal blooms, via substrate segregation (utilizing simple labile DOM versus complex HMW DOM and POM) and temporal separation (colonizing at early bloom phases versus at late bloom phases). Indeed, studies have shown that MRC bacteria are key pioneer surface colonizers and that *Bacteroidetes* are likely secondary surface colonizers of submerged surfaces in coastal seawater (17, 604). Marine *Bacteroidetes* may be specialized as secondary surface-colonizing experts, armed with T6SSs, EMVs, extracellular *N*-acyl homoserine lactonases (for disrupting QS-facilitated primary surface colonizer communities), and gliding predation capability for preying on and replacing some of the primary colonizers on the surface (733, 735–737, 825, 842, 843). However, both the MRC and *Bacteroidetes* groups are highly diverse (272, 594). Different species or strains in each group may have somewhat different ecophysiologies (such as distinct substrate spectra and different responses during bloom progression), and certain bacteria from different groups may have similar ecophysiologies and overlapping niche preferences (8, 272, 768, 844–846). Differentiation of the roles of the MRC bacteria and *Bacteroidetes* in algal bloom-related processes and ecofunctions may not be straightforward in some situations. Furthermore, although the species and physiological status of algae are important factors influencing the composition, succession, and function of alga-colonizing microbial communities (847), the composition, abundance, and dynamics of metabolizable organic compounds (such as labile DOM and HMW DOM and POM) from algal exudates and phytodetritus may play an even more important role (841, 848, 849). It is necessary to monitor the flows of matter and energy during blooms to gain a better understanding of bacterium-alga interactions and microbial community successions.

Recently, it was shown that the abundance of surface-associated MRC bacteria is decreased while that of *Bacteroidetes* is increased in response to increases in environmental temperature or elevated partial CO_2 pressure (pCO_2)-induced ocean acidification (322, 324). Similarly, the abundance of planktonic *Bacteroidetes* also increases in response to increased temperature and/or CO_2 content (and thus decreased pH) in both mesocosms and natural seawater environments (850–852). These results further emphasize the niche segregation and ecophysiological distinction of these two key groups of marine bacteria and indicate their distinct roles in marine carbon cycling and other critical biogeochemical processes, especially under the scenario of global change.

FUTURE PERSPECTIVES ON STUDIES OF MARINE SURFACE-ASSOCIATED MICROBIOTA

Although a wealth of information has been obtained regarding surface-associated microorganisms, major gaps in our knowledge remain, especially regarding community structure, dynamics, functions, and the impacts of the changing marine environment. The compositions and structures of the surface-associated microbiota and the processes and mechanisms of microbial surface colonization and biofilm development are highly complex, particularly in dynamic natural marine environments. Many working hypotheses regarding the marine surface-associated microbiota have been proposed in previous studies and throughout this review. Here we summarize a number of scientific questions that should be productive to pursue regarding marine surface- and biofilm-associated microbial communities.

- What are the physicochemical and nutritional environmental cues that marine microorganisms sense and respond to for initiating surface colonization and biofilm formation? Is there any consistency among these cues in different marine environments, such as in estuaries, coastal seas, and open oceans?
- What are the molecular apparatus and mechanisms employed by marine microorganisms to sense distinct environmental cues for initialization of surface colonization and biofilm formation? Do microorganisms in different phylogenetic or functional groups use the same sensing systems and mechanisms for the same environmental cue, or do they vary at group-, species-, or even strain-specific levels?
- How is an extracellular signal from an environmental cue relayed inside the microbial cell, and how is the intracellular response for surface colonization and biofilm formation elicited and regulated in the cell? How may the environmental signal be propagated among different microorganisms to induce a communal behavior in marine surface colonization and biofilm formation?
- What are the major cell surface components that are involved in surface sensing and surface colonization in marine microorganisms? Are *C. crescentus* flagellum-based surface mechanosensing and holdfast-based surface colonization common mechanisms in marine primary surface colonizers? What distinct functional roles may primary and secondary surface colonizers play in surface-associated microbial communities? What role may coaggregation play in the composition and succession of marine surface-associated microbial communities? How do the different mechanisms of microbial cooperation and competition influence the composition, structure, spatiotemporal dynamics, functions, and stability of marine surface-associated microbial communities?
- How may the composition, structure, and functions of surface-associated microbial communities be related to the physicochemical and nutritional differences of distinct surface or particle types in the ocean? How may the interactions of the surface-associated and free-living microbial communities influence each other? How may the surface-associated

microbial communities and functions be influenced by viruses, protozoa, and surface-grazing zooplankton?

