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THE ROLE OF QUORUM SENSING AND INFOCHEMICALS IN THE INTERACTION BETWEEN PRO- AND MICROEUKARYOTES IN AQUATIC ECOSYSTEMS

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This review presents key insights into the molecular interactions of unicellular organisms. Bacteria are characterized by quorum sensing (QS): an ability to modulate gene expression by microorganisms depending on cell population density. This can, in particular, lead to changes in behavior and the activation of virulence factors. Phytoplankton possesses an analogous system: cells produce infochemicals that can either increase the resistance of recipients to stress factors or trigger programmed cell death in them. While bacterial quorum sensing molecules (QSMs) can activate/inhibit phytoplankton cell growth, the infochemicals produced by the latter can affect the composition of the microbial community and suppress consumer development. Moreover, phytoplankton cells can affect bacterial QS by disrupting the activity of signaling molecules or by imitating them.

Keywords: quorum sensing, autoinducers, phytoplankton, bacteria, infochemicals

In multicellular organisms, cells establish close physical and chemical contacts. These interactions determine their differentiation, metabolism, and function [Brodskii, 2009]. Intercellular interactions are also important for the vital activities of unicellular organisms. This was first demonstrated in studies of autoluminescence in *Vibrio fischeri* [Kempner, Hanson, 1968]. Research showed that luminescence in these bacteria is activated in response to the appearance of extracellular secreted molecules, the synthesis of which is induced at high cell density in the mid-logarithmic phase [Nealson et al., 1970]. It took more than a decade to confirm that this process is transcriptionally regulated. Thus, genes involved in luminescence were discovered (*lux* operon) [Engebrecht, Silverman, 1984]. It was established that *luxCDABEG* genes are required for visible light emission, while *luxI* and *luxR* genes are involved in regulating the operon, controlling activation/inhibition of luminescence genes. The extracellular secreted molecule that activates luminescence at high cell density was identified as *N*-3-oxohexanoyl-L-homoserine lactone (3OC6-HSL) [Eberhard et al., 1981]. Its production requires *luxI* gene, which encodes autoinducer synthase. In turn, *luxR* recognizes 3OC6-HSL and, acting as a transcription factor, activates *lux* operon [Engebrecht, Silverman, 1984].

Gradually, similar gene systems began to be identified in other bacterial species, thereby expanding our understanding of their physiology. It became evident that bacteria produce signaling molecules that are recognized by cell–surface receptors. These molecules enter the cell and affect the transcription

of specific genes: a phenomenon termed quorum sensing (hereinafter QS) [Fuqua et al., 1994]. Studies of intercellular interactions have demonstrated that communication among phytoplankton cells is mediated by infochemicals [Pohnert et al., 2007]. Given that algae and bacteria coexist closely in aquatic environments and have coevolved, a system of interactions has developed between them.

Currently, bacterial QS is a field of active research, as it offers novel strategies for combating pathogenic bacteria. Still, studies on intercellular interactions in phytoplankton remain comparatively scarce. However, this field is important: it provides insight into the mechanisms regulating blooms of unicellular algae, which are an essential link in the trophic chains of water bodies and biogeochemical cycles, affect climate change, and also contribute to half of the Earth's oxygen production [Field et al., 1998]. Bacteria coexisting with phytoplankton in aquatic environments can regulate its abundance: enhance stress tolerance and promote cell division. On the other hand, such bacteria can induce algal death, and this is crucial to consider when developing strategies to mitigate toxic algal blooms, which pose a danger to animals and humans. Given the fragmented and limited nature of conducted studies, the aim of this review was to synthesize key concepts regarding bacterial QS, phytoplankton infochemicals, and the mechanisms of cross-domain interactions mediated by these systems, as well as to identify current knowledge gaps and research perspectives.

Bacterial quorum sensing system. QS enables the differential regulation of gene expression depending on bacterial population density, leading to biofilm formation, biosynthesis of essential enzymes and antibiotics, and shifts in motility and attachment. QS-controlled biofilm formation regulates bacterial virulence by hindering antibiotic access to cells [Preda, Săndulescu, 2019]. Consequently, identifying molecules that inhibit QS is a pressing issue.

QS molecules are referred to as autoinducers (AIs). Those are divided into five main groups (Fig. 1).

