

REVIEW

Open Access



# Bacterial–microalgal consortia for bioremediation of textile industry wastewater and resource recovery for circular economy

Ranju Kumari Rathour<sup>1</sup>, Deepak Sharma<sup>2</sup>, Saleem Ullah<sup>3</sup>, El-Hassan M. Mahmoud<sup>4</sup>, Nitish Sharma<sup>5</sup>, Pradeep Kumar<sup>6</sup>, Arvind Kumar Bhatt<sup>1</sup>, Irshad Ahmad<sup>4,7</sup> and Ravi Kant Bhatia<sup>1\*</sup>

## Abstract

Textile industries discharge significant amounts of toxic chemicals, including residual dyes and various other xenobiotic compounds, into the environment, leading to adverse effects such as toxicity, mutagenicity, and carcinogenicity. While physico-chemical methods are commonly used for dye removal, bioremediation with microorganisms offers a greener and more eco-friendly alternative. Many microorganisms, including fungi, bacteria, and microalgae, possess the ability to degrade textile dyes through their metabolic pathways. However, their biodegradation potential is often hindered by factors such as cytotoxic effects of dyes, unfavorable environmental conditions, dye composition, concentration, and microbial types. In recent years, different strains of fungi, bacteria, and microalgae have been employed individually or in consortia for textile dye biodegradation. Nevertheless, there is a notable gap in research regarding the use of “bacterial–microalgal consortia” as a novel approach for efficient textile dye detoxification. This review aims to provide updated insights into the symbiotic interactions between bacteria and microalgae in degrading textile dyes. It discusses various technological, resource recovery, and economic challenges, as well as future prospects of this approach for textile wastewater treatment, emphasizing its potential for environmental and economic benefits.

## Highlights

1. Textile effluent contribute to pollution due to presence of dyes and heavy metals
2. Bacterial–microalgal consortia emerged as promising technology for bioremediation
3. Symbiotic interaction among BMC members helps in better removal of pollutants
4. BMC could become a technology for the sustainable management of textile effluent
5. BMC could provide valuable products beside treatment of textile industry effluent

**Keywords** Textile wastewater, Dyes and colorants, Bioremediation, Natural consortia, Resource recovery, Sustainable approach

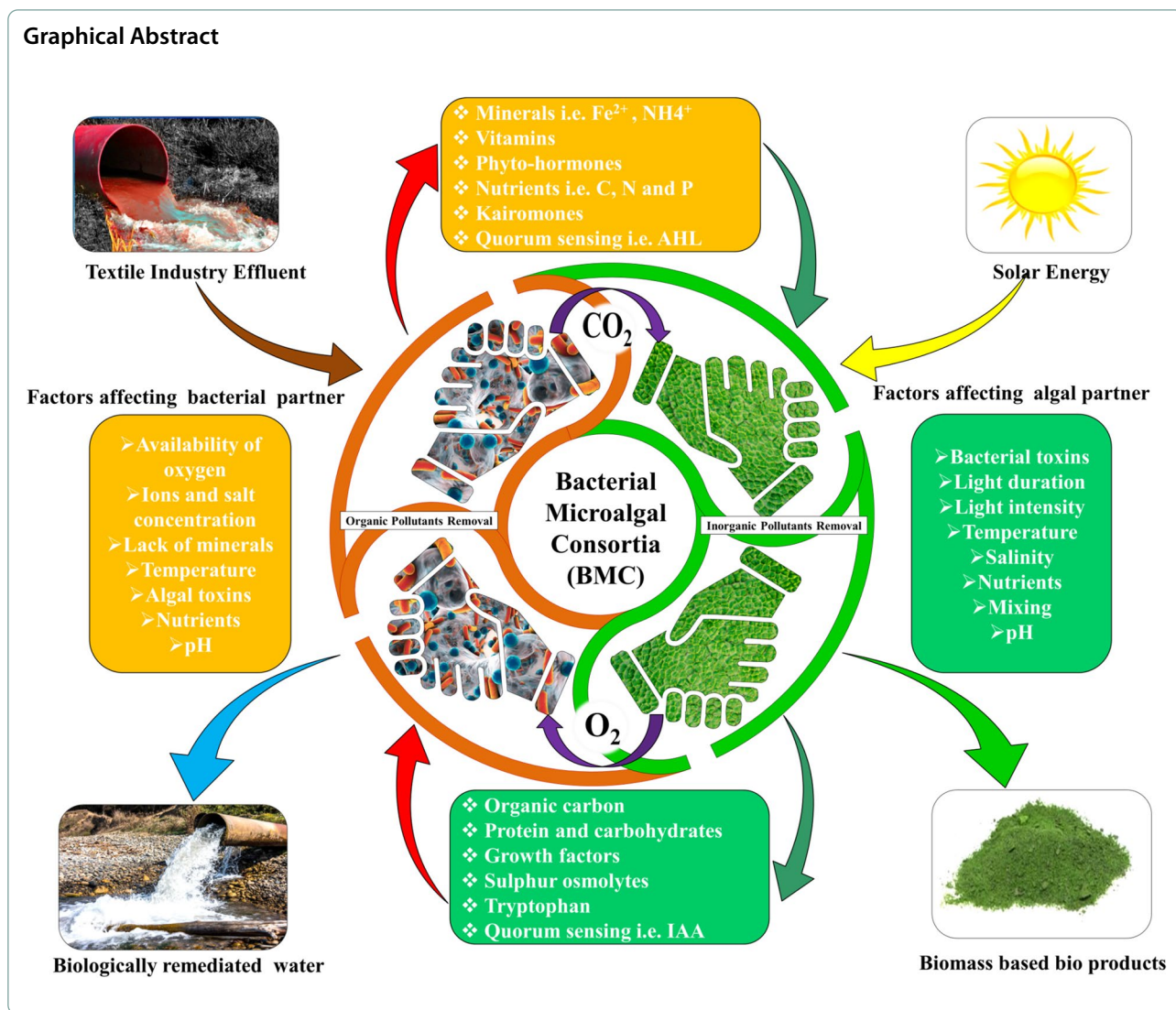
\*Correspondence:

Ravi Kant Bhatia  
ravibiotech07@gmail.com

Full list of author information is available at the end of the article



© The Author(s) 2024. **Open Access** This article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons licence, and indicate if changes were made. The images or other third party material in this article are included in the article's Creative Commons licence, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons licence and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this licence, visit <http://creativecommons.org/licenses/by/4.0/>.



**Introduction**

The textile industry plays a vital role in the global economy, contributing to sustainable development and the prosperity of nations. It encompasses the creation, manufacturing, and distribution of yarn, fabric, and clothing items [1]. Within various technological processes employed by the industry, dyes form a crucial component. These dyes, which belong to a diverse and heterogeneous group of chemicals, include azo dyes, triarylmethanes, phenothiazines, and anthraquinones, among others, and are extensively used in textile processing [2]. Unfortunately, during the dyeing process, a significant portion of these colors, estimated to be around 10–15%, is discharged into the environment as effluent, posing a serious risk to human health due to presence of carcinogenic toxic heavy metals and phenolic derivatives [3]. Hence, the presence of these toxic compounds

in the environment is a major concern and need an effective removal plan to safeguard the ecosystem. Various methods such as adsorption, chemical processing, ion-pair extraction, coagulation, and flocculation are utilized for decolorizing dye and treating textile effluents [4]. Although these techniques are efficient, they can also lead to secondary environmental issues in the future and are expensive [5]. On the other hand, the biological method of dye degradation, involving microbes and enzymes, has been effective and has fewer limitations [6]. However, there are certain limitations, such as the concentration of pollutants, their structural complexity, physicochemical behavior, and the type of microorganism when using a single microbial culture for effluent remediation [7]. This can be overcome by using a mixotrophic culture, i.e., bacterial–microalgal consortia (BMC), for bioremediation of textile effluent. The main advantages of using these

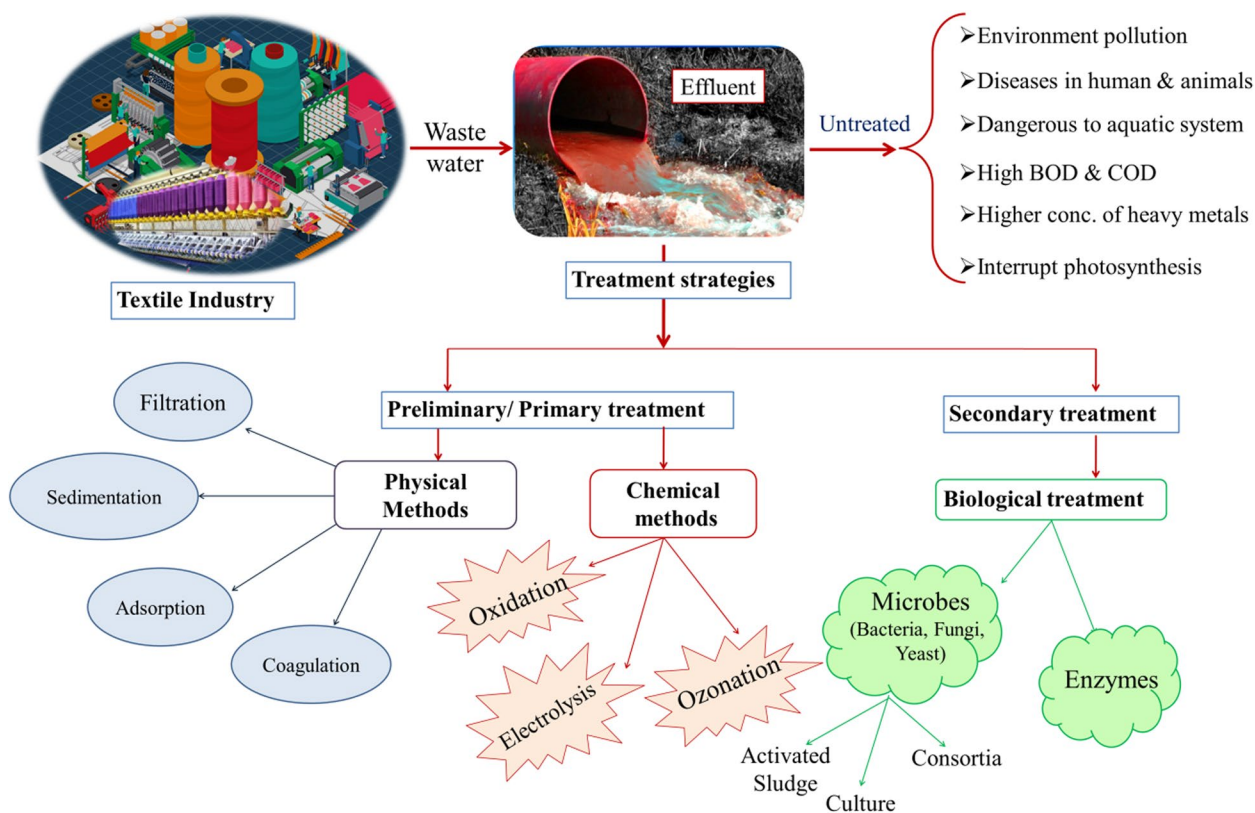
consortia are a fast rate of remediation, metabolic flexibility, and protection of cells from damage [8]. Wu et al. [9] used BMC for the bioremediation of textile effluent. Thus, in this review, authors provided comprehensive information regarding the types and compositions of textile effluents and advanced and conventional methods for treating textile effluent. The role of BMC in bioremediation and different aspects of interaction among bacteria and microalgae are discussed, emphasizing the effectiveness of BMC in textile effluent remediation. Additionally, the review delves into the techno-economic and environmental implications of implementing BMC for treating textile effluents, exploring the associated challenges and future prospects based on existing literature.

### Textile effluent treatment strategies

The elevated levels of hazardous chemicals pose obstacles to treatment procedures, complicating the process. Moreover, the presence of dyes obstructs sunlight and suppresses the growth of aquatic organisms such as plants, phytoplankton, and flora [10]. To address the removal of contaminants from textile wastewater, various treatment methodologies have been devised,

encompassing physical, chemical, biological, and hybrid approaches (Fig. 1).