- How may surface association influence the genetic, physiological, and ecological fitness of marine microorganisms? Do surface-associated microorganisms evolve faster, driven by more frequent horizontal gene transfer events, than their free-living counterparts? How do plasmids, chromids, GTAs, and other extrachromosomal elements impact surface-associated fitness and its dispersal among marine microorganisms? How can these genetic elements be engineered and employed to control microbial surface colonization and biofilm development, for instance, to prevent biofouling and biocorrosion?
- For clearly identified, commonly occurring marine surface colonizers such as MRC bacteria, *Bacteroidetes*, *Alteromonadaceae*, and *Vibrionaceae*, is there any interaction (cooperative or competitive) among these bacterial groups on surfaces and in biofilms? How may these interactions be influenced by changing marine environments?
- What are the quantitative contributions of marine particle-associated microbiota to the biogeochemical cycling of life-essential and environmentally important elements, primary production (in both photic zone and dark deep waters), and carbon sequestration of the ocean? How may these contributions be altered in response to anthropogenic perturbations and global environmental change impacts? Are surface-associated microbial communities functionally resilient in the face of these impacts? What are the roles of surface-associated microbiota in (accelerating or decelerating) global environmental change? How can we build a mechanistic and prediction-based model?

As microbial surface colonization and biofilm formation and development involve multiple levels of cell-surface and cell-cell interactions, by both direct contact and signal molecule- and metabolite-mediated communication and coordination, laboratory studies using single microbial species and simple mixtures of species are still necessary. Such studies are particularly important for gaining an in-depth understanding of the microbial physiological, biochemical, and genetic characteristics and their environmental responses during key stages of surface colonization and biofilm formation. For single bacterial species, transcriptomic and proteomic studies have revealed useful information about differences in gene expression and protein functions between planktonic and sessile bacterial populations and about the carbon and energy metabolic processes characteristic of distinct biofilm growth states (585, 853). For surface-associated microbial community analyses, molecular approaches such as gene clone library screening, fluorescence *in situ* hybridization (FISH) analyses, and activity assays (especially at the single-cell level) can provide vital information about the composition, abundance, and spatiotemporal variation of the major surface-colonizing microorganisms and their *in situ* activities and functions (854, 855). Mechanistic studies will provide more information about the functions and regulation of the surface-associated microbiota from an ecosystem perspective.

Marine surface-associated microbial communities are intrinsically complex and dynamic, involving diverse microbial species, functional groups, metabolic pathways, sensing and signaling networks, cooperative and competitive mechanisms, genetic exchange and evolutionary potentials, as well as spatiotemporal variation and acclimatization. Furthermore, many different surfaces (including various kinds of particles and aggregates) exist in marine environments (186). The differences among the colonizable substrata add another level of complexity and diversity to the surface-associated microbial communities and their ecophysiology and biogeochemical functions (245). Thus, systems biology approaches are necessary in order to gain an understanding of the community composition, dynamics, and especially the function and its regulation of the marine surface-associated microbiota (856). These approaches will be particularly helpful in decoding the higher-level characteristics of surface-associated microbial communities, such as various cooperative and other sociomicrobial functions (35, 61). "Omics" methods and related bioinformatics analytical tools, which are generally capable of dealing with high-throughput, rapid, and complex analyses, have been proposed as vital approaches (857).

Recently, the *in situ* gene expression of a chemolithoautotrophic *Epsilonproteobacteria*-dominated biofilm from a deep-sea hydrothermal chimney was analyzed by using metatranscriptomics (858). Although typical surface-associated microbial communities in marine waters may be much more complex than the biofilm communities in extreme environments such as deep-sea hydrothermal vents, the rapid development of omics-related approaches presents a promising opportunity to make strides in understanding the marine surface-associated microbiota (859). Omics techniques have already been adopted and are being investigated for marine biofilm microbiota studies (860, 861). Although there seems to be a multitude of opportunities to improve these techniques, it is reasonable to predict that substantial advances are in the offing.