1. **AI-1.** Acyl homoserine lactones (AHLs) characteristic of gram-negative bacteria [Papenfort, Bassler, 2016]. AHL molecule consists of a lactone ring and an acyl side chain. Variations in the number of carbon atoms in the acyl chain (from C₄ to C₁₈) and in the substituent groups (oxo and hydroxy) determine the vast diversity and specificity of AHLs. Their molecules are transported into cells and recognized by LuxR-type and CepR-type receptor proteins [Papenfort, Bassler, 2016; Slinger et al., 2019]. AHLs are produced by many genera of gram-negative bacteria; accordingly, various AHL synthases exist, encoded by *luxI* [Engbrecht, Silverman, 1984], *ainS* [Gilson et al., 1995], *hdtS* [Laue et al., 2000], and *CepI* [Slinger et al., 2019] genes.
2. **PQS.** *Pseudomonas* quinolone signal (PQS), 2-heptyl-3-hydroxy-4(1H)-quinolone, characteristic of gram-negative pseudomonads. Proteins involved in its synthesis constitute *PqsABCDEH* gene cluster [Lin et al., 2018]. Upon entering the cell, PQS binds to the transcription factor PqsR, resulting in the activation of virulence genes, particularly those required for biofilm formation [Lin et al., 2018].
3. **DSF.** Diffusible signal factors (DSFs), a family of cis-2-unsaturated fatty acids characteristic of gram-negative bacteria [He et al., 2023]. The mechanism of their action is governed by *rpf* (regulation of pathogenicity factor) gene cluster. In DSF synthesis, *rpfF* and *rpfB* proteins are involved. DSF is detected by *rpfC*, which subsequently activates *rpfG* [Feng et al., 2023]. DSF signals have emerged as important regulators of virulence and biofilm formation in a wide range of bacterial pathogens [Deng et al., 2010]. DSFs have been shown to mediate not only intra- and interspecies communication but also cross-domain one, particularly with fungi, plants, and insects [He et al., 2023; Ryan et al., 2015]. However, no effect on phytoplankton has been demonstrated to date.

4. **AI-2.** QS signal characteristic of both gram-negative and gram-positive bacteria; a group of interconverting furanones derived from dihydroxy-2,3-pentanedione (DPD), which undergoes a series of spontaneous rearrangements. In DPD synthesis, luxS enzyme is involved, conserved in many bacteria [Surette et al., 1999]. Two types of DPD-derived AI-2 have been described: boron-containing S-2-methyl-2,3,3,4-tetrahydroxytetrahydrofuran-borate (S-THMF-borate) and nonborated R-2-methyl-2,3,3,4-tetrahydroxytetrahydrofuran (R-THMF). These compounds are specific to various bacteria, are recognized by different receptors, but are interconvertible, enabling to facilitate interspecies bacterial communication. S-THMF-borate is recognized by LuxP (*Vibrio* spp.), whereas R-THMF targets LsrB (*Escherichia coli*, *Salmonella typhimurium*, *Bacillus anthracis* str. *ames*, and *Sinorhizobium meliloti*), RbsB (*Aggregatibacter actinomycetemcomitans*), and dCACHE domain of PctA and TlpQ chemoreceptors (*Pseudomonas aeruginosa*) [Rodrigues et al., 2023].
5. **AIP.** Autoinducing peptides characteristic of gram-positive bacteria. The mechanism of their action is similar across various species: peptides are synthesized by certain AIP synthases and later undergo post-translational modification, and are secreted *via* ABC transporters with ATP-dependent release. On the surface of recipient cells, AIPs are recognized by histidine kinase; it becomes activated and triggers a signaling cascade, ultimately leading to changes in the expression of genes involved in production of virulence factors [Verbeke et al., 2017].