Various physical methods, including sedimentation, adsorption, coagulation, and filtration, have been employed to remove suspended soil particles, lint pieces, and fibers from textile effluents [11]. Nano-filtration technology, coupled with a variety of coagulating and flocculating agents such as inorganic salts and organic substances like *Aloe vera* and *Cactus*, has emerged as effective for removing colorful impurities from effluents [12]. Madhav et al. [13] demonstrated the efficacy of natural adsorbents derived from plant biomass or biomass byproducts in treating textile effluents. However, a significant drawback of this technique is its low yield, efficiency, and generation of multiple by-products in the sludge [14, 15]. Chemical methods primarily involve oxidation, ozonation, and electrolysis. Zhang et al. [16] recently reported on the effectiveness of advanced oxidation techniques in treating textile effluents. Hutagalung et al. [17] corroborated the efficacy of these methods, noting a 51.7% reduction in COD through oxidative procedures [18]. Sala and Gutiérrez-Bouzán [19] utilized electrochemical methods for effluent treatment, facilitating the discoloration of effluents by degrading dyes. In



**Fig. 1** Different physical, chemical, and biological methods of effluent treatment

biological treatment, microorganisms such as bacteria (bioremediation), fungi (mycoremediation), and algae (phycoremediation), along with their enzymes, play a crucial role in effluent treatment [20]. Bacteria decompose organic matter into less toxic or useful by-products, which subsequently settle after sedimentation [21]. Bacteria were most effectively used for degradation of azo dyes with higher rate of remediation and less rate of formation of by-products while fungi degrade the non-soluble dyes by oxidation [22]. Microbial enzymes were also reported to degrade dyes and effluents by oxidation. Laccases, lignin peroxidase, lipases, hydrolases, protease, etc. are mainly used for this purpose [23]. The concentration of other constituents was also found to be higher in textile effluent as detailed in Table 1.

Recent studies have identified various microorganisms capable of degrading aromatic compounds present in industrial effluents [29]. While biological degradation methods are highly effective, they have drawbacks such as the specificity of a single microorganism toward a substrate and partial degradation of impurities [30]. To overcome these limitations, genetically modified microbes or microbial consortia have been developed for the degradation of toxic and hazardous industrial effluents [31]. These advanced technologies have proven to be more effective, eco-friendly, faster, and cost-effective compared to conventional methods [32].

#### Bacterial–microalgal consortia (BMC) for the degradation of textile effluent

Synthetic textile dyes have become an unavoidable component of several industries. According to a recent study by Morsy et al. [33], annually, 700,000 tons of diverse groups of dyes are produced, which are major contributors to various environmental pollutions and cause irreversible damage to ecosystems. While conventional

processes degrade dyes efficiently (coagulation-flocculation, adsorption, ion exchange etc.), they also produce toxic intermediates that further harm the environment [26]. Therefore, the scientific community highly recommends cheap and eco-friendly biological methods utilizing microbes, plants, biocatalysts, and consortia as alternative solutions [8]. Bacterial–microalgal consortia (BMC) have been used for the treatment of industrial effluent for decades and have been found to be more innovative and less time-consuming than engineered systems. BMC is a symbiotic association between bacteria and algae in which both positively affect each other's growth [34]. In these symbioses, algae help in the sorption of contaminants due to their large surface area and act as hosts to create favorable conditions for bacteria to survive in harsh environments. On the other hand, bacteria promote the growth of algae by degrading toxic pollutants and releasing phytohormones [35]. During such interactions, molecular signals and genetic information were also exchanged by both the organisms that facilitate genetic transformations [36]. Furthermore, before using such consortia in reactor system, selection of strains is necessary step and must be compatible towards each other w.r.t. size, growth rate, and genetic stability [37, 38].

#### Community structure of bacterial–microalgal consortia

The community structure of BMCs is dynamic and highly dependent on the environmental conditions in which they grow [39]. BMCs are typically composed of a few dominant algal species and a diverse array of bacterial taxa. The interactions between the different members of the BMC community are complex and involve a range of physical, chemical, and biological processes [34]. Understanding the community structure and dynamics of BMCs is important for the development of sustainable and efficient biotechnological applications for the treatment of textile effluent. Studies have shown that the composition of BMCs can be influenced by a range of factors, including nutrient availability, temperature, light intensity, and pH [40]. Importance of communication and signaling between the different members of the BMC community to sense members and their density for adjusting their behavior accordingly has also been studied by Venkata Mohan et al. [41]. An important aspect of the community structure of BMCs is the potential for functional redundancy that can provide a buffer against environmental fluctuations and disturbances. For example, if one bacterial species is unable to metabolize a particular nutrient, another species with similar metabolic capabilities may be able to fill the niche [42]. Overall, the community structure of BMCs is a complex and fascinating area of study that

**Table 1** Composition of different constituents of textile effluents

Sr. No	Constituent of effluent	Range	Reference
1.	Color	Dark brown to charcoal black	[24]
2.	Temperature (°C)	20–60	[25]
3.	pH	4–10	[26]
4.	TDS (mg/L)	1800–12,000	[24]
5.	TSS (mg/L)	15–8000	[25]
6.	Conductivity (µS/cm)	1000	[27]
7.	Chlorines (mg/L)	200–6000	[24]
8.	Heavy metals (mg/L)	2–15	[28]
9.	BOD (mg/L)	80–6000	[26]
10.	COD (mg/L)	150–12,000	
11.	Surfactants	20–100	[18]

has important implications for biotechnology, environmental management, and our understanding of microbial ecology require further research for better management of textile effluent.

In this mode of construction, the bacterial and microalgal species are grown together in the same culture medium to facilitate their interactions. Mubashar et al. [28] reported *Enterobacter* sp. MN17-inoculated with *C. vulgaris* to treat wastewater resulted into removal of 79% (Cr), 93% (Cd), 72% (Cu), and 79% (Pb). The co-cultivation of microalgae *Chlorella sorokiniana* strain DBWC2 and *Chlorella* sp. strain DBWC7 and bacteria *Klebsiella pneumoniae* strain ORWB1 and *Acinetobacter calcoaceticus* strain ORWB3 has been reported to produce biomass feedstock with simultaneous wastewater remediation [43]. The bacterial species enhanced the growth of the microalga by providing essential nutrients, resulting in efficient removal of nitrogen and phosphorus from the synthetic wastewater. Table 2 summarizes various BMCs with their efficiencies for the treatment of various wastewaters.

The sequential inoculation of bacterial and microalgal species into the culture medium facilitates specific interactions between them. This approach enables direct interaction between the microalgal and bacterial cells, fostering a more symbiotic relationship between the two species [39]. Genetically engineered BMCs are established to promote specific interactions, enhancing the development of beneficial strains and facilitating the sustainable production of commercial metabolites [32, 36]. BMCs also contribute to the formation of biofilms, aiding in the attachment of microalgal and bacterial cells to surfaces, thereby creating a complex ecosystem. This strategy can enhance the stability and productivity of the

consortium, particularly in wastewater treatment applications [51].

### Modes of interaction in BMCs

BMCs can interact with each other in different ways, including synergistic, commensal, and mutualistic interactions (Fig. 2). Here is a brief overview of each mode of interaction.

#### Synergistic interaction

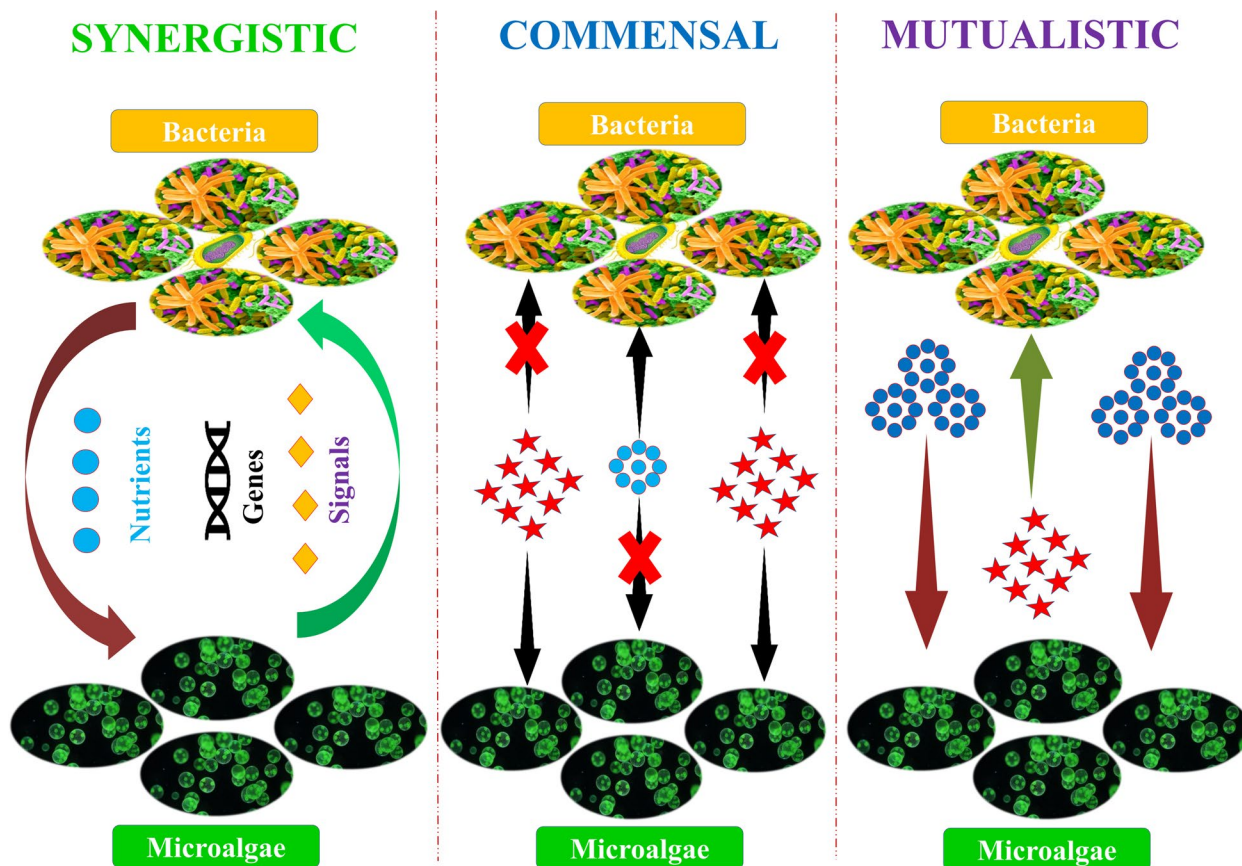
In this form of interaction, the bacterial and microalgal species within the consortium collaborate to improve its overall performance. Bacterial members may degrade toxic substances, providing essential nutrients or growth factors to the microalgae, while the microalgae may supply organic carbon for bacterial growth [52]. For instance, a *Chlorella-Exiguobacterium* and *Chlorella-Exiguobacterium/Bacillus licheniformis* consortium demonstrated a synergistic reduction in total nitrogen, total phosphorus, ammonia, and chemical oxygen demand by 78.3%, 87.2%, 84.4%, and 86.3%, respectively, during piggery wastewater treatment [53]. Through this synergy, bacterial species supported microalgal growth with essential nutrients, while microalgae supplied organic carbon for bacterial proliferation, resulting in the efficient removal of organic pollutants from the wastewater [52].

#### Commensal interaction

In a commensal interaction, one species benefits from the presence of another species without causing any harm or providing any benefit in return. For instance, certain bacterial species in the consortium may utilize the organic carbon excreted by the microalgae for their growth without offering any benefit in return [54]. Research indicates

**Table 2** BMCs and their efficiencies in various wastewater treatments

Bacterial–microalgal consortium	Wastewater	Efficiency	Reference
<i>Chlorella vulgaris</i> and <i>Staphylococcus</i> species	Real textile wastewater	Nitrogen-58.57%, phosphate-86.42%, and COD-91.5%	[6]
<i>Chlorella vulgaris</i> and <i>Enterobacter</i> sp. MN17	Textile wastewater	Reduction in chromium (79%), cadmium (93%), copper (72%), lead (79%), COD (74%), and color removal (70%)	[28]
<i>C. sorokiniana</i> DBWC2, <i>Chlorella</i> sp. DBWC7 and <i>K. pneumoniae</i> ORWB1, <i>Acinetobacter calcoaceticus</i> ORWB3	Artificial wastewater	Total biomass titer (93%), nitrate removal (82%), COD (90%) in both artificial wastewater and raw dairy wastewater	[43]
Algal–bacterial consortium	Wastewater treatment	Ammonium removal-100%, COD-90%	[44]
<i>C. vulgaris</i> and activated sludge	Synthetic wastewater	Nitrogen-89.4%, phosphorous-91.4%, and COD-83.6%	[45]
<i>Scenedesmus</i> sp. and bacteria group	Municipal wastewater	Nitrogen-95.7%, phosphate-98.1%, and COD-92.3%	[46]
<i>Picochlorum</i> sp and <i>Chitrimycetes</i> , <i>Pseudomonas</i> sp.	Saline wastewater	Carbon, nitrogen, and phosphorus-95%	[47]
<i>Chlorella</i> , <i>Chlamydomonas</i> , <i>Stichococcus</i> , and bacteria	Swine manure	Phosphorous-90%	[48]
<i>C. sorokiniana</i> and aerobic sludge	Swine wastewater	Nitrogen-82.7%, phosphate-58%, and COD-62.3%	[49]
<i>C. sorokiniana</i> and <i>Azospirillum brasilense</i>	Ammonia wastewater	Nitrogen-100%	[37]
<i>Chlorella vulgaris</i> and <i>Lemnamin uscula</i>	Recalcitrant effluent	Nitrogen-71.6%, phosphate-28%, and COD-61%	[50]



**Fig. 2** Mode of interaction between algae and bacteria in BMC

that the presence of the bacteria *Auxenochlorella protothecoides* and the microalga *Chlorella sorokiniana* in wastewater did not affect the growth of the algae, illustrating the occurrence of commensalism [55].

