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# Seaweed-associated microbes as a novel source of crop agrochemicals

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The climate crisis necessitates new and expanded agrochemical options to address the challenges in current agricultural production. The marine flora represents an attractive source of novel bioactive compounds with potential relevance to agriculture (including both crops and livestock applications), human health, and biomaterials. While significant research is currently underway focusing on discovering and characterising bioactives derived directly from algal biomass, an often-overlooked aspect of seaweeds – or marine macro-organisms in general – is their close association with a diverse array of microorganisms, forming what is now referred to as holobiont systems. As such, the marine flora hosts a variety of microbes, including epiphytic and endophytic bacteria and fungi. This reservoir of microbial biodiversity itself offers a promising, yet largely untapped, source of novel bioactives with potential applications in the agriculture and healthcare industries. This mini-review aims to discuss the recent findings in the bioactivities of the Seaweed-Associated Microbiome (SAM) and specifically explore the potential applications of seaweed microbiome-derived bioactives as a novel source of agrochemicals relevant to crop growth, health, and pest management.

## KEYWORDS

seaweed associated microbiome, plant growth promoting (PGP) activities, phytohormones, defence elicitors, antimicrobials

## 1 Introduction

Climate change forecast predicts an increase in overall temperatures and longer wet spells, intensifying (a)biotic pressure on crops as warmer and wetter days stimulate pathogen growth, particularly fungi & moulds (Chaloner et al., 2021). This may in turn necessitate more pesticides application to maintain yields, with known negative impacts on the ecosystem and human health (Sharma et al., 2019). Consequently, the discovery of novel natural compounds that enhance crop yields or resilience to biotic and abiotic pressures is crucial for “climate-proofing” agricultural systems.

Significant research efforts are directed towards identifying alternative microbial sources for sustainable crop protection and biostimulation. Terrestrial microbial sources,

such as *Bacillus* (Fira et al., 2018; Radhakrishnan et al., 2017) and *Pseudomonas* species (Mehmood et al., 2023; Raio and Puopolo, 2021), are well-established for their biopesticidal and plant growth-promoting properties, while certain marine-derived fungi and bacteria have also shown promise in controlling plant diseases via their secondary metabolites (Nguyen et al., 2022; Qi et al., 2023) and enhancing growth in various agricultural settings, including as biofertilisers (Joshi et al., 2020; Rathod et al., 2023). Among these diverse microbial reservoirs, the marine environment offers a unique and largely underexplored biodiversity that could be leveraged for these critical needs. Specifically, the SAM may produce a plethora of compounds relevant to crop production and health, such as SAM-derived growth regulators, AHLs, defence elicitors or antimicrobials against crop pathogens (Figure 1).

The role and diversity of the seaweed microbiome has garnered significant attention in recent years. Those include non-specific associations, where the seaweed biomass serves as substrate to colonising microbes (Saha and Weinberger, 2019), to symbiotic relationships where seaweed growth and development is directly dependent of the presence of their symbiotic bacteria (Spoerner et al., 2012). Other examples of associations include the protection against pathogens conferred by colonising bacteria – chemically recruited by the seaweed host (Saha and Weinberger, 2019) –, to increased environmental resilience (Ghaderiardakani et al., 2020). Another example showed that *Ulva*'s microbiome quickly undergoes taxonomic modifications when introduced in a

different environment (van der Loos et al., 2024), and similar restructuring occurs between *U. rigida* grown in an integrated multi-trophic aquaculture site and the surrounding lagoon area (Califano et al., 2020).

Metabarcoding studies regularly find hundreds of bacterial genera from seaweed samples, with variations in composition based on the hosts, abiotic parameters, and geography (Burgunter-Delamare et al., 2023; Burke et al., 2011; Deutsch et al., 2023; Paix et al., 2021; Ramírez-Puebla et al., 2022; van der Loos et al., 2023; Wood et al., 2022). Of particular note is the presence of “functional guilds” within seaweed-associated microbes that specialise in the degradation of seaweed-specific polysaccharides (Khan et al., 2024). The use of metagenome-assembled genomes (MAG) from seaweed holobionts (Weigel Brooke et al., 2022) is likely to yield novel enzymes and pathways that can have biotechnological implications, such as in the degradation of halogenated compounds (Lavecchia et al., 2024), nutrient cycling (Weigel Brooke et al., 2022), or the production of plant growth regulators (Wang et al., 2022). Significant efforts are currently underway to better characterise and understand the role, diversity and dynamics of the seaweed microbiome, a topic extensively reviewed by Saha et al. (2024). A deeper understanding of the seaweed holobiont is expected to lead to higher yields or the creation of tailored biomass through optimising the three-way interaction between seaweed genotype, its environment and microbiome (Li et al., 2023; Simon et al., 2022), or through improved microbiome design (Wichard, 2023).