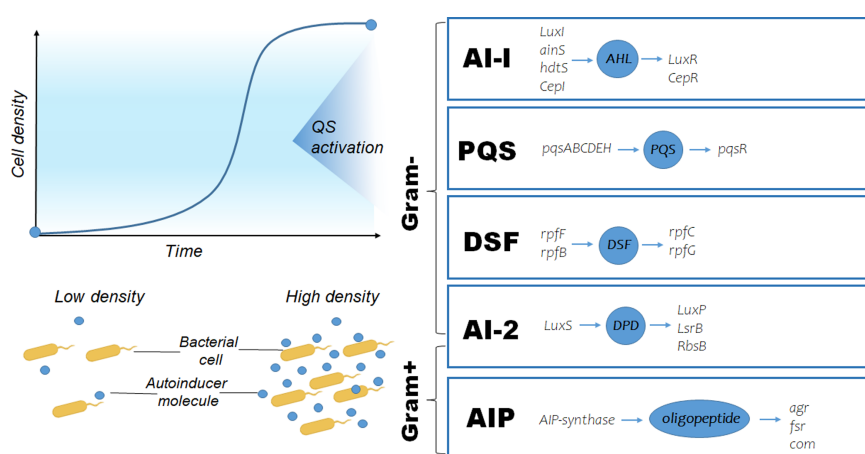


Fig. 1. Quorum sensing regulation. Schematic representation of quorum sensing activation (left) and the main types of autoinducers with key genes involved in their synthesis and perception by cells (right). The autoinducer molecule is represented by a blue circle. AI, autoinducer; AHL, acyl homoserine lactone; PQS, *Pseudomonas* quinolone signal; DSF, diffusible signal factors; DPD, dihydroxy-2,3-pentanedione; AIP, autoinducing peptide

The diversity of quorum sensing molecules enables not only intraspecies but also interspecies communication. AI-2 molecules mediate signal exchange between gram-positive and gram-negative bacteria. Moreover, gram-negative bacteria have been shown to regulate their metabolism using different AIs. Thus, epibionts of *Trichodesmium* use QS to enhance phosphate uptake *via* alkaline phosphatases (a process regulated by AI-1); AI-2 production governs a decrease in phosphate uptake [Van Mooy et al., 2012].

Infochemicals of phytoplankton. The best-studied signaling molecules of phytoplankton are oxylipins: short-chain polyunsaturated aldehydes (PUAs) and other degradation products of oxygenated fatty acids (Fig. 2). To date, PUAs under investigation include decadienal, decatrienal, octadienal, octatrienal, and heptadienal [Cutignano et al., 2006; Wichard et al., 2005]. In addition to diatoms,

haptophytes [Hansen et al., 2004] and chrysophytes [Rashash et al., 1995] are capable of producing these compounds. PUA production increases upon membrane disruption following grazing by consumers, as well as during the stationary growth phase, at high cell density. PUAs serve as a defense against grazers, regulate the bacterial community composition in the phycosphere of microalgae, and participate in their stress responses, either enhancing adaptation or leading to programmed cell death.

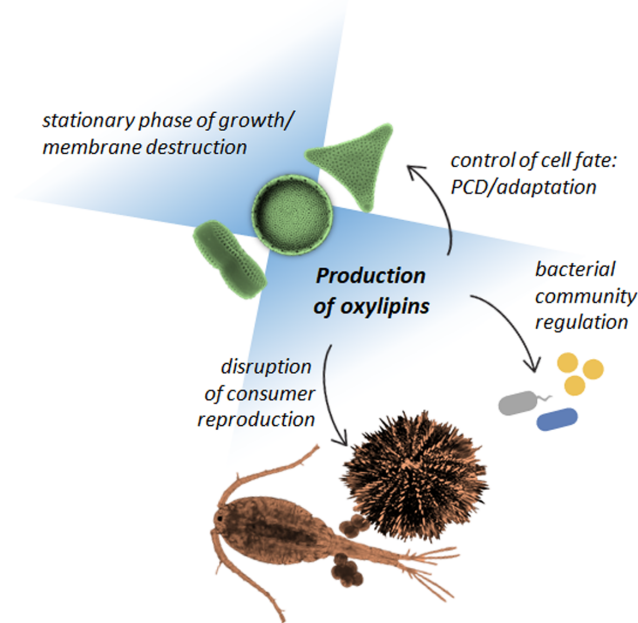


Fig. 2. Effects of oxylipins produced by diatoms on coexisting organisms in the environment

It was found as follows: when copepods feed on diatoms, cell and chloroplast membranes of the latter are damaged, and this results in the release of polyunsaturated fatty acids. Oxidation and enzymatic cleavage of these fatty acids (by phospholipases and glycolipases) mediates the formation of PUAs [Cutignano et al., 2006; Pohnert, 2002], which exert teratogenic effects on copepods [Caldwell et al., 2002; Ianora et al., 2004] and disrupt their embryonic development [Miralto et al., 1999]. Furthermore, PUAs were found to induce embryonic cleavage abnormalities in sea urchins, polychaetes, and ascidians [Lettieri et al., 2015; Ruocco et al., 2019].