#### Mutualistic interaction

In a mutualistic interaction, both bacterial and microalgal species in the consortium benefit from each other's presence. For instance, when *Ostreococcus tauri* and *Dinoroseobacter shibae* were co-cultured, it provided both species with the B vitamins they required, leading to a mutualistic association [56]. Similarly, Palacios et al. [57] demonstrated a symbiotic relationship for mutual growth, where *Azospirillum brasilense* produced indole acetic acid and *Chlorella sorokiniana* produced thiamine, with both species consuming tryptophan for growth.

#### Functional modes of BMCs

##### BMCs in environment maintenance

Bacterial–microalgal consortia (BMC) have emerged as key players in preserving environmental health, notably in treating textile and other effluents [58]. Utilizing industrial flue gas and wastewater for cultivating

microalgae–bacteria consortium enables the utilization of nutrients and organic matter, thereby aiding in CO<sub>2</sub> mitigation [59]. Additionally, BMCs prove valuable in remediating persistent organic pollutants from water streams and industrial effluents through mechanisms such as biosorption, bioaccumulation, and biodegradation [58]. Researchers have explored the use of microalgae in consortia systems alongside other microorganisms, predominantly bacteria, to enhance their efficiency in pollutant removal [60]. Microalgae perform photosynthesis, producing oxygen that supports bacterial populations, while also assimilating contaminated nutrients throughout their growth cycle [61]. A synthetic BMC was developed for crude oil degradation, comprising *Sphingomonas* GY2B, *Burkholderia cepacia* GS3C, *Pseudomonas* GP3A, *Pandoraea pnomenus* GP3B, and an oil-tolerant microalga, *Scenedesmus obliquus* GH2 [62].

##### Nutrient exchange in BMC

Bacterial–microalgal consortia plays a crucial role in nutrient exchange within aquatic ecosystems, particularly in environments where nutrients are scarce. These consortia facilitate the exchange of metabolites, nutrients,

vitamins, growth-promoting factors, phytohormones, carbon uptake, oxygen generation, and removal, thereby enhancing biomass productivity and quality [63]. For instance, the freshwater green alga *Lobomonas rostrata*, which requires organic micronutrients for growth, obtains vitamin B12 from the bacterium *Mesorhizobium loti*, while providing photosynthate to the bacteria in return [64]. Additionally, bacteria may produce specific antibiotics to either lyse algal cells (parasitism, for controlling algal blooms) or protect algae from other microorganisms (mutualism/commensalism) [65]. Acyl homoserine lactones (AHLs), signaling molecules produced by bacteria, facilitate biofilm formation between bacterial and algal cells, potentially aiding in biomass harvesting and wastewater treatment [66].

**Signal exchange in BMCs**

Signal exchange plays a pivotal role in the functioning of bacterial–microalgal consortia (BMCs) in the treatment of textile effluents. Bacteria and microalgae communicate through the exchange of signaling molecules, enabling them to coordinate their actions and respond to environmental changes [67]. For instance, symbiotic bacteria from the *Roseobacter* group release quorum sensing signals, such as rosmarinic acid, which facilitate the colonization of *Asterionellopsis glacialis* and enhance biofilm formation. This enhances the bacteria’s ability to attach to diatom microalgae [68]. The interactions between bacteria and phytoplankton are intricate, affecting various processes that can either positively or negatively impact BMC productivity [69]. Research has shown that quorum

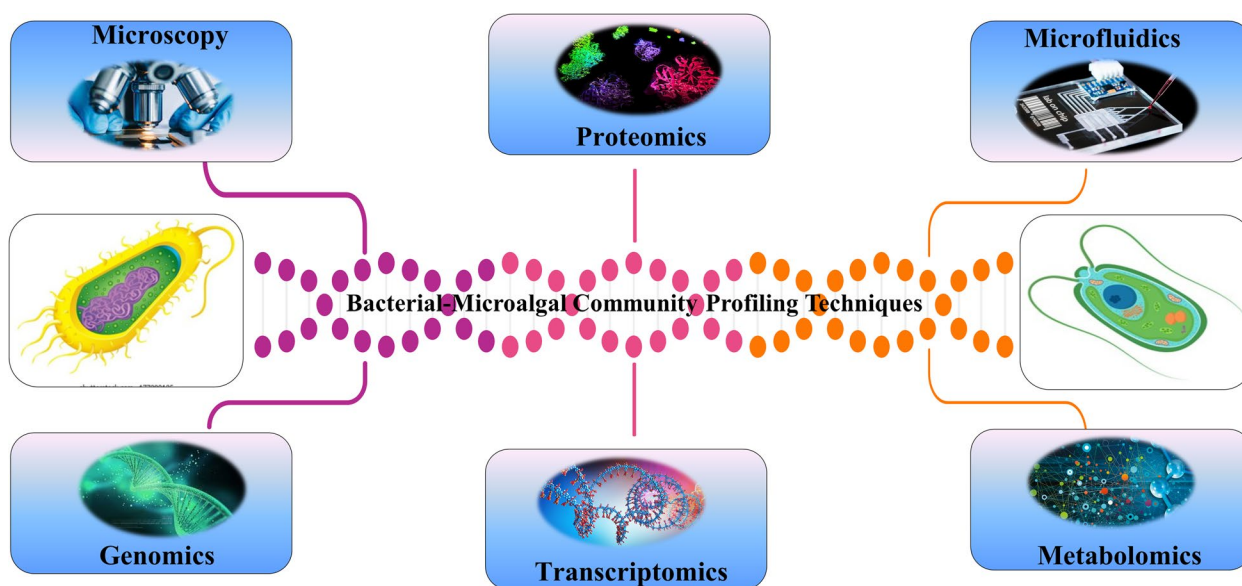
sensing molecules isolated from microbial consortia in wastewater can boost lipid synthesis in *Chlorophyta* sp. microalgae by 86%, albeit with a slight decrease in algal biomass [70]. In another study, *Chlorococcum sorokiniana* microalgae cultivated in a photo-bioreactor with bacterial quorum sensing molecules extracted from anaerobic bacterial sludge exhibited a 2.25-fold increase in algal biomass, along with elevated lipid and protein content [66].

**Technologies for BMC community profiling**

Precise identification and characterization of microalgae and bacteria within a consortium are essential for optimizing these communities and harnessing their potential applications. Researchers employ various techniques, including physical, biochemical, and molecular methods, to identify bacterial–microalgal consortia [40]. As technology advances, novel approaches have emerged to study microorganism interactions within consortia as shown in Fig. 3, aiming to improve wastewater treatment efficiency and facilitate biotechnological applications [36].

**Microscopy**

Microscopic observation is a fundamental method for studying the morphology, organization, and function of microalgae and bacteria in the phycosphere. Epifluorescence microscopy is commonly utilized to examine bacteria and microalgae, which are typically fixed with 2% formaldehyde and stained with 4',6'-diamidino-2-phenylindole (DAPI) before observation under an inverted



**Fig. 3** BMC profiling techniques

optical microscope [71]. Laser confocal fluorescence microscopy is another valuable technique used to detect the accumulation and utilization of fluorescent organic compounds, such as BaP, in algal cells [72]. Scanning electron microscopy (SEM) analysis of bacterial–microalgal consortia involves fixing the sample in glutaraldehyde for 24 h, dehydration in a series of alcohol solutions for 10 min, and mounting onto a support material coated with gold particles for SEM analysis [73]. Similarly, Biswas et al. [74] analyzed bacterial–microalgal consortia by preparing a thin smear of the consortium, air-drying it, coating it with an 8-nm-thick layer of gold in a sputter coater, and observing it using light microscopy, SEM, and field emission SEM. Confocal laser scanning microscopy has been employed to identify the presence of microalgae in natural consortia found in municipal wastewaters, enabling visualization of the three-dimensional microstructure of bacterial–microalgal consortia [75].

#### Microfluidics

Microfluidic devices have emerged as valuable tools for creating controlled environments conducive to the growth of bacterial biofilms, enabling real-time observation and measurement of their properties [76]. These devices facilitate the analysis of complex environmental conditions, such as concentration gradients, by allowing researchers to observe the responses of individual cells through live-cell imaging [77]. In a recent advancement, a microfluidic photo-bioreactor was successfully developed and tested for the photoautotrophic cultivation of *C. sorokiniana* [78]. Additionally, Syed et al. [79] designed a low-cost spiral micro channel capable of efficiently separating and purifying *Tetraselmis suecica* from invasive diatoms, such as *Phaeodactylum tricorutum*, at optimal flow rates. This method achieved up to 95% separation of *P. tricorutum* cells from the culture without impacting cell viability [80].

#### Genomics

One of the key advantages of genomics lies in its capacity to analyze the genetic sequences and gene expression patterns of individual organisms, revealing pertinent biological functions [36]. Polymerase chain reaction-denaturing gradient gel electrophoresis (PCR-DGGE) is a molecular technique commonly paired with 16S rDNA sequencing to explore microbial diversity in environmental samples [81]. Cho et al. [75] employed DGGE in conjunction with pyrosequencing to assess bacterial diversity associated with microalgae in untreated municipal wastewater, identifying prevalent genera such as *Chlorella* sp., *Acutodesmus* sp., and *Scenedesmus* sp. [48]. Quantitative polymerase chain reaction (qPCR) utilizing specific markers like rRNA gene and plastid DNA is employed

to examine bacteria and microalgae in consortia under specific conditions [54]. Pyro-tag sequencing is another genomic technique used to analyze the BMC community in fixed-bed photo-bioreactors [47]. Additionally, quantitative PCR and metagenomic analyses have shown that microalgae stimulate bacterial growth, establishing a symbiotic relationship with *C. vulgaris* compared to indigenous bacteria [82]. Fluorescence in situ hybridization (FISH) is employed for identifying and quantifying specific microbial populations by hybridizing fluorescently labeled oligonucleotide probes to complementary sequences in target microbial cells [36, 83]. Next-generation sequencing (NGS) provides a comprehensive understanding of genetic stability by identifying interspecies variants in consortia exposed to extreme conditions. The genomic features of these bacterial cells suggest the critical role of heterotrophy in this bacterial phylum. Furthermore, fluorescence-activated cell sorting (FACS) in enrichment cultures, combined with single-amplified genomics/amplicon sequencing and fluorescence microscopy, aids in identifying various metabolic capabilities and interactions of BMC members [84].

#### Transcriptomics

Analyzing the transcriptome sequence provides a detailed insight into the physiological processes occurring in individual microorganisms or consortia comprising bacteria and microalgae [52]. For instance, during consortia development, the diatom *Thalassiosira pseudonana* was found to produce a protein that transports and catabolizes 2,3-dihydroxypropane-1-sulfonate (DHPS), which serves as a food source for bacteria in the consortium [85]. Co-culturing *T. pseudonana* with DHPS enables *Ruegeria pomeroyi* to utilize DHPS as a carbon source, resulting in the transcriptional expression of its metabolism and up-regulation of genes involved in C2-sulfonate N-acetyltaurine transport and catabolism [86]. Although green algae typically cannot synthesize vitamin B12, they can utilize a cobalamin-independent pathway to produce methionine necessary for protein synthesis, thus bypassing the need for vitamin B12 [64]. These approaches are crucial for obtaining a comprehensive understanding of the interactions between different organisms within a consortium and their roles in the ecosystem.

#### Proteomics

Proteomics offers valuable insights into the metabolic and signaling pathways involved in the interactions between organisms within a consortium [87]. By identifying bioactive compounds and growth factors influencing BMC survival, proteomics guides the cultivation of the consortium [88]. For instance, proteomics analysis



elucidated molecular mechanisms between *Chlorella vulgaris* and *Bacillus licheniformis* supplemented with vitamin B12, revealing significant enrichment in pathways like carbon fixation, amino acid metabolism, and nitrogen metabolism [64]. In the presence of vitamin B12, upregulation of proteins activated the quorum-sensing pathway, enhancing the algae–bacteria interaction [89]. Moreover, interactions between microalgae and associated microbiomes enable metabolic adaptation, allowing bacteria to metabolize nutrients from injured or dead algal cells, sustaining the microbial community [90].

### Metabolomics

Comprehending the metabolic interactions within BMCs and their responses to environmental stimuli is pivotal for their engineering, as these interactions are modulated by environmental changes, genetic modifications, and organismal physiology [37, 86]. Recent investigations have focused on metabolic responses in microalgae, particularly under nutrient-deprived conditions. For instance, Chen et al. [91] observed changes in the metabolome profile of co-cultures of *C. sorokiniana* and *Pseudomonas* sp. compared to individual microorganisms. The metabolomics analysis, employing orthogonal partial least squares discriminate analysis (OPLS-DA), revealed an augmentation of secondary metabolites with high economic value in both *C. sorokiniana* and the consortia developed with *Pseudomonas* sp. [57, 92]. Integrating multiple omics techniques, including genomics, transcriptomics, proteomics, and metabolomics, is imperative for a comprehensive understanding of microalgae–bacteria interactions within a consortium.