Recent omics investigations of marine particle-associated microbial communities revealed a wealth of information about certain common characteristics of microbial particle colonizers. Metagenomic investigations showed that MRC bacteria are abundant on particles in estuarine, coastal, and polar waters (151, 758, 862), consistent with previous 16S rRNA clone library-, 454 pyrosequencing-, genomics-, and FISH-based study results that found that these bacteria are key primary surface colonizers in coastal waters (8, 13, 20, 54, 173, 272, 450, 594). Metagenomic investigations have also indicated that particle-associated microbial communities generally harbor a more diverse and complex gene repertoire than free-living communities, such as higher genetic potential for transporters of particle biopolymer degradation products and adaptations to life under hypoxic and anoxic conditions. This includes enrichment in genes related to sulfate reduction, methanogenesis, and anammox (151, 161, 863). Recently, high rates of N_2 fixation and *nifH* gene expression by heterotrophic diazotrophs were detected in fully oxygenated marine waters, suggesting that particle association may be the key mechanism to provide the hypoxic or anoxic conditions necessary for this process in such environments (155, 864). Metatranscriptomics studies indicate that different microorganisms may employ distinct adaptive strategies for the use of either free-living or particle-associated habitats in the ocean (865). Particle-associated communities usually harbor more genes that mediate microbial surface colonization, cell-cell interactions, signaling, and transposase-based mobile genetic element activity, all of which are important for surface living and fitness on marine particles (151, 161). In line with these findings, particle-associated microbial

communities transcribed more copies of genes encoding signaling and surface adhesion cellular components that are related to biofilm formation than free-living communities (866). Particle-associated microbial communities also transcribed more copies of genes encoding metabolic pathways that are related to reducing environments (153). For example, transcripts encoding enzymes for microbial denitrifying N_2O and N_2 production were enriched up to 28-fold in particle-associated samples found in the OMZ of the Eastern Tropical North Pacific (167). Although there have been no metaproteomic studies on size-fractionated particles to date, preliminary metaproteomic studies without size fractionation have inferred certain key properties of particle-associated microbial groups in marine environments. For example, these studies have shown that MRC bacteria are rich in membrane transporter expression for the uptake of labile organic substrates, especially during algal blooms (867, 868). Metaproteomic studies have also suggested that marine *Bacteroidetes* (mainly the *Flavobacteria* group) are specialists in attachment to and growth on algal surfaces or detrital particles (194, 841, 867). A recent proteomic study revealed the major functional proteins in *V. cholerae* vesicles (750). These approaches are also suitable for studying microbial surfomes (869) to decode key surface-associated processes such as signaling, adhesion, transport, and cell-cell and cell-environment interactions. Metaproteomics also have great potential for studies of marine extracellular enzymes, vesicles, and cell surface proteinaceous determinants of surface-associated microbiota. In addition to the identification of surface-induced gene expression and functional adaptivity, metatranscriptomic and metaproteomic approaches show the potential to identify fine-scale spatiotemporal dynamics and interspecies interactions (such as cooperation and competition) in complex microbial communities (870, 871), suitable for process and functional analyses of surface-associated microbiota.