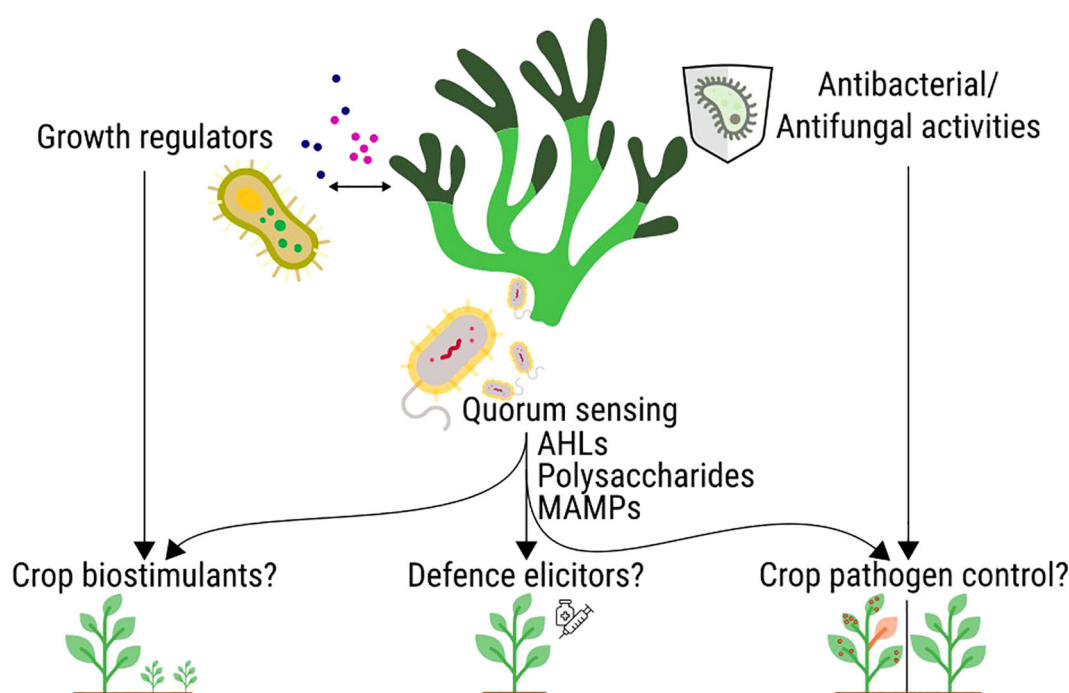


FIGURE 1

Potential for seaweed-associated microbes to produce bioactive compounds for crop health and as crop biostimulants. Left: Growth regulators produced by the SAM could be used to stimulate crop growth and development. Middle: Quorum sensing molecules, such as AHLs, can display biostimulants, defence elicitor and antimicrobial activities. Right: antimicrobial and antifungal compounds have been described as originating from the SAM, which may be used as novel pesticides for crop pathogen control.

The reported role(s) of the SAM are likely due, in part, to the microbial community's production of bioactive compounds. For example, a number of microorganisms such as *Maribacter* sp. MS6 (Alsufyani et al., 2020), *Bacillus pumilus* (Singh et al., 2011a) or *Azotobacter* species (Head and Carpenter, 1975) have been identified as Seaweed Beneficial Microorganisms (SBMs) producing algal growth and morphogenesis-promoting factors (AGMPF), including phytohormones (e.g. auxins-like, cytokinins-like), vitamin B<sub>12</sub>, and providing nutrient fixation (Li et al., 2023). Other beneficial effects of SAMs in disease protection have been uncovered. For example, *Phaeobacter* sp. BS52 and *Pseudoalteromonas* sp. PB2-1 can reduce the impact of the macroalgal pathogen *Pseudoalteromonas arctica* G-MAN6, responsible for bleaching disease in *Agarophyton vermiculophyllum* and *Delisea pulchra* (Li et al., 2022). Similarly, the production of pyrenocines by *Phaeosphaeria* sp. AN596H can inhibit the infection of *Ectocarpus siliculosus* by several protistan pathogens (Vallet et al., 2018). Finally, the role of SAM in protecting their host against disease may also be modulated by a stimulation of its immune response (Li et al., 2023), although a direct elicitation of algal immune responses by the SAM has yet to be reported.