### BMC interactions in textile effluent treatment

In BMCs, bacteria and algae play significant roles in shaping physiology, environmental chemistry, and microbial diversity. The interaction between bacteria and microalgae is both mutualistic and competitive [51]. In a study by Mandal et al. [93], it was observed that the microalgae *Amphidinium carterae* produce extracellular polymeric compounds that enhance the growth of *B. pumilus*. Similarly, bacteria produce growth-promoting elements such as vitamins and siderophores, which facilitate algal growth, particularly in iron-deficient environments. Kim et al. [94] reported the role of rhizobium in promoting algal growth in nitrogen-fixation-deficient algae. Bacteria and algae degrade organic matter through mixotrophic and heterotrophic metabolism without significantly altering the system's pH [95]. The mucus produced by some blue-green algae creates a specialized microenvironment for specific bacteria. In competitive relationships, both partners can have adverse effects on each other, with metabolites excreted by microalgae having bactericidal

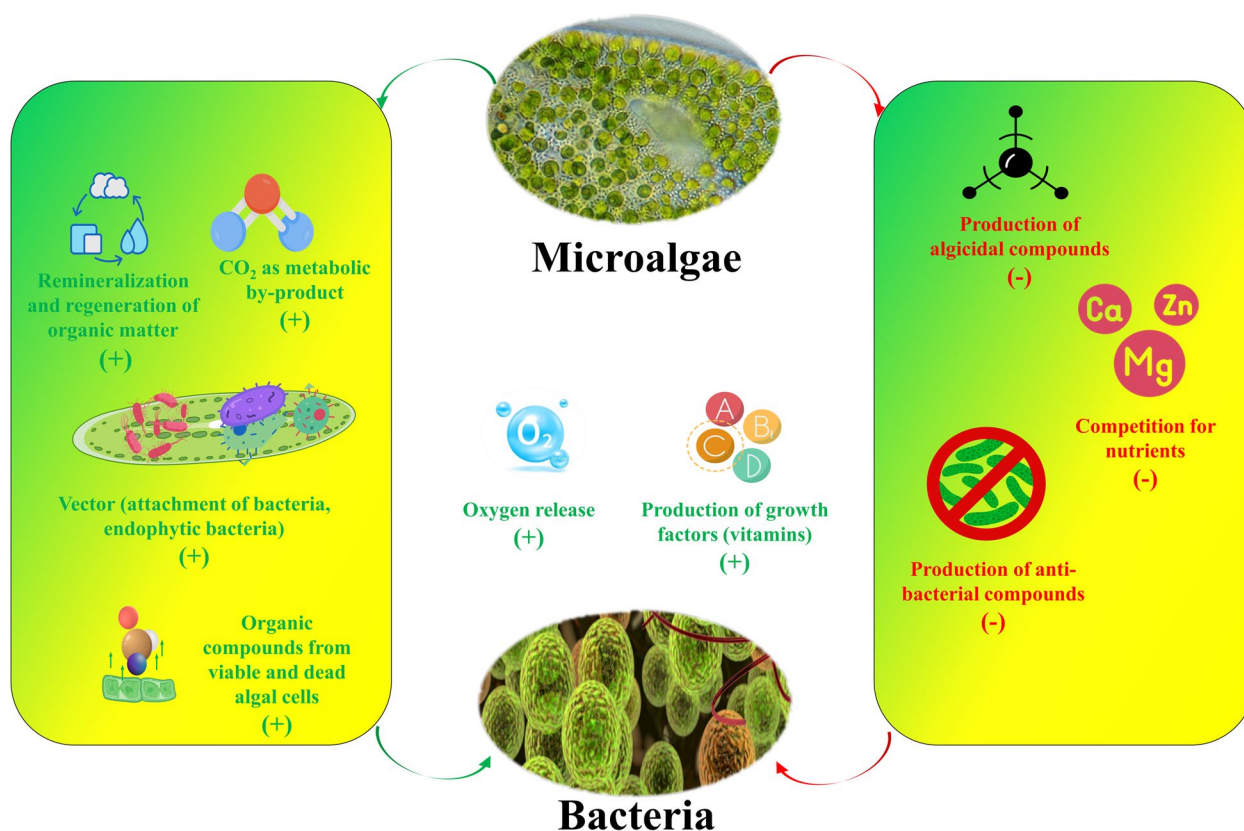
effects and vice versa [51, 96]. Reports indicate the inhibition of bacteria such as *B. subtilis*, *E. coli*, and *P. aeruginosa* by microalgae. Changes in dissolved oxygen, temperature, and pH during photosynthesis can also have harmful effects on bacteria [95]. Figure 4 is depicting the exchange of various nutrients and metabolites among bacteria and microalgae during their consortia formation for the treatment of wastewater.

### Stimulation of growth by nutrient regeneration

In nutrient-limiting environments, heterotrophic bacteria play a vital role in re-mineralizing nutrients to promote algal growth. Kim et al. [94] observed that bacteria synthesize vitamins and other growth-promoting metabolites essential for algal growth. This interaction offers benefits such as nutrient provision, biological material cycling, and the development of ecological niches for symbiotic organisms [97]. Many bacteria form symbiotic associations, and chemicals synthesized by microbes aid in their communication; for instance, bacteria and algae employ chemotaxis for communication [60]. Bacteria also synthesize specific antibiotics that protect algae from parasites [98]. Inorganic phosphorus, produced during ATP hydrolysis by bacteria, is utilized by algae for growth. Metabolites released during algal blooms and cell death significantly influence bacterial metabolism [99]. Certain algae can produce transparent exopolymer particles, granular organic molecules that reveal the species and bacterial activity of symbiotic algae. Algae also synthesize polysaccharides, carbohydrates, and other growth nutrients to enhance bacterial growth [100].

### Inhibition of growth by metabolites

Both algae and bacteria synthesize antibacterial and algicidal metabolites, such as chlorellin and lysozyme, which have inhibitory effects [101]. Algae are known to produce several compounds with antibacterial potential, including fatty acids (e.g., eicosapentaenoic acid, hexadecatrienoic acid), terpenes, glycosides, and chlorophyll derivatives (e.g., pheophytin and chlorophyllide) [102]. Similarly, bacteria synthesize compounds such as quinolones, pyrroles, glucosidases, indoles, chitinases, peptides, amino acids, and alkaloids, which exhibit algicidal activity [103]. Rajamani et al. [104] reported the formation of lumichrome, a derivative of the vitamin riboflavin, by *Chlamydomonas reinhardtii*, which acts as an AHL (acyl-homoserine lactone) antagonist to inhibit *Pseudomonas aeruginosa*, LasR. Additionally, microalgae produce quorum quenching (QQ) molecules, such as lactonases, acylases, and oxidases, to inhibit bacterial AHL signaling molecules and protect themselves from harmful bacteria [105].



**Fig. 4** Positive and negative interactions among bacterial–microalgal consortia by exchange of nutrients and metabolites

#### Signal transduction in BMC for mutualistic and antagonistic effect

In consortia, bacteria and algae respond to chemical signals and toxins. Microalgae produce quorum-sensing mimics, likely to interfere with bacterial communication. Additionally, molecules in the algal–bacterial symbiosis regulate virulence factor synthesis and reproductive activity [106]. It was reported that by blocking bacterial QS signals, *Chlamydomonas reinhardtii* and *Chlorella saccharophila* protect themselves from pathogenic *Vibrio harveyi* [105]. These signaling molecules that mediate communication in BMC are divided into lipid-based molecules (AHLs) and microalgal allelochemicals (e.g., flavonoids and ectocarpene) [96]. Indole acetic acid (IAA) is one such signal molecule secreted by bacteria that encourages mutualism in both partners [67]. Additionally, some toxins are secreted by bacteria that inhibit algae or alter the algal life cycle [107]. Proteases secreted as QS by *Flavobacterium Kordia algicida* target its algal symbiotic hosts (*Thalassiosira* and *Phaeodactylum*) [85]. It has been discovered that microalgae react to bacterial QS signaling molecules (AHLs) in a specific way, producing associated biological reactions and steadily influencing microalgae growth, biofilm formation, spore

generation, and nutrient digestion [71, 108]. Inter-kingdom signaling, discovered between eukaryotes and bacteria, is a category for signal transduction between algae and bacteria [66]. Additionally, it was reported that algae have the ability to excrete specific chemicals that prevent bacteria from quorum sensing, and simultaneously bacterial quorum-sensing compounds (acyl homoserine lactones) hinder the germination and development of zoospores [109].

#### Factors affecting efficiency of BMC in textile effluent treatment

For efficient working of any consortia, different working as well as physiological conditions plays a significant role. Every microorganism has some working condition and requirement. The role of these conditions in working of BMC to treat textile effluent is discussed below.

##### Aeration

The balance of CO<sub>2</sub> and O<sub>2</sub> gases holds significance in algae metabolism, as both are essential at the catalytic site of ribulose 1,5 diphosphate oxygenase/carboxylase, a key enzyme in the Calvin cycle [99]. High rates of aeration can impede CO<sub>2</sub> fixation by algae due to an abundance

of O<sub>2</sub> [110]. Additionally, bacteria outpacing algae growth leads to insufficient oxygen production in BMCs, accelerating CO<sub>2</sub> consumption by algae. Excessive aeration exacerbates this issue by depleting CO<sub>2</sub> levels, sparking a competition between algae and bacteria for carbon sources and nutrient assimilation [100]. Thorough mixing of BMCs through shaking can enhance the availability of CO<sub>2</sub> and O<sub>2</sub> for both algae and bacteria [82].

#### Light irradiation

Several studies have highlighted the significant influence of lighting on algae growth, nutrient utilization, and pollutant degradation, considering factors like photoperiod, light intensity, and wavelength [111, 112]. In their research, Ferro et al. [113] utilized a BMC system consisting of *C. vulgaris* and its associated bacterium, *Rhizobium* sp., within artificial municipal wastewater. While increased light irradiation has been shown to enhance nitrogen removal in algal–bacterial granules, BMCs face limitations in light exposure due to bacterial/algae cell shading, the dark hue of wastewater, and lighting duration. Exposure to a surface light intensity of 3000 lx can lead to severe photo-inhibition in algal–bacterial granules, potentially causing chloroplast degradation [92].

#### Variety of partners in BMC

In BMCs, the selection of microalgae and bacteria partners significantly influences wastewater treatment, as their metabolic processes vary, affecting contaminant removal rates and efficiencies [114]. Certain microalgae excel in photosynthesis, producing higher oxygen levels that aid wastewater aeration, facilitating aerobic bacteria in contaminant degradation [115]. Others secrete extracellular polymeric substances, fostering biofilm formation for enhanced contaminant removal [116]. Similarly, specific bacteria exhibit superior abilities in degrading particular contaminants, underscoring the importance of selecting suitable bacterial species for the consortium to optimize textile effluent treatment [94]. A well-designed consortium can yield an effective and durable wastewater treatment system [95].

#### Ratios of algal and bacterial partners

Achieving a balance in the proportions of algae and bacteria is crucial to establish commensal or mutualistic relationships, preventing parasitism. Toyama et al. [117] found that *Emticicia* sp. presence stimulated *Euglena gracilis* growth, indicating the significance of microbial ratios. Increasing bacterial concentration enhances nutrient removal efficiency and chlorophyll content, as evidenced by studies employing various *C. vulgaris* and *B. licheniformis* inoculation ratios in artificial wastewater

[118]. However, optimal phosphate and nitrogen removal occurred at a 1:3 algae-to-bacteria ratio [119].

#### Temperature and pH

Several studies have highlighted the correlation between the diversity of bacterial communities, particularly in aquatic environments, and water temperature, which directly impacts BMC productivity. During the summer, microalgae can flourish in high-temperature environments and predominate in aquatic ecosystems [120]. For instance, Proteobacteria have been found to be associated with microalgae. In an experiment, it was observed that *Actinomycetes* were present only in the group treated at 20 °C and disappeared when exposed to higher temperatures [121]. This indicates that temperature influences both bacterial and microalgal communities in wastewater simultaneously. There are various factors contributing to pH changes within BMC, such as a reduction in carbon dioxide concentration due to the activity of photosynthetic plankton [122]. While the microalgae community tends to be less tolerant of acidic conditions compared to the bacterial community, paradoxically, bacterial communities may be less suited to alkaline conditions than microalgal communities, potentially due to carbon dioxide absorption dynamics [123]. An acidic environment is more conducive for BMC to break down organic pollutants, as the consortium requires lower pH conditions. Therefore, BMC can adapt its community composition to optimize pollutant degradation efficiency while creating a suitable growth environment for the consortium [110]. Studies have shown that BMC exhibits higher efficiency in removing heavy metals from acid mine drainage at lower pH levels (between 3.0 and 5.0) [122]. Hence, optimizing pH is crucial to meet the diverse requirements of BMC and achieve maximal pollutant degradation.