Oxylipins were discovered as a defensive response of phytoplankton to grazing by consumers. However, during subsequent research, it was found that their environmental significance is much higher. Oxylipins not only function as intraspecific signals but also affect various phytoplankton taxa and thereby contribute to the structuring of aquatic communities.

It has been demonstrated that PUA production increases with culture age and under nutrient depletion [Ribalet et al., 2007; Vidoudez, Pohnert, 2008]. Mechanical disruption of the cell membrane (as occurs during copepod grazing) is not strictly required for PUA production: during the terminal stages of *Skeletonema marinoi* blooms, PUA production was positively correlated with abundance of cells and the rate of their lysis [Ribalet et al., 2014]. PUAs produced by diatoms have been shown to affect the division of other phytoplankton species: haptophytes, chrysophytes, and dinoflagellates [Pichierri et al., 2016; Ribalet et al., 2007]. Additionally, PUAs participate in regulating abundance and metabolic activity of phytoplankton-associated bacteria [Ribalet et al., 2008].

Under stress conditions, phytoplankton cells produce aldehyde (2E,4E/Z)-decadienal (DD) [Pohnert, 2002]. At high concentrations, DD induces intracellular signaling *via* nitric oxide (NO), culminating in programmed cell death [Vardi et al., 2006]. However, at low concentrations, DD initiates a cascade of reactions that confer resistance to stress, including elevated DD levels [Dolch et al., 2017; Vardi et al., 2006].

Bacteria–phytoplankton interactions. Research into the mechanisms of bacteria–phytoplankton interactions is of great practical importance: its results are useful for wastewater treatment and mitigation of algal blooms [Wu et al., 2022]. Furthermore, scientists continue the search for QS-inhibiting compounds for effective treatment of diseases caused by multidrug-resistant bacterial strains [Pacheco et al., 2021; Ćirić et al., 2019].

The primary site of interaction between microalgae and bacteria is the phycosphere (Fig. 3). This region, that surrounds a phytoplankton cell, contains higher concentrations of nutrients and secondary metabolites as compared to environment [Seymour et al., 2017].

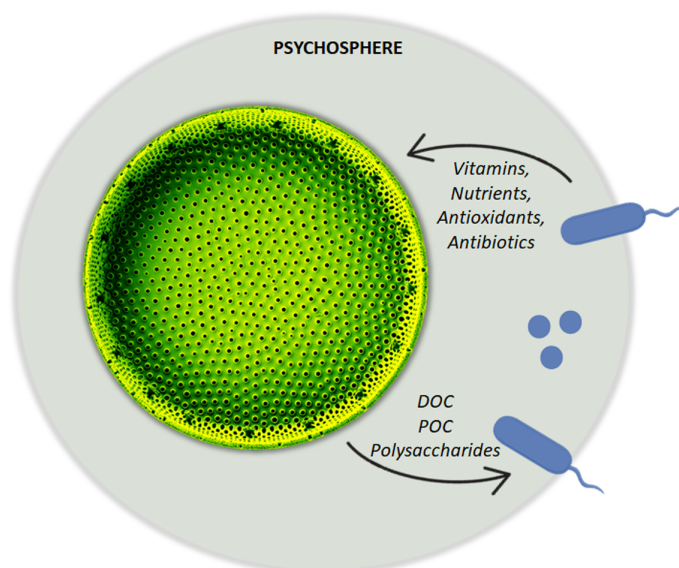


Fig. 3. Scheme of interaction of microalgae and bacteria in the phycosphere (DOC, dissolved organic carbon; POC, particulate organic carbon)

Interactions between bacteria and microalgal cells are remarkably diverse, ranging from mutualism to parasitism [Amin et al., 2012]. In this review, we consider the aspects of bacteria–phytoplankton interactions that are directly related to bacterial QS and phytoplankton-derived infochemicals.