This mini-review will shift focus from seaweed holobiont systems to explore the potential uses of SAM-derived bioactives in agriculture, specifically as a reservoir of crop biostimulants.

## 2 Potential for SAM-derived microbes and their bioactives in crop agriculture

### 2.1 Plant growth promoting regulatory compounds

Among SAM bioactives are phytohormones. For example, *Ulva*'s microbiome produces cytokinins-like and auxins-like phytohormones, originating from *Roseovarius* sp. MS2, and *Maribacter* sp. MS6, respectively (Ghaderiadekani et al., 2017). Those hormones have been shown to induce morphogenesis in *Ulva* species via promoting cell division and cell differentiation (Wichard, 2023). Other strains and species that phenocopy *Roseovarius* and *Maribacter* role have been isolated (i.e. *Sulfitobacter* sp. BPC-C4, and *Maribacter* sp. BPC-D8) demonstrating the diversity of algae growth-promoting bacteria present within the seaweed holobiont (Ghaderiadekani et al., 2024). In another example, thallusin, a steroid-like compound produced by *Maribacter* associated with both *Monostroma oxyspermum* (Matsuo et al., 2005) and *Ulva* spp (Alsufyani et al., 2020), exert numerous bioactivities, ranging from growth stimulation to morphogenesis and cell wall formation (Alsufyani et al., 2020; Dhiman et al., 2022; Yamamoto et al., 2018). Those bioactivities are structure-dependent as (–)-thallusin and its synthetic derivatives display differential activities in *Ulva* (Dhiman et al., 2022). Phytohormone production is not limited to *Ulva*'s microbiome (De Clerck et al., 2018) and has been demonstrated in other phyla including in brown (e.g. *Ectocarpus*) (Burgunter-Delamare et al., 2020), and red algae [e.g. *Porphyridium*

*purpureum* and *Pyropia yezoensis* (Kim et al., 2024; Matsuda et al., 2018; Mori et al., 2017)]. Therefore, phytohormone/AGMPF production is likely a common feature of SAM. Outside of the SAM, marine bacteria associated with phytoplankton have also been shown to contain biosynthetic genes for plant growth-promoting phytohormones and conversely produce 6 out of the 7 plant growth hormones tested (Khalil et al., 2024), highlighting their potential as a reservoir of plant growth regulators.

The type and structural diversity of plant growth regulators originating from SAM could be leveraged for the biodiscovery of novel crop growth-promoting compounds. Indeed, auxins, cytokinins and steroid compounds are major plant phytohormones controlling a wide range of cellular and developmental processes. For this, plant trials could indicate 1) if those marine-derived growth regulators can be recognised by plant receptors, and 2) whether SAM-derived growth regulators are indeed effective in modulating crop growth, development, and response to environmental stresses. Screening for an impact of SAM-derived growth regulators on plants could be relatively straightforward, using high-throughput phenotyping platforms that measure biomass growth over time (Fort et al., 2019, 2016), following the application of SAM-derived extracts. However, the characterisation of the growth regulators within, and their mode of action *in planta* will require more extensive research.

Another mechanism by which plant growth & resilience could be modulated by marine bacteria is through the use of plant growth promoting rhizobacteria (PGPR) isolated from the marine environment, as demonstrated by several studies showing improved crop growth and stress responses (notably salt-stress) following inoculation; via a combination of growth-promoting effects or the production of osmoprotectants (Aizaz et al., 2023; Carreiras et al., 2023). These studies underscore the broader potential of marine microbes to act as biofertilizers (Singh et al., 2023).

### 2.2 Plant defence elicitors

Beyond plant growth regulators are molecules produced by the SAM - such as N-Acyl homoserine lactones (AHLs) - that also hold promise as crop biostimulants and defense elicitors. AHLs represent a class of signalling molecules involved in quorum sensing and biofilm formation in bacteria. AHLs produced by the SAM are involved in seaweed-microbiome interactions. For example, *Pseudoalteromonas galathea* isolated from *Porphyra haitanensis*, was found to produce four types of AHL molecules that stimulate biofilm formation on the seaweed surface (Aslam et al., 2023). In another example, *Vibrio anguillarum*'s production of three AHLs was reported, with the AHL 3-oxo-C10-HSL involved in the attraction of *Ulva* zoospores (Joint et al., 2007; Tait et al., 2005). *Shewanella algae* produces five types of AHLs, with its C<sub>4</sub> and C<sub>6</sub> AHLs able to induce carpospore liberation in *Gracilaria dura* (Singh et al., 2015a). Those studies highlight the wide composition and roles of AHLs produced by the SAM.