#### Dissolved oxygen (DO)

The concentration of dissolved oxygen (DO) in water plays a crucial role in shaping the community structure of bacterial–microalgal consortia. In eutrophic water bodies, the agglomeration and decomposition of cyanobacterial cells can lead to a reduction in DO levels, potentially creating anoxic conditions. Li et al. [116] examined how low DO levels (DO 0.5 mg/L) resulting from blooms in Taihu Lake affected the bacterial community structure. They found that *Clostridium prazmowski* dominated in the early stages of hypoxia, while *Desulfovibrio* and *Comamonas* sp. persisted throughout the hypoxia process. Parakh et al. [124] investigated a system combining a photobioreactor for microalgae growth and a sequential batch reactor for sludge treatment. They observed that prolonged low oxygen levels in the sequential batch reactor led to sludge adhesion

to the membrane. Despite this, dissolved oxygen is essential for the oxidation of pollutants in wastewater treatment by aerobic microorganisms [99]. However, excessive dissolved oxygen can inhibit anaerobic processes. Therefore, maintaining a balance between bacterial and microalgal communities is crucial for regulating DO levels and optimizing wastewater treatment. While high dissolved oxygen concentrations can hinder photosynthesis-based microalgal growth, aerobic bacteria can consume oxygen produced by algae, potentially mitigating the issue of excessive DO that limits microalgal growth [116].

### Nutrients (C/N/P)

Interactions between bacteria and microalgae play a pivotal role in carbon and nitrogen transport [125]. For instance, a study unveiled a mutualistic relationship between *Phaeodactylum* and *Donghicola* sp., where *Donghicola* sp. converts methylamine into inorganic nitrogen, facilitating algae growth [80]. Furthermore, the removal of ammonia nitrogen from a system, exceeding 95%, results in residual nitrate nitrogen, fostering increased biomass of both bacteria and algae [126]. Wang et al. [127] found that a BMC comprising an algae-cyanobacteria consortium is 6.3 times more effective at removing nitrous nitrogen in wastewater plants. The synergy between algae and bacteria enhances bacterial capacity to solubilize phosphorus in wastewater, augmenting microalgal phosphate uptake [128]. Algae's ability to absorb inorganic phosphate is bolstered when coexisting with compatible bacterial partners, shaping BMC communities in the phycosphere. Arias et al. [126] concluded from their research

that a high N/P ratio enhances biomass production in microalgal and cyanobacterial consortia.

### Resource recovery and techno-economic impacts of BMC in textile effluent treatment

The symbiotic relationship between bacteria and microalgae mutually supports efficient pollutant removal from textile wastewater. However, for successful implementation of BMC in textile effluent treatment at a commercial scale, conducting techno-economic and environmental analyses is crucial (Table 3). Although biomass from the microalgae–bacteria consortium holds potential for various applications, including biofuel, biochemicals, animal feed, biofertilizers, nutraceuticals, cosmetics, and food ingredients, certain applications may be unsuitable for a consortium system due to the input of wastewater and the bacterial component. Therefore, only compatible applications are discussed below, considering the type of microalgae for each desired end product.

### Renewable biofuel production

Numerous studies and research have highlighted the high biomass production efficiency of both microalgae and bacteria, but the BMC stands out as particularly effective for textile effluent treatment. Microalgae exhibit a much faster doubling time compared to land-based energy crops, with lipid yields surpassing those of traditional oil crops by 15–300 times, making them an ideal source for biofuel production [136, 137]. Microalgae lipid composition typically includes approximately 0.7–30.6% free fatty acids and 4.1–77.5% triglycerides, which can be readily converted into biodiesel [138, 139]. Indole-3-acetic acids released by plant growth-promoting bacteria have been found to double lipid content and productivity, indicating the potential for enhanced biofuel production [140]. The

**Table 3** Techno-economic impact and challenges of applying BMC in textile effluent treatment

	Impact	Details	References
Techno-economic impact	Improved treatment efficiency	Enhance inorganic carbon fixation and increase microalgae biomass	[70]
	Cost-effectiveness	Reduce the cost of treatment as well as growth nutrient because microalgae biomass was used as substrate by bacteria	[129]
	Renewable energy production	Energy-rich biomass is generated during utilization of N, P, and other inorganic nutrients during nitrification and photosynthesis	[130]
	Resources recycling	Convert nutrients from the effluent into biomass, e.g., conversion of phosphorous found in the textile effluent into polyphosphate	[131]
	Reduced discharge of pollutants	Convert toxic metals into less toxic ones before discharge	[132]
	Greenhouse gas emissions	Microalgae consume high levels of CO <sub>2</sub> and convert it into chemical energy with the help of sunlight	[45]
Challenges	Inhibition of microalgal growth	Competition for nutrients Production of antifungal metabolites by bacteria	[133]
	Inhibition of bacterial partner	Production of antibacterial metabolites by algae	[134]
	Non-availability of information	Lack of information regarding co-cultivation and scale-up strategies	[135]

high-lipid content in microalgae may be partly attributed to nutritional deficiency resulting from microbial competition within the BMC, making this method advantageous for large-scale biofuel production [74]. While some microalgae species like *T. maculata* exhibit relatively low lipid concentrations, others like *Schizochytrium* sp. boast lipid concentrations exceeding 80% [141]. Blending BMC biomass with palm oil is suggested for use as biofuel due to its low monounsaturated acid content [142]. Moving forward, proper planning, optimization, and simulation will be essential for reducing operational costs and ensuring sustainable biofuel recovery from BMC cultivated in textile wastewater.

### Resources recycling

The bacterial–microalgal consortium (BMC) can effectively convert phosphorus found in textile effluent into polyphosphate, which finds diverse applications in medicine, biomaterials, and the food industry [131]. The carbon sources present in algal cells can be readily converted into polysaccharides and bio-fats, serving various purposes in disciplines such as pharmacology, diagnostics, and cosmetics [143]. Additionally, the consortium demonstrates a highly efficient mechanism for recovering nitrogen from textile effluent, which can be reused as organic fertilizer or as a substitute for fish feed [129]. Microalgae also serve as excellent sources for producing lipids, carbohydrates, proteins, and other specific biochemicals. Certain microalgae species contain high percentages of fatty acids, such as *C. reinhardtii* with 49.9% and *I. galbana* with 47% fatty acid content [144, 145]. These fatty acids hold potential for nutritional and therapeutic purposes. Examples like *C. stigmatophora* (~55%) and *C. vulgaris* (>52%) highlight microalgae with high carbohydrate contents [146]. Carbohydrates derived from microalgae, aside from serving as a source for alcohol, can be converted into bioplastics and produced using wastewater. Moreover, cyanobacteria produce exopolysaccharides that can be utilized as gelling agents, thickeners, stabilizers, biolubricants, and anti-inflammatory agents. Protein in microalgae primarily exists in the form of amino acids. Species like *S. maxima* and *S. platensis* contain all necessary amino acids in quantities suitable for treating conditions such as diabetes and obesity [147]. Proteins from microalgae or plants can activate cholecystokinin, aiding in lowering cholesterol levels and facilitating human enzymatic processes. Incorporating bacteria into microalgae cultures significantly alters the biochemical composition [148]. For instance, a microalgae–bacteria consortium of *A. brasilense* Cd and *A. protothecoides* UTEX 2341 improved protein content by 40–60% [108]. Similarly, the consortium system of *M. capsulatus* and *C. sorokiniana* enhanced carbohydrates by 42% and lipids

by 15% [149]. However, due to interactions with bacteria, lipid enhancement may occur in the form of extracellular polymeric compounds. Microalgae cultivated in wastewater can serve as a biofertilizer or soil additive, enriching soil nitrogen and phosphorus levels, as well as other trace elements essential for plant growth [66]. The biomass derived from landfill leachate can be directly converted into biofertilizer.

### Animal feed

Microalgae represent a valuable resource for dietary supplements in aquaculture and livestock farming, offering various benefits for animal health and growth. For example, feeding ornamental goldfish with microalgae has been shown to enhance their coloration, while the use of *Nannochloropsis* sp. in finfish hatcheries has resulted in elevated levels of DPA/EPA, essential fatty acids for fish development [150]. Poultry birds, including chickens, ducks, turkeys, and quail, have experienced significant increases in body weight when fed with microalgae. Specifically, feeding chickens with *H. pluvialis*, *N. gaditana*, and *Spirulina* sp. has led to improvements in muscle pigmentation, antioxidant components in the liver, and carotenoid coloration in egg yolks [151].

Astaxanthin, a red pigment found in microalgae, possesses antioxidant properties and offers various health benefits, including cancer prevention and heart disease protection. While synthetic astaxanthin has been traditionally used in farmed salmon feed to achieve the desired pink coloration, concerns over its impurities have led to bans in certain countries. Microalgae like *H. pluvialis* offer a natural alternative, providing salmon with a source of astaxanthin that result in flesh coloration 90 times more intense than synthetic astaxanthin, without any associated toxicity risks [152].

Moreover, the microalgae–bacteria consortium system enhances the aroma of feed, making it more appealing to animals. However, it is important to note that consortium systems often form flocs, which can pose health risks to animals if ingested. Agro-industrial wastewater serves as an ideal substrate for producing animal feed using the microalgae–bacteria consortium, offering a sustainable solution for both waste management and animal nutrition [153].

### Reduced discharge of pollutants

The environmental impact of bacterial–algal consortia lies in their capacity to mitigate the release of pollutants into the environment, particularly heavy metals that pose risks to both human health and ecosystem integrity [132]. While microalgae offer valuable applications in various sectors such as food, medicine, and agriculture, there are limitations to their utilization. Advancements

in biomass utilization research are focused on enhancing the removal of additional heavy metals or persistent substances from economically viable resources [40]. Additionally, the conversion of such biomass into biogas through anaerobic digestion presents a more environmentally friendly solution, as it eliminates direct contact between the biomass and humans, thereby reducing potential health risks.

#### **Reduce greenhouse gas emission**

The rise in carbon dioxide emissions from various sources, particularly industrial activities, has significantly contributed to the greenhouse effect, a leading cause of global warming. Recent studies indicate that atmospheric CO<sub>2</sub> levels have surpassed 400 parts per million (ppm), reaching the highest recorded levels in over 800,000 years [154]. Microalgae play a crucial role in mitigating this issue, as they possess the ability to consume substantial amounts of CO<sub>2</sub> and convert it into chemical energy through photosynthesis. In comparison to terrestrial plants, microalgae exhibit a much higher rate of carbon dioxide fixation, ranging from 10 to 50 times that of their land-based counterparts [45]. Within a bacterial–algal consortium (BMC), the symbiotic relationship between microalgae and bacteria becomes paramount for efficient CO<sub>2</sub> to O<sub>2</sub> exchange, which is essential for algae growth and carbon dioxide fixation. This underscores the importance of photosynthetic microalgae as valuable assets for carbon dioxide sequestration, thereby promoting the advancement of a low-carbon economy and contributing to the reduction of greenhouse gas emissions [134].

#### **Improved treatment efficiency**

Bacteria co-cultured with microalgae play a crucial role by secreting vitamins that enhance the efficiency of bacterial–microalgal consortia (BMCs) and support the specific functions of the microalgal partner. Several studies have highlighted the benefits of co-culturing vitamin B12-dependent microalgae with bacteria, resulting in improved microalgal growth [64]. Moreover, maintaining a mutualistic relationship between microalgae and bacteria has been shown to enhance nitrate consumption and pollutant removal [155]. For instance, mutualisms between *Azospirillum brasilense* and microalgae such as *Scenedesmus*, *Chlorella*, and *Chlamydomonas* have led to increased microalgal populations and biomass, along with improved inorganic carbon fixation [82]. Traditional aeration methods often lead to carbon dioxide stripping and elevated dissolved oxygen levels, both of which hinder microalgae growth. However, employing techniques like algal biofilms or membrane aeration can address these issues, thereby enhancing the efficiency of textile wastewater treatment. In a study by Zhang et al. [70], it

was demonstrated that increasing the CO<sub>2</sub> concentration from 0.04% to 2% resulted in improved algae growth within algal biofilms, ultimately enhancing the BMC efficiency.

#### **Cost-effectiveness**

The economic analysis of BMCs should prioritize the costs and returns associated with recovering valuable products to ensure the cost-effectiveness of this technology. In a study focused on treating piggery biogas slurry, the approximate value of the products generated by the consortium was found to be \$15.06 per kg based on market prices. However, the costs associated with wastewater treatment were approximately \$0.75 per ton, with a biomass production cost of \$0.47 per ton [129]. Algae have the potential to produce compounds applicable in various industries, including biofuels, pharmaceuticals, and agriculture. Similarly, bacteria can produce extracellular polymeric substances (EPS) that facilitate biological flocculation and phosphorus removal in textile effluent [156]. Therefore, if valuable products such as vitamins, biofertilizers, and essential oils can be extracted from the microbial biomass cultivated in textile wastewater using BMC technology, it has the potential to become both cost-effective and sustainable.