Regulation of algicidal activity in bacteria. The hypothesis that bacteria–microalgae interactions are mediated by QS is supported by metagenomic data, which have revealed bacterial gene sequences involved in the synthesis of autoinducers within actively developing phytoplankton populations in aquatic environments [Huang et al., 2018]. Under such conditions, QS may be directed toward protecting bacteria from antibacterial compounds produced by rapidly dividing phytoplankton cells, as well as toward securing the supply of additional nutrients released from dead algal cells. Moreover, occurrence of compounds released during decomposition of phytoplankton can trigger QS induction in bacteria. For example, cells of *Phaeobacter gallaeciensis*, strain BS107, which coexist with *Emiliania huxleyi*, provide coccolithophores with the phytohormone auxin (a growth promoter) during their exponential growth

phase, while also protecting them from pathogens *via* antibiotic production. In turn, *E. huxleyi* produces dimethylsulfoniopropionate (DMSP), which bacteria utilize as a source of sulfur. During the stationary growth phase, when products of algal decomposition, such as *n*-coumaric acid, are accumulated in the environment, *P. gallaeciensis* metabolism shifts in response to the production of algicidal compounds (in this case, roseobactericides) [Seyedsayamdost et al., 2011]. A flavobacterium *Kordia algicida* also uses QS to control its algicidal activity. Thus, upon reaching high densities, its cells produce an algicidal protease that affects *Skeletonema*, *Thalassiosira*, and *Phaeodactylum* representatives [Paul, Pohnert, 2011]. However, the same study showed that the algicide produced did not affect *Chaetoceros didymus*. Further investigation revealed that *C. didymus* releases its own proteases, which, upon sensing *K. algicida* proteins, may serve as a chemical defense mechanism [Paul, Pohnert, 2013]. The mechanism of QS-mediated activation of algicidal substance production has been demonstrated in *Aeromonas* [Guo et al., 2016], *Ponticoccus* [Chi et al., 2017], and *Bacillus subtilis* [Zhang et al., 2020].

Effects of quorum sensing molecules on phytoplankton cells. Quorum sensing molecules themselves can be a source of stress for phytoplankton, as they lead to lipid accumulation and a slight reduction in biomass, as demonstrated in Chlorophyta [Zhang et al., 2018]. Cultivation of *Chlorella sorokiniana* with bacterial quorum sensing molecules, specifically AHLs, resulted in increased algal biomass, as well as a significant boost in lipid and protein content [Das et al., 2019]. Marine *Roseobacter* isolates have been found to produce AHLs, and some isolates can inhibit cell division of a diatom *Skeletonema costatum* [Ziesche et al., 2015]. Spontaneous rearrangement of AHLs can occur, with formation of tetramic acids (TAs) [Stock et al., 2019]. A high diversity of TAs has been reported. These compounds exhibit antibacterial, antifungal, and antiviral activities [Jiang et al., 2020], and also algicidal effects. Notably, the rearrangement product of oxo-C12-AHL (TA12) suppresses cell division and photosynthesis in *Phaeodactylum tricornutum* [Stock et al., 2019]. Also, the effect of TA14 (oxo-C14-HSL) has been shown on *Seminavis robusta* [Stock et al., 2020]. However, C14-HSL enhanced cell division of this species. Transcriptomic analysis revealed that the mechanism of action of C14-HSL and oxo-C14-HSL involves activation of gene expression related to intracellular signaling, and also alteration of the cell cycle-dependent gene expression in diatoms. Lipid metabolism was altered as well, leading the researchers to suggest that *S. robusta* may utilize AHLs (C14-HSL) as an external energy source [Stock et al., 2020].

Quinolones exert a strong toxic effect on phytoplankton. Pentylquinolone isolated from *Alteromonas* sp. KNS-16 was shown to suppress the growth of *Heterosigma akashiwo*: a bloom-forming toxic microalga [Cho, 2012]. A marine bacterium *Pseudoalteromonas piscicida* produces heptylquinolone, which is toxic to *E. huxleyi* at a low concentration (1 μ M) [Harvey et al., 2016]. The mechanism of its action differs slightly among phytoplankton species. When affecting *E. huxleyi*, heptylquinolone disrupted photosynthesis by inhibiting photosystem II and a cytochrome b6f [Harvey et al., 2016], and also suppressed cell cycle and DNA repair [Pollara et al., 2021]. In a green alga *Dunaliella tertiolecta*, photosynthesis was inhibited *via* inactivation of photosystem II, whereas in a diatom *P. tricornutum*, the compound hindered electron transport by blocking the cytochrome b6f complex [Dow et al., 2020]. A positive effect of heptylquinolone on *E. huxleyi* was also observed: the induction of resistance to viral infection [Pollara et al., 2021].