AHLs can act as strong plant defence elicitors (i.e. priming the plant pathogen defence pathways) (Schenk et al., 2014; Schikora et al., 2016). For example, AHLs can induce resistance against plant

pathogens (i.e. *Aternaria alternata*) when applied to tomatoes (Schuhegger et al., 2006), brassicas (Duan et al., 2023; Shrestha et al., 2020) and barley (Han et al., 2016). AHLs work in plants via priming the induced systemic resistance (ISR) pathway – typically modulated by the plant rhizosphere, and leading to the production of reactive oxygen species, phenolic compounds, callose and lignin accumulation as well as stomatal closure (Zhu et al., 2022). All of which lead to a faster and stronger response when the plant is exposed to pathogens.

In addition to their role in plant pathogen defence, AHLs can also act as crop biostimulants by stimulating root and biomass growth (Nawaz et al., 2020; Moshynets et al., 2019; Ortiz et al., 2024; Shrestha et al., 2020), particularly when applied on plants under salt stress (Zhao et al., 2020). The action of AHLs on plants depend on their structure and given the variety of AHLs produced by the seaweed associated microbiome, an investigation of their potential impact on crop defence and/or growth is warranted.

Outside of AHLs, other potential plant defence elicitors could be produced by the SAM or its enzymatic activity on seaweed polysaccharides, such as specific polysaccharides and Microbe Associated Molecular Patterns (MAMPs). These include oligosaccharides, chitin fragments, lipopolysaccharides (LPS), and peptidoglycan derivatives, all of which are classes of molecules that have been shown to activate immune responses in plants (Erbs et al., 2010). Alginate oligosaccharides, for example, can induce defence-related gene expression and improve resistance to pathogens when applied exogenously (Peng et al., 2025). LPS from gram negative bacteria are recognised by plant receptors and can trigger an immune responses or act as elicitors (Meena et al., 2022). Some marine bacteria, including SAM-derived ones such as *Staphylococcus equorum* and *Bacillus tropicus*, isolated from *Gracilaria* sp., possess chitinase activity (Ginting et al., 2024) and are able to produce chitin fragments that are well established elicitors that interact with plant lysin motif receptors to activate signalling cascades that bolster plant defence (Saber Risch et al., 2024). Marine bacteria, including member of the SAM such as *Pseudoalteromonas* spp., are known to produce diverse extracellular polysaccharides (EPS) (Daly et al., 2023; Meunier et al., 2024; Xu et al., 2021), some of which may mimic these immune triggering molecules or interfere with host signalling.

Altogether, SAM's diversity may represent a reservoir of molecules with plant defence elicitor activities, offering a promising, largely unexplored means of natural crop protection and immune modulation. Using reporter gene systems, such as plants carrying a reporter gene (e.g. GFP), under the control of a promoter activated by plant defences pathways such as *PATHOGENESIS RELATED 1* (PR1) or *NONEXPRESSOR OF PR GENES 1* (NPR1) (Halder and Kombrink, 2015), could allow for rapid screening of SAM extracts for plant elicitor bioactivities.

## 2.3 Antimicrobial compounds against crop pathogens

Finally, while SAM bioactives could be recognised and act on crops, they could also impact crop pathogens themselves. Most

research in this area focuses on antimicrobial bioactivities against human-relevant pathogens (Asharaf et al., 2022; Girão et al., 2019; Karthick and Mohanraju, 2018; Manam et al., 2025; Martinez-Delgado and Benitez-Campo, 2025; Vega-Portalatino et al., 2024; Tangestani et al., 2021; Manam et al., 2025). In the case of Manam et al. (2025), the bioactive originates from *Bacillus subtilis*, an endophyte isolated from *Gracilaria edulis*. The compound was identified via GC-MS and FT-IR as Pyrrolo[1,2- $\alpha$ ] pyrazine-1,4-dione, hexahydro-3-(2-methylpropyl) (PPDHMP), and possess beta-lactamase and cell wall inhibitory activities. Through the use of bioactivity-guided isolation - a systematic approach to purify bioactive compounds from complex mixtures by iteratively separating the mixture into fractions and testing each fraction for bioactivity; followed by mass spectrometry and NMR, decylprodigiosin, a compound with anticancer and antibacterial activity was identified (Girão et al., 2024). The compound was produced by *Streptomyces violaceoruber*, a bacteria associated with the green seaweed *Codium tomentosum*. Bioactivities from SAM-derived microbes have also been reported against aquaculture pathogens. A study by Deutsch et al. (2021), found 23 endophytes originating from twenty seaweed species with antimicrobial activities against four aquaculture pathogens. In this example however, the bioactives responsible are not known.