#### **Challenges of applying BMC in textile effluent treatment**

Although the role of bacteria in the growth of algae and the treatment of textile effluent is obvious because bacteria provide both growth-promoting signals and the nutrients required, this consortium must overcome the challenge of non-target bacterial blooms in order to be sustainable and stable [117]. In order to implement this technology at commercial level number of challenges need to be addressed as given below:

##### **Inhibition of microalgal growth**

Bacterial biotic stress can significantly hinder algal growth, particularly in oligotrophic environments where both bacteria and algae compete for essential nutrients such as nitrogen, phosphorus, and various organic molecules present in effluent [48]. Studies have shown that algal bioactivities are often suppressed under phosphorus-deficient conditions because bacteria have a higher efficiency in phosphate absorption compared to microalgae [128]. Similarly, ammonia-oxidizing bacteria can outcompete microalgae for ammonia, leading to a reduction in microalgal growth [111]. However, under specific circumstances, microalgae may prevail over ammonia-oxidizing bacteria for limited phosphorus resources [116]. Moreover, certain bacteria in natural environments can release substances that are detrimental to algae, and

specific bacterial strains have been found to produce inhibitory molecules against algal growth [157]. Bacteria can also disrupt algal microenvironments by lowering pH levels below the optimal neutral or alkaline range for algae. Some nitrifying and plant growth-promoting bacteria can generate acidic substrates, leading to acidification of the culture system and a decrease in chlorophyll content in microalgae [94]. Maintaining the pH of the algal–bacterial consortium at or near 7 has been shown to enhance nitrogen removal and increase chlorophyll-a levels [14].

BMCs may also be susceptible to diseases caused by protozoa, fungi, or zooplankton. Investigation into algae extracts revealed the presence of antifungal substances such as phenolic and carotenoid compounds, although their effectiveness is influenced by various culture parameters such as light exposure, growth stage, and temperature [133]. This suggests that while algae possess some degree of fungal resistance, it may be limited by the overall health of the algae and the environmental conditions in which they are cultivated. Furthermore, the presence of pathogenic bacteria can directly impede algal growth, potentially compromising the algal defense mechanisms and increasing susceptibility to other infections [96].

#### **Parasitic attack on microalgal partner**

Bacteria that parasitize algae have the ability to consume internal substances of algae using enzymes like glucosidases, aminopeptidases, cellulases, alkaline phosphatases, lipase, among others [90]. However, this process raises concerns about the utilization of algal products, as it can potentially reduce biomass yield and compromise its quality [107].

#### **Inhibition of bacterial partner**

Bacteria and microalgae have the ability to inhibit each other's growth and even cause mortality by producing inhibitory metabolites. Yang et al. [134] illustrated that microalgae can generate toxins that impede bacterial growth. Additionally, microalgae produce extracellular secretions such as soluble amino acids and antibiotics, which serve as examples of substances capable of inhibiting or even killing bacteria and pathogens [133].

#### **Impact of wastewater antibiotics on BMC**

The existence of antibiotics in wastewater presents a formidable hurdle for bacterial–microalgal consortia (BMC) employed in wastewater treatment processes. Commonly present in wastewater effluents from pharmaceutical manufacturing, hospitals, and household use, antibiotics can negatively affect the microbial communities within BMC [158]. Research conducted by Liu et al. [159] delved into the repercussions of tetracycline antibiotics on BMC

microbial communities, revealing that exposure to sub-lethal doses of tetracycline resulted in changes to community structure and reduced microbial diversity within the consortia. Additionally, antibiotic exposure has been shown to foster the emergence of antibiotic-resistant bacteria within BMC, potentially compromising the efficiency of wastewater treatment processes and contributing to the spread of antibiotic resistance genes in the environment [160].

In addition to impacting bacterial populations, antibiotics can also adversely affect microalgae within BMC. Studies have indicated that certain antibiotics, such as sulfonamides and fluoroquinolones, can hinder the growth and photosynthetic activity of microalgae, resulting in diminished biomass production and decreased nutrient removal efficiency in BMC. Furthermore, antibiotic-induced stress on microalgae can impair their capacity to produce extracellular polymeric substances (EPS), crucial for biofilm formation and pollutant adsorption in wastewater treatment systems [161].

Overall, the presence of antibiotics in wastewater can substantially alter the structure and function of bacterial–microalgal consortia, posing significant challenges to their effectiveness in wastewater treatment. However, strategies to mitigate the inhibitory effects of antibiotics on BMC include utilizing antibiotic-resistant strains, optimizing treatment processes, and implementing advanced treatment technologies to eliminate antibiotics from wastewater before BMC treatment.

#### **Future perspectives**

The future prospects of BMC in textile effluent management are promising, with several potential developments on the horizon: (a) isolation and development of new bacterial and microalgal strains optimized for bioremediation of textile industry effluent. (b) Utilization of synthetic biology to engineer BMC for enhanced efficiency and specificity towards target pollutants. (c) Scaling up BMC systems from laboratory to pilot and commercial-scale to establish feasibility and economic viability. (d) Bioreactor design and optimization to improve BMC performance in large-scale bioremediation projects. (e) Integration of genetic tools like CRISPR-Cas9 to enhance BMC performance in textile effluent bioremediation. (f) Application of nanotechnology to develop nanomaterials enhancing pollutant uptake, degradation, and BMC colonization. (g) Integration of AI to design BMC systems capable of predicting and adapting to changing environmental conditions for improved performance. (h) Collaboration between academia and industry to develop more efficient and cost-effective BMC-based bioremediation technologies. Technological innovations and multidisciplinary

approaches are expected to drive the future of BMC for textile effluent bioremediation, leading to more efficient and sustainable strategies. With further research and development, BMC could become a valuable tool for mitigating the environmental impact of the textile industry.

## Conclusion

Bacterial–microalgal consortia (BMC) have emerged as a promising solution for remediating textile industry effluent by efficiently removing pollutants and generating value-added products. Recent research trends have focused on optimizing BMC composition and cultivation conditions, exploring novel functionalities, and employing immobilized BMCs for enhanced stability and reusability, thus making them more cost-effective and practical for industrial use. Looking ahead, BMCs are poised to play an increasingly vital role in wastewater treatment, addressing environmental pollution concerns sustainably. Future efforts will likely concentrate on enhancing BMC efficiency and resilience through genetic engineering and synthetic biology methods. Moreover, BMCs' potential to yield high-value commodities like biofuels and nutraceuticals will continue to be investigated for cost-effectiveness. In essence, BMCs offer a promising avenue for textile effluent bioremediation, offering pollutant removal and value-added product generation for a cleaner, more sustainable environment.

## Acknowledgements

The authors would like to acknowledge the National Mission on Himalayan Studies Project Management Unit (NMHS-PMU) MoEF&CC Govt. of India New Delhi for the financial support this research and Department of Biotechnology HPU Shimla for necessary facilities (grant number: NMHS/2022-23/SG 81/01/280).

## Authors' contributions

Ranju Kumari Rathour and Deepak Sharma Writing original draft. Nitish Sharma and El-Hassan M. Mahmoud Data curation and formal analysis. Pradeep Kumar and Saleem Ullah Investigation and visualization. Arvind Kumar Bhatt, Irshad Ahmad, and Ravi Kant Bhatia Conceptualization, review, and editing.

## Funding

All sources of funding for the research reported.

## Availability of data and materials

No datasets were generated or analysed during the current study.

## Declarations

### Ethics approval and consent to participate

Not applicable.

### Consent for publication

Not applicable.

### Competing interests

The authors declare no competing interests.

## Author details

<sup>1</sup>Department of Biotechnology, Himachal Pradesh University, Shimla H.P. 171005, India. <sup>2</sup>Department of Biotechnology, Chandigarh Group of Colleges, Mohali, Punjab 140307, India. <sup>3</sup>Biomaterial Processing and Products, VTT Technical Research Centre of Finland Ltd, P.O. Box 1000, N02044 VTT, Espoo, Finland. <sup>4</sup>Department of Bioengineering, King Fahd University of Petroleum and Minerals (KFUPM), 31261 Dhahran, Saudi Arabia. <sup>5</sup>Centre of Innovative and Applied Bioprocessing (CIAB) Sector 81, Sahibzada Ajit Singh Nagar, Mohali Punjab 140306, India. <sup>6</sup>Department of Forensic Sciences, Himachal Pradesh University, Shimla H.P. 171005, India. <sup>7</sup>Interdisciplinary Research Center for Membranes and Water Security, King Fahd University of Petroleum and Minerals (KFUPM), 31261 Dhahran, Saudi Arabia.

Received: 1 April 2024 Accepted: 25 April 2024

Published online: 17 June 2024

## References

- Kumar D, Patel Z, Pandit P, Pandit R, Patel A, Joshi M, et al. Textile industry wastewaters from Jetpur, Gujarat, India, are dominated by *Shewanellaceae*, *Bacteroidaceae*, and *Pseudomonadaceae* harboring genes encoding catalytic enzymes for textile dye degradation. *Front Environ Sci* 2021;9. <https://doi.org/10.3389/fenvs.2021.720707>
- Singh AK, Bilal M, Iqbal HMN, Raj A. Lignin peroxidase in focus for catalytic elimination of contaminants—a critical review on recent progress and perspectives. *Int J Biol Macromol*. 2021;177:58–82. <https://doi.org/10.1016/j.jbiomac.2021.02.032>.
- Chen X, Ning X, Lai X, Wang Y, Zhang Y, He Y. Chlorophenols in textile dyeing sludge: pollution characteristics and environmental risk control. *J Hazard Mater*. 2021;416:125721. <https://doi.org/10.1016/j.jhazmat.2021.125721>.
- Chowdhary P, More N, Yadav A, Bharagava RN. Ligninolytic enzymes: an introduction and applications in the food industry. *Enzymes Food Biotechnol* 2019;181–95. <https://doi.org/10.1016/b978-0-12-813280-7.00012-8>
- Wu X, Xiang X, Dong X, Chai G, Song Z, Wang Y, et al. Profitable wastewater treatment by directly recovering organics for volatile fatty acids production. *J Water Proc Eng*. 2021;40:101881. <https://doi.org/10.1016/j.jwpe.2020.101881>.
- Raza ZA, Khalil S, Ayub A, Banat IM. Recent developments in chitosan encapsulation of various active ingredients for multifunctional applications. *Carbohydr Res*. 2020;492:108004. <https://doi.org/10.1016/j.carres.2020.108004>.
- Vipul G, Kant BN, Kumar RR. Remediation of chlorophenolic compounds from paper mill effluent using high-quality activated carbon from mixed plastic waste. *Water Air Soil Pollut* 2021;232. <https://doi.org/10.1007/s11270-021-05266-1>
- Nagarajan D, Lee D-J, Varjani S, Lam SS, Allakhverdiev SI, Chang J-S. Microalgae-based wastewater treatment-microalgae-bacteria consortia, multi-omics approaches and algal stress response. *Sci Total Environ*. 2022;845: 157110. <https://doi.org/10.1016/j.scitotenv.2022.157110>.
- Wu J-Y, Lay C-H, Chen C-C, Wu S-Y, Zhou D, Mohamed Abdula P. Textile wastewater bioremediation using immobilized *Chlorella* sp. Wu-G23 with continuous culture. *Clean Technol Environ Policy*. 2020;23:153–61. <https://doi.org/10.1007/s10098-020-01847-6>.
- Adane T, Adugna AT, Alemayehu E. Textile industry effluent treatment techniques. *J Chem*. 2021;2021:1–14. <https://doi.org/10.1155/2021/5314404>.
- Sabbar Y, Din A, Kiouach D. Predicting potential scenarios for wastewater treatment under unstable physical and chemical laboratory conditions: a mathematical study. *Results Phys*. 2022;39:105717. <https://doi.org/10.1016/j.rinp.2022.105717>.
- Musa MA, Idrus S. Physical and biological treatment technologies of slaughterhouse wastewater: a review. *Sustainability*. 2021;13:4656. <https://doi.org/10.3390/su13094656>.
- Madhav S, Ahamad A, Singh P, Mishra PK. A review of textile industry: wet processing, environmental impacts, and effluent treatment methods. *Environ Qual Manage*. 2018;27:31–41. <https://doi.org/10.1002/tqem.21538>.