Effects of phytoplankton on bacterial quorum sensing. Certain phytoplankton species are capable of mimicking bacterial signals, thereby suppressing QS (Table 1). This mechanism is termed quorum quenching (QQ) [Sikdar, Elias, 2020].

Table 1. Quorum quenching system in phytoplankton

Producer	Compound	Effect on recipient	Reference
<i>Chlamydomonas reinhardtii</i>	Not identified	Activation of QS in <i>Sinorhizobium meliloti</i>	Teplitski et al., 2004
	Not identified, with a lactone ring	Effect on CepR QS receptors in <i>Aeromonas veronii</i> : reduction of biofilm formation	Rajamani et al., 2011
	Lumichrome	Activation of QS in <i>Pseudomonas aeruginosa</i>	Rajamani et al., 2008
<i>Asterionellopsis glacialis</i>	Rosmarinic acid	Inhibition of motility, and biofilm formation in <i>Roseobacter</i>	Fei et al., 2020
<i>Anabaena</i> sp.	Acylase	Degradation of AHL	Romero et al., 2008
<i>Nitzschia</i> cf. <i>pellucida</i>	Haloperoxidase	Degradation of AHL	Syrpas et al., 2014

Upon prolonged cultivation, cells of a green alga *Chlamydomonas reinhardtii* produce a number of compounds that mimic AHLs by stimulating QS receptors: LasR or CepR. Exposure of *S. meliloti* cells at low density to such a mimic (partially purified and of unidentified chemical nature) altered the bacterial proteome to an extent similar to that caused by genuine AHLs [Teplitski et al., 2004]. Treatment with lactonase (a metalloenzyme) abolished the effect of the *C. reinhardtii* mimic on *Aeromonas veronii* CepR receptors, suggesting that the QS-mimicking compound produced by this alga contains a lactone ring with an amide bond, the same as bacterial AHLs [Rajamani et al., 2011]. Another study showed that *C. reinhardtii* cells produce riboflavin, that subsequently forms lumichrome; the latter can stimulate LasR receptors in *P. aeruginosa* [Rajamani et al., 2008].

Bacteria of the *Roseobacter* group colonize the phycosphere and are symbionts of a diatom *Asterionellopsis glacialis*. The alga, in turn, can use mimics of quorum sensing molecules to trigger inhibition of bacterial motility and biofilm formation [Fei et al., 2020]. Rosmarinic acid produced by *A. glacialis* may facilitate colonization of the phycosphere by bacteria *via* impairing their motility [Fei et al., 2020].

Filamentous cyanobacteria, *Anabaena* sp., possess AHL-acylase activity and genes encoding acylases (homologous sequences of the acylase-encoding gene have also been found in *Nostoc punctiforme*, *Gloeobacter violaceus*, and *Synechocystis* sp.). Its production probably allows it to avoid interference from external signals in its own signaling system or makes it possible to affect other organisms [Romero et al., 2008].

A diatom *Nitzschia* cf. *pellucida* is capable of degrading AHLs *via* bromine-mediated halogenation of oxo-AHLs, leading to hydrolysis of both the acyl and lactone moieties [Syrpas et al., 2014]. It is hypothesized that this mechanism is available to many diatoms, but further investigation is required. Bioinformatic analysis revealed that the genome of a diatom *Fragilariopsis cylindrus* contains a candidate gene encoding a haloperoxidase, which may inhibit bacterial QS through halogenation of AHL acyl chains [Amin et al., 2012]. Thus, diatoms can degrade AHLs, thereby inhibiting not only algicidal effects but also QS-mediated changes in bacteria.

Effects of phytoplankton oxylipins on bacterial cells. As was shown, the composition of the bacterial community in the phycosphere is dependent on the growth stage of algal cells and may be associated with the release of secondary metabolites. Differential effects of oxylipins have been observed among

bacterial strains isolated during the active growth phase of *S. marinoi* population, with these compounds either stimulating or inhibiting cell division [Ribalet et al., 2008]. However, several studies have failed to detect a correlation between bacterial diversity and the production of PUAs [Eastabrook et al., 2020; Paul et al., 2012]. Apparently, oxylipins, while not the sole determinant, constitute an important factor in algae–bacteria interactions. A recent study has demonstrated that *Cyclotella cryptica* modulates its PUA profile depending on co-cultivated bacteria [Hernanz-Torrijos et al., 2023].