Regarding crop pathogens, compounds like haliangicin, produced by marine bacteria associated with seaweeds [*Haliangium luteum* (Fudou et al., 2001)] have been found to have strong antibacterial and antifungal effects, which could be useful in protecting plants from harmful pathogens, such as the oomycete *Phytophthora capsica* (Sun et al., 2016). In addition, the recently identified antibiotic compound kocumarin (4-[(Z)-2-phenylethyl] benzoic acid), produced by the actinobacterium *Kocuria marina* CMG S2, isolated from the brown seaweed *Pelvetia canaliculata*, exhibited significant antimicrobial activities against both fungi and pathogenic bacteria, including crop pathogens such as *Aspergillus* (Uzair et al., 2018). Other examples of antimicrobials characterised from SAM-derived bacteria include furan derivatives (Karthick and Mohanraju, 2018), bacteriocins (Luz Prieto et al., 2012), alkaloids (Cui et al., 2009; Ravisankar et al., 2013), polyketides (Chakraborty et al., 2018) and massetolides (Desriac et al., 2013). Notably, massetolide A displays antifungal activities against the major crop pathogen *Phytophthora infestans* (Tran et al., 2007). Marine fungi isolated from seaweed have also been shown to produce interesting compounds like griseofulvin (Petit et al., 2004), known for its antifungal properties, and utilised in crop protection (Aris et al., 2022). Finally, a recent report has shown that *Sargassum*'s endophyte *Bacillus halotolerans* is producing antifungal compounds effective against the fungi responsible for chili fruit rot, *Fusarium incarnatum* (Suji et al., 2024). The above-mentioned studies are of particular importance as they highlight the potential for SAM-derived extracts to contain new crop-relevant compounds with a direct connection between SAM compounds and crop protection. The extensive biodiversity present within the SAM is therefore likely to contain numerous compounds that have not yet been tested specifically against plant pathogens.



### 3 Challenges in isolation of seaweed-associated microbes

Leveraging the SAM diversity to discover novel compounds with applications in crops first require the isolation of the bacteria and fungi associated with seaweeds. This presents several challenges, including the need for a wide variety of specialised culture media to encompass the SAM metabolic diversity; to separate microbes from different niches (e.g., epiphytes and endophytes), replicating natural growth conditions in the laboratory (Kaur et al., 2023); and account for the “One Strain Many Compounds” (OSMAC) phenomenon, where a single strain can produce different compounds depending on growth conditions (Romano et al., 2018), or when bioactivities -including that of SAM bacteria such as *Roseovarius aestuarii* or *Rathayibacter festucae*-change under environmental stress (Hmani et al., 2024).

A fundamental approach involves general isolation and culturing on agar plates. Epiphytes are typically isolated from swabs or streaks of seaweed thalli, while endophytes require surface sterilisation (Abdelrazek et al., 2024; Deutsch et al., 2021). This plating technique is widely used to cultivate a broad range of bacteria and fungi, as demonstrated in studies characterizing bacterial communities associated with green, and brown and red seaweeds often using nutrient-rich media like Zobell Marine Agar or potato dextrose agar to screen for antibacterial activity (Karthick and Mohanraju, 2018), and for fungi focusing on seaweed-associated endophytes (Abeygunawardane et al., 2025; Fan et al., 2020).

Specialised media are required for specific groups like fungi or bacteria with metabolic capabilities difficult to replicate on *ex situ* cultivation. Using host homogenate as nutrient/carbon source during isolation (e.g adding sterile host biomass to culture media), could significantly improve the diversity of isolated microbial species. While this method was used in plant

microbiome research (Armanhi et al., 2018; Sarhan et al., 2019), to our knowledge this has not been employed on seaweed samples and could yield many novel isolates.