14. Liang C-Z, Sun S-P, Li F-Y, Ong Y-K, Chung T-S. Treatment of highly concentrated wastewater containing multiple synthetic dyes by a combined process of coagulation/flocculation and nanofiltration. *J Membr Sci.* 2014;469:306–15. <https://doi.org/10.1016/j.memsci.2014.06.057>.
15. Pirzadeh B. Physical wastewater treatment. *Wastewater Treatm.* 2022. <https://doi.org/10.5772/intechopen.104324>.
16. Zhang Y, Shaad K, Vollmer D, Ma C. Treatment of textile wastewater using advanced oxidation processes—a critical review. *Water.* 2021;13:3515. <https://doi.org/10.3390/w13243515>.
17. Hutagalung SS, Muchlis I, Khotimah K. Textile wastewater treatment using advanced oxidation process (AOP). *IOP Confer Ser: Mater Sci Eng.* 2020;722:012032. <https://doi.org/10.1088/1757-899x/722/1/012032>.
18. Lotito AM, Fratino U, Bergna G, Di Iaconi C. Integrated biological and ozone treatment of printing textile wastewater. *Chem Eng J.* 2012;195–196:261–9. <https://doi.org/10.1016/j.cej.2012.05.006>.
19. Sala M, Gutiérrez-Bouzáán MC. Electrochemical techniques in textile processes and wastewater treatment. *Int J Photoenergy.* 2012;2012:1–12. <https://doi.org/10.1155/2012/629103>.
20. Sanghamitra P, Mazumder D, Mukherjee S. Treatment of wastewater containing oil and grease by biological method—a review. *J Environ Sci Health Part A.* 2021;56:394–412. <https://doi.org/10.1080/10934529.2021.1884468>.
21. Ngo ACR, Tischler D. Microbial degradation of azo dyes: approaches and prospects for a hazard-free conversion by microorganisms. *Int J Environ Res Public Health.* 2022;19:4740. <https://doi.org/10.3390/ijerph19084740>.
22. Rathour RK, Sharma V, Rana N, Bhatia RK, Bhatt AK. Bioremediation of simulated textile effluent by an efficient bio-catalyst purified from a novel *Pseudomonas fluorescens* LIP-RL5. *Curr Chem Biol.* 2020;14:128–39. <https://doi.org/10.2174/2212796814666200406100247>.
23. Kiran, Rathour RK, Bhatia RK, Rana DS, Bhatt AK, Thakur N. Fabrication of thermostable and reusable nanobiocatalyst for dye decolorization by immobilization of lignin peroxidase on graphene oxide functionalized MnFe<sub>2</sub>O<sub>4</sub> superparamagnetic nanoparticles. *Bioresource Technology.* 2020;317:124020. <https://doi.org/10.1016/j.biortech.2020.124020>.
24. Yaseen DA, Scholz M. Textile dye wastewater characteristics and constituents of synthetic effluents: a critical review. *Int J Environ Sci Technol.* 2018;16:1193–226. <https://doi.org/10.1007/s13762-018-2130-z>.
25. Kehinde F, Aziz HA. Textile waste water and the advanced oxidative treatment process, an overview. *Int J Innov Res Sci Eng Technol.* 2014;03:15310–7. <https://doi.org/10.15680/ijirset.2014.0308034>.
26. Ghaly A, Ananthashankar R, Alhattab M, Ramakrishnan V. Production, characterization and treatment of textile effluents: a critical review. *Chem Eng Proc Technol J.* 2014;5:1–18. <https://doi.org/10.4172/2157-7048.1000182>.
27. Islam MR, Mostafa MG. Characterization of textile dyeing effluent and its treatment using polyaluminum chloride. *Appl Water Sci* 2020;10. <https://doi.org/10.1007/s13201-020-01204-4>
28. Mubashar M, Naveed M, Mustafa A, Ashraf S, Shehzad Baig K, Alamri S, et al. Experimental investigation of *Chlorella vulgaris* and *Enterobacter* sp. MN17 for decolorization and removal of heavy metals from textile wastewater. *Water.* 2020;12:3034. <https://doi.org/10.3390/w12113034>.
29. Zafar S, Bukhari DA, Rehman A. Azo dyes degradation by microorganisms—an efficient and sustainable approach. *Saudi J Biol Sci.* 2022;29:103437. <https://doi.org/10.1016/j.sjbs.2022.103437>.
30. Rathour RK, Sharma D, Sharma N, Bhatt AK, Singh SP. Engineered microorganisms for bioremediation. *Curr Dev Biotechnol Bioeng* 2022:335–61. <https://doi.org/10.1016/b978-0-323-88504-1.00002-9>
31. Khoo KS, Chia WY, Chew KW, Show PL. Microalgal-bacterial consortia as future prospect in wastewater bioremediation, environmental management and bioenergy production. *Indian J Microbiol.* 2021. <https://doi.org/10.1007/s12088-021-00924-8>.
32. Ortiz-Marquez JCF, Do Nascimento M, Zehr JP, Curatti L. Genetic engineering of multispecies microbial cell factories as an alternative for bioenergy production. *Trends Biotechnol.* 2013;31:521–9. <https://doi.org/10.1016/j.tibtech.2013.05.006>.
33. Morsy SAGZ, Ahmad Tajudin A, Ali MohdSM, Shariff FMohd. Current development in decolorization of synthetic dyes by immobilized laccases. *Front Microbiol* 2020;11. <https://doi.org/10.3389/fmicb.2020.572309>
34. Raza N, Rizwan M, Mujtaba G. Bioremediation of real textile wastewater with a microalgal-bacterial consortium: an eco-friendly strategy. *Biomass Convers Bioref.* 2022;14:7359–71. <https://doi.org/10.1007/s13399-022-03214-5>.
35. Samo TJ, Kimbrel JA, Nilson DJ, Pett-Ridge J, Weber PK, Mayali X. Attachment between heterotrophic bacteria and microalgae influences symbiotic microscale interactions. *Environ Microbiol.* 2018;20:4385–400. <https://doi.org/10.1111/1462-2920.14357>.
36. Perera IA, Abinandan S, Subashchandrabose SR, Venkateswarlu K, Naidu R, Megharaj M. Advances in the technologies for studying consortia of bacteria and cyanobacteria/microalgae in wastewaters. *Crit Rev Biotechnol.* 2019;39:709–31. <https://doi.org/10.1080/07388551.2019.1597828>.
37. de Bashan LE, Mayali X, Bebout BM, Weber PK, Detweiler AM, Hernandez J-P, et al. Establishment of stable synthetic mutualism without co-evolution between microalgae and bacteria demonstrated by mutual transfer of metabolites (NanoSIMS isotopic imaging) and persistent physical association (Fluorescent in situ hybridization). *Algal Res.* 2016;15:179–86. <https://doi.org/10.1016/j.algal.2016.02.019>.
38. Li X, Li S, Xie P, Chen X, Chu Y, Chang H, Sun J, Li Q, Ren N, Ho SH. Advanced wastewater treatment with microalgal- indigenous bacterial interactions. *Environ Sci Ecotechnol.* 2024;1(20):100374. <https://doi.org/10.1016/j.ese.2023.100374>.
39. Sial A, Zhang B, Zhang A, Liu K, Imtiaz SA, Yashir N. Microalgal-bacterial synergistic interactions and their potential influence in wastewater treatment: a review. *BioEnergy Res.* 2020;14:723–38. <https://doi.org/10.1007/s12155-020-10213-9>.
40. Mu R, Jia Y, Ma G, Liu L, Hao K, Qi F, et al. Advances in the use of microalgal-bacterial consortia for wastewater treatment: community structures, interactions, economic resource reclamation, and study techniques. *Water Environ Res.* 2021;93:1217–30. <https://doi.org/10.1002/wer.1496>.
41. Venkata Mohan S, Rohit MV, Chiranjeevi P, Chandra R, Navaneeth B. Heterotrophic microalgae cultivation to synergize biodiesel production with waste remediation: progress and perspectives. *Biores Technol.* 2015;184:169–78. <https://doi.org/10.1016/j.biortech.2014.10.056>.
42. Sörenson E, Capo E, Farnelid H, Lindehoff E, Legrand C. Temperature stress induces shift from co-existence to competition for organic carbon in microalgae-bacterial photobioreactor community-enabling continuous production of microalgal biomass. *Front Microbiol* 2021;12. <https://doi.org/10.3389/fmicb.2021.607601>
43. Makut BB, Das D, Goswami G. Production of microbial biomass feedstock via co-cultivation of microalgae-bacteria consortium coupled with effective wastewater treatment: a sustainable approach. *Algal Res.* 2019;37:228–39. <https://doi.org/10.1016/j.algal.2018.11.020>.
44. Yang J, Gou Y, Fang F, Guo J, Lu L, Zhou Y, et al. Potential of wastewater treatment using a concentrated and suspended algal-bacterial consortium in a photo membrane bioreactor. *Chem Eng J.* 2018;335:154–60. <https://doi.org/10.1016/j.cej.2017.10.149>.
45. Xu X, Gu X, Wang Z, Shatner W, Wang Z. Progress, challenges and solutions of research on photosynthetic carbon sequestration efficiency of microalgae. *Renew Sustain Energy Rev.* 2019;110:65–82. <https://doi.org/10.1016/j.rser.2019.04.050>.
46. Lee J, Lee J, Shukla SK, Park J, Lee TK. Effect of algal inoculation on COD and nitrogen removal, and indigenous bacterial dynamics in municipal wastewater. *J Microbiol Biotechnol.* 2016;26:900–8. <https://doi.org/10.4014/jmb.1512.12067>.
47. Babatsouli P, Fodelianakis S, Paranychianakis N, Venieri D, Dialynas M, Kalogerakis N. Single stage treatment of saline wastewater with marine bacterial-microalgae consortia in a fixed-bed photobioreactor. *J Hazard Mater.* 2015;292:155–63. <https://doi.org/10.1016/j.jhazmat.2015.02.060>.
48. Wang L, Liu J, Zhao Q, Wei W, Sun Y. Comparative study of wastewater treatment and nutrient recycle via activated sludge, microalgae and combination systems. *Biores Technol.* 2016;211:1–5. <https://doi.org/10.1016/j.biortech.2016.03.048>.
49. Charriá-Girón E, Amazo V, De Angulo D, Hidalgo E, Villegas-Torres MF, Baganz F, et al. Strategy for managing industrial anaerobic sludge through the heterotrophic cultivation of *Chlorella sorokiniana*: effect of iron addition on biomass and lipid production. *Bioengineering.* 2021;8:82. <https://doi.org/10.3390/bioengineering8060082>.