Research perspectives. Chemical interactions between unicellular organisms are mainly explored *in vitro*, that undoubtedly provides the foundation for investigating natural phenomena. This approach certainly allows the detection of various compounds responsible for cellular signaling and the elucidation of basic principles of cell interactions. Under laboratory conditions, we can model specific processes to study cellular responses, examine changes in gene expression induced by various infochemicals, isolate novel compounds from cells, and use genetic engineering approaches to investigate the effects of turning on and off genes involved in the synthesis of target compounds. However, it is impossible to model *in vitro* all environmental factors that affect an organism, and consequently, to capture all possible cellular responses. Numerous questions remain unsolved, including the following ones: how does microbiome of the algal phycosphere affect its response to environmental changes, and what concentrations of infochemicals are sufficient to transmit signals in the water column? To understand the role of bacteria in the mechanisms of phytoplankton population development, interdisciplinary laboratory studies need to be complemented by comprehensive *in vivo* investigations: metagenomic (to identify bacteria associated with various phytoplankton species), metatranscriptomic (to elucidate cellular responses to environmental changes), and metabolomic ones (to detect induced signaling compounds).

Understanding the processes of cellular interactions provides fundamental knowledge about development of phytoplankton population that has several practical applications. First, obtaining stable and high biomass of unicellular algae is a key issue in biotechnology. Elucidating the mechanisms of population regulation will open up relevant opportunities. Second, phytoplankton metabolites are a source of bioactive compounds, particularly for the production of new antibiotics [Pradhan, Ki, 2022]. In turn, bacterial compounds can be used for species-specific control of algal overgrowth in water bodies, which is crucial for mitigating harmful algal blooms [Sun et al., 2018].

Conclusion. Molecular interactions between unicellular organisms in aquatic ecosystems play a key role in shaping both competitive and cooperative dynamics within population. A wide diversity of signaling molecules produced by microorganisms facilitates not only intra- and interspecific communication but also interactions between pro- and microeukaryotes. Bacterial quorum sensing (QS) enables colonization of the microalgal phycosphere and can affect algal physiology. The production of algicidal compounds is known to be a quorum-dependent mechanism capable of regulating phytoplankton population dynamics. In turn, microalgae can modulate bacterial development through their own infochemicals and interfere with bacterial QS by either degrading autoinducers or mimicking them. Nevertheless, the prevalence of quorum quenching across different phytoplankton species, as well as the mechanisms by which oxylipins affect the microbial community of the phycosphere, remain poorly understood. Numerous unresolved questions underscore the need for further research aimed at elucidating the principles of coexistence of organisms in aquatic ecosystems, cellular adaptation to environmental changes, and the search for novel compounds for controlling pathogenic bacteria and mitigating harmful algal blooms.

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РОЛЬ ЧУВСТВА КВОРУМА И ИНФОХИМИЧЕСКИХ ВЕЩЕСТВ ВО ВЗАИМОДЕЙСТВИИ ПРО- И МИКРОЭУКАРИОТ В ВОДНЫХ ЭКОСИСТЕМАХ

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В обзоре представлены ключевые знания о молекулярных взаимодействиях одноклеточных организмов. Для бактерий характерно чувство кворума (quorum sensing, QS) — способность к регулированию экспрессии генов микроорганизмами в зависимости от плотности клеточной популяции. Это, в частности, может приводить к изменению поведения и к активации факторов вирулентности. У фитопланктона есть аналогичная система: клетки продуцируют инфохимические вещества, которые могут либо повышать устойчивость реципиентов к стрессовым воздействиям, либо запускать в них программируемую гибель. В то время как бактериальные молекулы чувства кворума (quorum sensing molecules, QSM) могут активировать/ингибировать рост клеток фитопланктона, продуцируемые последними инфохимические вещества могут влиять на состав микробного сообщества и подавлять развитие консументов. Кроме того, клетки фитопланктона могут воздействовать на QS бактерий, нарушая активность сигнальных молекул либо имитируя их.

Ключевые слова: чувство кворума, аутоиндукторы, фитопланктон, бактерии, инфохимические вещества