### 4 Conclusion & perspectives

Seaweed-associated microbiomes have been identified as promising sources of bioactive compounds with antimicrobial properties, offering new opportunities for sustainable crop protection strategies (Singh et al., 2015b). Of note, whether some SAM-derived bioactives could act on insects, weeds or nematodes has not been investigated to date. Other potential, more speculative since they have not been tested yet to the authors knowledge, include using SAM extracts as crop biostimulants and defence elicitors. Systematic testing of those SAM-derived compounds on crops/crop pathogens could yield significant impacts on plants given that these compounds might interact differently with land plant receptors or pathways; or offer novel modes of action due to their structural diversity. These represent important avenues for future research. Several SAM-derived compounds that have been characterised to date could already be potential targets for these uses, including the plant growth regulators and AHLs described above, and summarised in Table 1.

However, while potential is significant, practical application of SAM-derived bioactives in agriculture will likely face hurdles. Focused and systematic research is needed to bridge this gap, particularly in i) isolating and characterising individual potential compounds, ii) understanding their mode of action in crops/soils; and iii) assess their effectiveness and environmental impact(s) compared to existing phytochemicals. These, particularly the characterisation of the compounds (e.g via bioactivity-guided fractionation), the use of specialised instrumentation, and cost in both time and expertise needed, represent major challenges. The

TABLE 1 Type of molecules, origins and roles of SAM-derived classes of bioactives with a potential on crops.

Bioactive functions	Type of molecule	Examples of SAM origin(s)	Seaweed host	Role
Crop growth promoting compounds	Auxin-like	<i>Maribacter</i> sp. MS6 (Spoerner et al., 2012), <i>Neptunomonas</i> spp (Matsuda et al., 2018)	<i>Ulva</i> spp., <i>Pyropia yezoensis</i>	Proposed impact on crop growth and development
	Cytokinin-like	<i>Roseovarius</i> sp. MS2 (Spoerner et al., 2012); <i>Halomonas</i> sp. MS1 (Morales-Reyes et al., 2022)	<i>Ulva</i> spp.	Proposed impact on crop growth and development
	Thallusin	<i>Maribacter</i> sp. BPC-D8 & <i>Sulfitobacter</i> sp. BPC-C4 (Ghaderiardakani et al., 2024); <i>Maribacter</i> sp. MS6 (Spoerner et al., 2012)	<i>Ulva</i> spp.	Proposed impact on crop growth and development
	N-Acyl Homoserine Lactones (AHLs)	<i>Pseudoalteromonas galathea</i> (Aslam et al., 2023); <i>Vibrio anguillarum</i> (Joint et al., 2007); <i>Shewanella</i> algae (Singh et al., 2015a)	<i>Porphyra haitanensis</i> ; <i>Ulva</i> spp.; <i>Gracilaria dura</i>	Proposed as crop biostimulants

(Continued)