Diverse sensing mechanisms and cell surface and extracellular components are involved in microbial surface interactions and surface living. Several key cellular components or systems can thus be defined specifically for surface- or biofilm-associated microbial communities, such as the metasensoritomes, metasecretomes, and metasurfomes (343). These systems are involved in key steps of microbial surface colonization and biofilm development on surfaces, such as initial cell-surface interactions of the pioneer colonizing species, interspecies cell-cell interactions between primary colonizers and secondary colonizers for recruiting new microorganisms and metabolic pathways, and microbial interpopulation interactions leading to spatial variation and temporal succession of the colonizing community. Furthermore, genome-scale metabolic network reconstructions have become a powerful tool for systematic understanding, prediction, and discovery of the genetic and biochemical potentials of an organism (872). This technique also serves as a platform for constraint-based analyses and modeling of microbial communities (873). The integration of community metabolic network reconstructions (constrained by the community signaling and regulatory networks) with ecological and biogeochemical modeling may provide a fundamental framework for mechanism- and prediction-based modeling of both the biological components and the biogeochemical functions of marine ecosystems (874, 875). Thus, omics approaches, along with cultivation and conventional molecular approaches, provide the means for targeted investigation of surface-specific community-level microbial features, which may lead to an enhanced understanding of surface-associated microbial community ecology and biogeochemical functions, at the levels of both molecular mechanistic details and systems biological comprehension.

APPENDIX

Definitions

remineralization depth The depth at which particulate organic carbon is consumed and respired by marine animals and microorganisms. The remineralization of marine organic particles follows an exponential decay pattern with water depth. The remineralization depth determines the degree to which the respired CO_2 that is returned to the water column can influence air-sea CO_2 partitioning and, thus, climate.

POC (particulate organic carbon) The organic carbon in particulate form that is large enough to be retained on a filter (typically with a filter with a pore size of 0.7, 0.45, or 0.22 μm).

DOC (dissolved organic carbon) The organic carbon remaining in the filtrate after the sample is filtered (typically with a filter with a pore size of 0.7, 0.45, or 0.22 μm).

marine snow Mostly biogenic particles with a diameter of >0.5 mm. These organic particles are usually formed in the euphotic zone of the ocean and sink at high rates to serve as the principal means by which organic carbon is transported to the deep ocean and sediments.

transparent exopolymer particles Small organic particles (less than a few hundred micrometers) that are visible under a light microscope only by staining with an acidic polysaccharide-specific dye, such as alcian blue, or are otherwise transparent and invisible by light microscopy. They are abundant in marine waters and formed by extracellular biopolymeric substances exuded by phytoplankton and bacteria.

biological pump The vertical transportation of photosynthetically produced organic carbon, mainly in the particulate form, from the euphotic surface ocean to the dark deep ocean. The biological pump provides one of the biological mechanisms contributing to the oceanic sink of atmospheric CO_2 via the settlement of biogenic organic particles out of the ocean surface waters.

microbial carbon pump The process of microbial transformation of labile dissolved organic carbon to recalcitrant dissolved organic carbon, contributing to ocean carbon sequestration in the dissolved organic phase.

microbial loop The pathway of carbon and energy flow, via heterotrophic *Bacteria* and *Archaea*, from dissolved organic matter to bacteriovorous protists and further to other animals at higher trophic levels in the aquatic food web.

epipelagic zone Also referred to as the "euphotic zone," the water layer from the air-sea interface down to the depth at which the light intensity falls to 0.1% of that at the ocean's surface. This illuminated portion of the water column, usually in the upper 200 m in the clearest ocean water where sufficient sunlight is available, sustains net photosynthesis.

mesopelagic zone Also referred to as the "twilight zone," the water layer immediately below the euphotic zone and usually between depths of 200 m and 1,000 m where sunlight is measurable but insufficient to support net photosynthesis. The mesopelagic zone is usually characterized by intense microbial heterotrophic activities.

bathypelagic zone The water layer from 1,000 m down to ~4,000 m, where only chemoautotrophs (but not photoautotrophs) contribute to marine primary production due to the complete lack of sunlight.

chemolithoautotroph A microorganism that uses CO_2 as its source of carbon for biomass production and cell growth and derives its metabolic energy from the oxidation of reduced inorganic compounds.

mixotroph A microorganism that can obtain its metabolic energy or carbon from more than one conventional source. For example, many chemolithoautotrophic microorganisms can assimilate some organic compounds as supplements to CO_2 fixation.

anaplerotic CO_2 fixation Heterotrophic CO_2 fixation (i.e., heterotrophic

CO_2 assimilation) processes that usually employ carboxylation reactions to incorporate CO_2 into organic intermediate metabolites to replenish the tricarboxylic acid cycle. This carbon assimilation reaction is an important metabolic activity for carbon acquisition, biomass production, and growth in some heterotrophic microorganisms that do not harbor autotrophic CO_2 fixation pathways.