TABLE 1 Continued

Bioactive functions	Type of molecule	Examples of SAM origin(s)	Seaweed host	Role
	Osmoprotectants promotion	Marine microbes consorsium (Carreiras et al., 2023), possible SAM-derived	n/a	Proposed as stimulating plant stress tolerance (Carreiras et al., 2023)
	Plant Growth Promoting Rhizobacteria (PGPR)	Marine microbes ( <i>Bacillus subtilis</i> , <i>Nitratireductor aquimarinus</i> , <i>Halopseudomonas pachastrellae</i> (Aizaz et al., 2023)), possible SAM-derived	n/a	Proposed as biofertilizers (Aizaz et al., 2023; Carreiras et al., 2023)
Antimicrobials	PPDHMP	<i>Bacillus subtilis</i> (Manam et al., 2025)	<i>Gracilaria edulis</i>	Antimicrobial. Role against crop pathogens to be determined
	Decylprodigiosin	<i>Streptomyces violaceoruber</i> (Girão et al., 2024)	<i>Codium tomentosum</i>	Antimicrobial. Role against crop pathogens to be determined
	Haliangicin	<i>Haliangium luteum</i> (Fudou et al., 2001)	n.d	Antimicrobial. Role against <i>Phytophthora capsica</i> (Sun et al., 2016)
	Kocumarin	<i>Kocuria marina</i> (Uzair et al., 2018)	<i>Pelvetia canaliculata</i>	Antimicrobial, role against <i>Aspergillus</i> spp (Uzair et al., 2018)
	Furan derivatives	<i>Pseudomonas stutzeri</i> , <i>Alcanivorax dieselolei</i> , <i>Exiguobacterium profundum</i> , <i>Vibrio</i> sp (Karthick and Mohanraju, 2018)	<i>Gracilaria corticata</i> ; <i>Ulva lactuca</i> ; <i>Turbinaria ornata</i> ; <i>Mastophora rosea</i>	Antimicrobials, including crop pathogens
	Bacteriocins	<i>Bacillus</i> spp (Luz Prieto et al., 2012)	<i>Ulva</i> spp.	Antibacterials, including crop pathogens
	Alkaloids	<i>Pseudomonas</i> sp (Ravisankar et al., 2013); <i>Aspergillus ochraceus</i> (Cui et al., 2009)	<i>Padina tetrastromatica</i> ; <i>Sargassum kjellmanianum</i>	Antimicrobials, including crop pathogens
	Polyketides	<i>Bacillus amyloliquefaciens</i> (Chakraborty et al., 2018)	<i>Kappaphycus alvarezii</i>	Antimicrobials, griseofulvin effective against crop fungal pathogens (Aris et al., 2022)
	Massetolides	<i>Pseudomonas</i> sp. (Gerard et al., 1997)	n.d	Antifungal, massetolide A effective against <i>Phytophthora infestans</i> (Tran et al., 2007)
	Other Antifungal compounds (unspecified chemical nature)	<i>Bacillus halotolerans</i> (Suji et al., 2024)	<i>Sargassum wightii</i>	Antifungal ( <i>Fusarium incarnatum</i> , Suji et al., 2024). Other <i>B. halotolerans</i> strains induced resistance against <i>Botrytis cinerea</i> (Tsalgatidou et al., 2023)
Plant defence elicitors	N-Acyl Homoserine Lactones (AHLs)	<i>Pseudoalteromonas galathea</i> (Aslam et al., 2023); <i>Vibrio anguillarum</i> (Joint et al., 2007); <i>Shewanella algae</i> (Singh et al., 2015a)	<i>Gracilaria corticata</i> ; <i>Ulva lactuca</i> ; <i>Turbinaria ornata</i> ; <i>Mastophora rosea</i>	Priming of plant defence system, polyphenols & ROS production (Zhu et al., 2022)

(Continued)

TABLE 1 Continued

Bioactive functions	Type of molecule	Examples of SAM origin(s)	Seaweed host	Role
	Alginate derived oligosaccharides	General class of molecules (from seaweed, processed by SAM)	n/a	Priming of plant defence system & polyphenols production (Peng et al., 2025)
	Chitin fragments	<i>Staphylococcus equorum</i> and <i>Bacillus tropicus</i> (Ginting et al., 2024)	<i>Gracilaria</i> sp.	Priming of plant defence system & phytoalexin production (Saberri Riseh et al., 2024)
	Lipopolysaccharides (LPS)	General class of molecules (gram-negative bacteria)	n/a	Priming of plant defence system & hypersensitive response (Erbs et al., 2010)
	Peptidoglycan derivatives	General class of molecules	n/a	Priming of plant defence system, chitinase activity & polyphenols production (Erbs and Newman, 2012)
	Extracellular Polysaccharides (EPS)	<i>Bacillus licheniformis</i> (Singh et al., 2011b) <i>Pseudoalteromonas</i> spp (Xu et al., 2021)	<i>Gracilaria. dura</i> ; <i>Fucus evanescens</i>	Priming of plant defence system, hypersensitive response & ROS production (Drira et al., 2021)

n/a, Not applicable; nd, Not determined.

industrial production and purification of those compounds similarly require extensive research, as large batch cultivation of the target marine microorganism could be difficult. An attractive option could be to first decipher the metabolic pathways leading to bioactive accumulation in the desirable microbe itself via genomics and metabolomics (Castro-Falcón et al., 2025; Molina et al., 2025; Tsalgatiidou et al., 2022), and then transfer the genes responsible via synthetic biology to microbial factories for heterologous production (Chaudhary et al., 2024). Finally, matrix/synergistic effects between compounds within the SAM should also be considered, and creating rhizosphere SAM-derived communities will require extensive testing.

In conclusion, while the exploration of seaweed-associated microbiomes as sources of crop protective bioactives & biostimulants is still in its early stages, the diversity of SAM-derived metabolites offers a compelling case for further investigation.

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