oligotroph A microorganism that tends to live in an oligotrophic environment, such as the subtropical gyres of the ocean, which offers very low levels of organic carbon. An oligotroph is usually characterized by its genetic and ecophysiological adaptation to low-nutrient conditions and may also display slow growth and low rates of metabolism.

copiotroph A microorganism that tends to live in an environment that is rich in nutrients (particularly organic carbon). A copiotroph is usually characterized by its genetic and ecophysiological adaptation to high-nutrient conditions, fast growth, and high rates of metabolism when concentrations of suitable substrates are sufficient.

priming effect The positive influence of a labile organic matter input on the increased utilization and decomposition of originally refractory organic matter in the environment. This effect may result from enhanced microbial activity stimulated by the supply of labile organic matter.

biofouling The impairment or degradation of underwater surfaces, equipment, and structures as a result of the gradual and undesirable accumulation, growth, or activity of living organisms such as bacteria (and their extracellular products), protozoa, algae, barnacles, and other fouling animals on surfaces. Biofouling usually results in corrosion, clogging, contamination, or a decrease in the efficiency of moving parts. Biofouling is a major concern in bioinvasion as well.

biocorrosion Also called microbiologically influenced corrosion or microbially induced corrosion, corrosion caused or promoted by bacteria and other microorganisms, due mainly to their activities on the surfaces and/or in biofilms of the corroding material.

ALWC (accelerated low water corrosion) A particularly aggressive form of localized biocorrosion that affects marine steel structures in seawater near the low water tide mark in virtually all the world's oceans and climates. ALWC usually results in very high rates of metal wastage, up to or even greater than 1 mm $year^{-1}$, whereas the steel corrosion rate in seawater without ALWC is 0.05 to 0.15 mm $year^{-1}$.

phycosphere The region surrounding a phytoplankton cell that represents a high-nutrient environment. This microhabitat usually harbors a unique microbiome and stimulates specific phytoplankton-bacterium interactions such as parasitism, communalism, or mutualism.

plastisphere A unique (micro)environment surrounding human-made plastic debris that is colonized by various microorganisms in the ocean. Plastic debris provides durable surfaces and vehicles for attachment, survival, and long-distance transportation of marine microorganisms (including human pathogens).

chromid An extrachromosomal genetic element that carries some core genes and has similar nucleotide composition (such as G+C content) and codon usage as chromosomes but instead harbors the plasmid-type maintenance and replication systems. Chromids are sometimes called "megaplasmids."

gene transfer agent A bacteriophage-like extrachromosomal genetic element produced by some bacteria that mediates horizontal gene transfer via genomic DNA transduction from the donor bacterium to a recipient bacterium.

sensoritome The complete set of the diverse microbial surface-sensing machinery and its regulated response products that are involved in a microorganism's sensing, signaling, and responsive reactions to extracellular environmental cues and population size signals.

metasensoritome The whole set of sensoritomes of all the participating microorganisms in a community or a specific environment that are involved in the sensing, signaling, and responsive reactions of the microbial assemblage to extracellular environmental cues and interorganism communications.

secretome The complete set of secretion systems and their secreted/translocated products, such as those involved in the surface colonization, biofilm formation, and development processes of a surface-associated microorganism.

metasecretome The whole set of secretomes of all the participating microorganisms in a community or a specific environment, such as those involved in the establishment, development, and maturation of a surface-associated microbiota.

surfome The complete set of microbial surface-exposed proteinaceous moieties that play important roles in signaling, adhesion, and transport of a microorganism.

metasurfome The whole set of surfomes of all the participating microorganisms in a community or a specific environment, such as those involved in the signaling, adhesion, and transport processes of a surface-associated microbiota.

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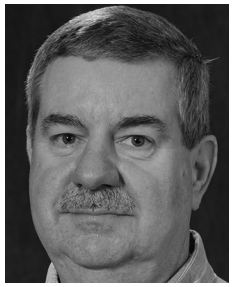

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