50. Valderrama LT, Del Campo CM, Rodríguez CM, de Bashan LE, Bashan Y. Treatment of recalcitrant wastewater from ethanol and citric acid production using the microalgae *Chlorella vulgaris* and the macrophyte *Lemna minuscula*. *Water Res.* 2002;36:4185–92. [https://doi.org/10.1016/S0043-1354\(02\)00143-4](https://doi.org/10.1016/S0043-1354(02)00143-4).
51. Gonçalves AL, Pires JCM, Simões M. A review on the use of microalgal consortia for wastewater treatment. *Algal Res.* 2017;24:403–15. <https://doi.org/10.1016/j.algal.2016.11.008>.
52. Ashraf N, Ahmad F, Lu Y. Synergy between microalgae and microbiome in polluted waters. *Trends Microbiol.* 2023;31:9–21. <https://doi.org/10.1016/j.tim.2022.06.004>.
53. Wang Y, Wang S, Sun L, Sun Z, Li D. Screening of a *Chlorella*-bacteria consortium and research on piggery wastewater purification. *Algal Res.* 2020;47:101840. <https://doi.org/10.1016/j.algal.2020.101840>.
54. Perera IA, Abinandan S, Subashchandrabose SR, Venkateswarlu K, Cole N, Naidu R, Megharaj M. Extracellular polymeric substances drive symbiotic interactions in bacterial-microalgal consortia. *Microb Ecol.* 2022;83:596–607. <https://doi.org/10.1007/s00248-021-01772-1>.
55. Higgins BT, Gennity I, Fitzgerald PS, Ceballos SJ, Fiehn O, VanderGheynst JS. Algal-bacterial synergy in treatment of winery wastewater. *Npj Clean Water* 2018;1. <https://doi.org/10.1038/s41545-018-0005-y>
56. Cooper MB, Kazamia E, Helliwell KE, Kudahl UJ, Sayer A, Wheeler GL, et al. Cross-exchange of B-vitamins underpins a mutualistic interaction between *Ostreococcus tauri* and *Dinoroseobacter shibae*. *ISME J.* 2018;13:334–45. <https://doi.org/10.1038/s41396-018-0274-y>.
57. Palacios OA, Gomez-Anduro G, Bashan Y, de Bashan LE. Tryptophan, thiamine and indole-3-acetic acid exchange between *Chlorella sorokiniana* and the plant growth-promoting bacterium *Azospirillum brasilense*. *FEMS Microbiol Ecol.* 2016;92:fiw077. <https://doi.org/10.1093/femsec/fiw077>.
58. Chan SS, Khoo KS, Chew KW, Ling TC, Show PL. Recent advances biodegradation and biosorption of organic compounds from wastewater: microalgae-bacteria consortium-a review. *Biores Technol.* 2022;344:126159. <https://doi.org/10.1016/j.biortech.2021.126159>.
59. Chia SR, Chew KW, Leong HY, Ho S-H, Munawaroh HSH, Show PL. CO<sub>2</sub> mitigation and phycoremediation of industrial flue gas and wastewater via microalgae-bacteria consortium: possibilities and challenges. *Chem Eng J.* 2021;425:131436. <https://doi.org/10.1016/j.cej.2021.131436>.
60. Lachnit T, Blümel M, Imhoff J, Wahl M. Specific epibacterial communities on macroalgae: phylogeny matters more than habitat. *Aquat Biol.* 2009;5:181–6. <https://doi.org/10.3354/ab00149>.
61. Jia H, Yuan Q. Removal of nitrogen from wastewater using microalgae and microalgae-bacteria consortia. *Cogent Environ Sci.* 2016;2:1275089. <https://doi.org/10.1080/23311843.2016.1275089>.
62. Tang X, He LY, Tao XQ, Dang Z, Guo CL, Lu GN, et al. Construction of an artificial microalgal-bacterial consortium that efficiently degrades crude oil. *J Hazard Mater.* 2010;181:1158–62. <https://doi.org/10.1016/j.jhazmat.2010.05.033>.
63. González-González LM, de Bashan LE. Toward the enhancement of microalgal metabolite production through microalgae-bacteria consortia. *Biology.* 2021;10:282. <https://doi.org/10.3390/biology10040282>.
64. Grant MAA, Kazamia E, Cicuta P, Smith AG. Direct exchange of vitamin B12 is demonstrated by modelling the growth dynamics of algal-bacterial cocultures. *ISME J.* 2014;8:1418–27. <https://doi.org/10.1038/ismej.2014.9>.
65. Lépinay A, Turpin V, Mondeguer F, Grandet-Marchant Q, Capioux H, Baron R, et al. First insight on interactions between bacteria and the marine diatom *Haslea ostrearia*: algal growth and metabolomic fingerprinting. *Algal Res.* 2018;31:395–405. <https://doi.org/10.1016/j.algal.2018.02.023>.
66. Das S, Das S, Ghangrekar MM. Quorum-sensing mediated signals: a promising multi-functional modulators for separately enhancing algal yield and power generation in microbial fuel cell. *Biores Technol.* 2019;294:122138. <https://doi.org/10.1016/j.biortech.2019.122138>.
67. Amin SA, Hmelo LR, van Tol HM, Durham BP, Carlson LT, Heal KR, et al. Interaction and signalling between a cosmopolitan phytoplankton and associated bacteria. *Nature.* 2015;522:98–101. <https://doi.org/10.1038/nature14488>.
68. Fei C, Ochsenkühn MA, Shibl AA, Isaac A, Wang C, Amin SA. Quorum sensing regulates 'swim-or-stick' lifestyle in the phycosphere. *Environ Microbiol.* 2020;22:4761–78. <https://doi.org/10.1111/1462-2920.15228>.
69. Seymour JR, Amin SA, Raina J-B, Stocker R. Zooming in on the phycosphere: the ecological interface for phytoplankton-bacteria relationships. *Nat Microbiol* 2017;2. <https://doi.org/10.1038/nmicrobiol.2017.65>
70. Zhang C, Li Q, Fu L, Zhou D, Crittenden JC. Quorum sensing molecules in activated sludge could trigger microalgae lipid synthesis. *Biores Technol.* 2018;263:576–82. <https://doi.org/10.1016/j.biortech.2018.05.045>.
71. Li Q, Gu P, Zhang H, Luo X, Zhang J, Zheng Z. Response of submerged macrophytes and leaf biofilms to the decline phase of *Microcystis aeruginosa*: antioxidant response, ultrastructure, microbial properties, and potential mechanism. *Sci Total Environ.* 2020;699:134325. <https://doi.org/10.1016/j.scitotenv.2019.134325>.
72. Subashchandrabose SR, Krishnan K, Gratton E, Megharaj M, Naidu R. Potential of fluorescence imaging techniques to monitor mutagenic PAH uptake by microalgae. *Environ Sci Technol.* 2014;48:9152–60. <https://doi.org/10.1021/es500387v>.
73. Sátiro J, Cunha A, Gomes AP, Simões R, Albuquerque A. Optimization of microalgae-bacteria consortium in the treatment of paper pulp wastewater. *Appl Sci.* 2022;12:5799. <https://doi.org/10.3390/app12125799>.
74. Biswas T, Bhushan S, Prajapati SK, Ray CS. An eco-friendly strategy for dairy wastewater remediation with high lipid microalgae-bacterial biomass production. *J Environ Manage.* 2021;286:112196. <https://doi.org/10.1016/j.jenvman.2021.112196>.
75. Cho HU, Kim YM, Park JM. Enhanced microalgal biomass and lipid production from a consortium of indigenous microalgae and bacteria present in municipal wastewater under gradually mixotrophic culture conditions. *Biores Technol.* 2017;228:290–7. <https://doi.org/10.1016/j.biortech.2016.12.094>.
76. Kou S, Cheng D, Sun F, Hsing I-M. Microfluidics and microbial engineering. *Lab Chip.* 2016;16:432–46. <https://doi.org/10.1039/c5lc01039j>.
77. Kim S, Moon JH, Jung GY. Recent progress in the development of droplet-based microfluidic technologies for phenotypic screening using cell-cell interactions. *Biotechnol Bioprocess Eng.* 2022;28:929–35. <https://doi.org/10.1007/s12257-022-0081-1>.
78. Westerwalbesloh C, Brehl C, Weber S, Probst C, Widzowski J, Grünberger A, et al. A microfluidic photobioreactor for simultaneous observation and cultivation of single microalgal cells or cell aggregates. *PLoS ONE.* 2019;14:e0216093. <https://doi.org/10.1371/journal.pone.0216093>.
79. Syed MS, Raféie M, Vandamme D, Asadnia M, Henderson R, Taylor RA, et al. Selective separation of microalgae cells using inertial microfluidics. *Biores Technol.* 2018;252:91–9. <https://doi.org/10.1016/j.biortech.2017.12.065>.
80. Suleiman M, Zecher K, Yücel O, Jagmann N, Philipp B. Inter-kingdom cross-feeding of ammonium from marine methylamine-degrading bacteria to the diatom *Phaeodactylum tricorutum*. *Appl Environ Microbiol.* 2016;82:7113–22. <https://doi.org/10.1128/aem.01642-16>.
81. Su Y, Zhang Y, Wang J, Zhou J, Lu X, Lu H. Enhanced bio-decolorization of azo dyes by co-immobilized quinone-reducing consortium and anthraquinone. *Biores Technol.* 2009;100:2982–7. <https://doi.org/10.1016/j.biortech.2009.01.029>.
82. Choix FJ, López-Cisneros CG, Méndez-Acosta HO. *Azospirillum brasilense* increases CO<sub>2</sub> fixation on microalgae *Scenedesmus obliquus*, *Chlorella vulgaris*, and *Chlamydomonas reinhardtii* cultured on high CO<sub>2</sub> concentrations. *Microb Ecol.* 2018;76:430–42. <https://doi.org/10.1007/s00248-017-1139-z>.
83. Kumar G, Zhen G, Kobayashi T, Sivagurunathan P, Kim SH, Xu KQ. Impact of pH control and heat pre-treatment of seed inoculum in dark H<sub>2</sub> fermentation: a feasibility report using mixed microalgae biomass as feedstock. *Int J Hydrogen Energy.* 2016;41:4382–92. <https://doi.org/10.1016/j.ijhydene.2015.08.069>.
84. Li W, Podar M, Morgan-Kiss RM. Ultrastructural and single-cell-level characterization reveals metabolic versatility in a microbial eukaryote community from an ice-covered Antarctic lake. *Appl Environ Microbiol.* 2016;82:3659–70. <https://doi.org/10.1128/aem.00478-16>.
85. Paul C, Pohnert G. Interactions of the Algalicidal Bacterium *Kordia algicida* with diatoms: regulated protease excretion for specific algal lysis. *PLoS ONE.* 2011;6:e21032. <https://doi.org/10.1371/journal.pone.0021032>.
86. Durham BP, Sharma S, Luo H, Smith CB, Amin SA, Bender SJ, et al. Cryptic carbon and sulfur cycling between surface ocean plankton. *Proc Natl Acad Sci.* 2014;112:453–7. <https://doi.org/10.1073/pnas.1413137112>.

87. Scognamiglio V, Giardi MT, Zappi D, Touloupakis E, Antonacci A. Photoautotrophs–bacteria co-cultures: advances, challenges and applications. *Materials*. 2021;14:3027. <https://doi.org/10.3390/ma14113027>.
88. Krohn-Molt I, Alawi M, Förstner KU, Wiegandt A, Burkhardt L, Indenbirken D, et al. Insights into microalga and bacteria interactions of selected phycosphere biofilms using metagenomic, transcriptomic, and proteomic approaches. *Front Microbiol* 2017;8. <https://doi.org/10.3389/fmicb.2017.01941>
89. Ji X, Luo X, Zhang J, Huang D. Effects of exogenous vitamin B12 on nutrient removal and protein expression of algal-bacterial consortium. *Environ Sci Pollut Res*. 2020;28:15954–65. <https://doi.org/10.1007/s11356-020-11720-0>.
90. Hoeger A-L, Jehmlich N, Kipping L, Griehl C, Noll M. Associated bacterial microbiome responds opportunistic once algal host *Scenedesmus vacuolatus* is attacked by endoparasite *Amoebaophelidium protococcarum*. *Sci Rep* 2022;12. <https://doi.org/10.1038/s41598-022-17114-1>
91. Chen T, Zhao Q, Wang L, Xu Y, Wei W. Comparative metabolomic analysis of the green microalga *Chlorella sorokiniana* cultivated in the single culture and a consortium with bacteria for wastewater remediation. *Appl Biochem Biotechnol*. 2017;183:1062–75. <https://doi.org/10.1007/s12010-017-2484-6>.
92. Fan J, Chen Y, Zhang TC, Ji B, Cao L. Performance of *Chlorella sorokiniana*-activated sludge consortium treating wastewater under light-limited heterotrophic condition. *Chem Eng J*. 2020;382:122799. <https://doi.org/10.1016/j.cej.2019.122799>.
93. Mandal SK, Singh RP, Patel V. Isolation and characterization of exopolysaccharide secreted by a toxic dinoflagellate, *Amphidinium carterae* Hulbert 1957 and its probable role in harmful algal blooms (HABs). *Microb Ecol*. 2011;62:518–27. <https://doi.org/10.1007/s00248-011-9852-5>.
94. Kim B-H, Ramanan R, Cho D-H, Oh H-M, Kim H-S. Role of Rhizobium, a plant growth promoting bacterium, in enhancing algal biomass through mutualistic interaction. *Biomass Bioenerg*. 2014;69:95–105. <https://doi.org/10.1016/j.biombioe.2014.07.015>.
95. Unnithan VV, Unc A, Smith GB. Mini-review: a priori considerations for bacteria-algae interactions in algal biofuel systems receiving municipal wastewaters. *Algal Res*. 2014;4:35–40. <https://doi.org/10.1016/j.algal.2013.11.009>.
96. Najdenski HM, Gigova LG, Iliev II, Pilarski PS, Lukavský J, Tsvetkova IV, et al. Antibacterial and antifungal activities of selected microalgae and cyanobacteria. *Int J Food Sci Technol*. 2013;48:1533–40. <https://doi.org/10.1111/ijfs.12122>.
97. Helliwell KE, Wheeler GL, Leptos KC, Goldstein RE, Smith AG. Insights into the evolution of vitamin B12 auxotrophy from sequenced algal genomes. *Mol Biol Evol*. 2011;28:2921–33. <https://doi.org/10.3390/ijms20081978>.
98. Stocker R, Seymour JR. Ecology and physics of bacterial chemotaxis in the ocean. *Microbiol Mol Biol Rev*. 2012;76:792–812. <https://doi.org/10.1128/mmb.00029-12>.
99. Zhang H, Gong W, Bai L, Chen R, Zeng W, Yan Z, et al. Aeration-induced CO<sub>2</sub> stripping, instead of high dissolved oxygen, have a negative impact on algae-bacteria symbiosis (ABS) system stability and wastewater treatment efficiency. *Chem Eng J*. 2020;382:122957. <https://doi.org/10.1016/j.cej.2019.122957>.
100. Zhang Z, Chen M, Li J, Zhao B, Wang L. Significance of transparent exopolymer particles derived from aquatic algae in membrane fouling. *Arab J Chem*. 2020;13:4577–85. <https://doi.org/10.1016/j.arabcj.2019.10.004>.
101. Liu ZZ, Zhu JP, Li M, Xue QQ, Zeng Y, Wang ZP. Effects of freshwater bacterial siderophore on *Microcystis* and *Anabaena*. *Biol Control*. 2014;78:42–8. <https://doi.org/10.1016/j.biocontrol.2014.07.010>.
102. Atasoy M, Eyice O, Schnürer A, Cetecioglu Z. Volatile fatty acids production via mixed culture fermentation: revealing the link between pH, inoculum type and bacterial composition. *Biore Technol*. 2019;292:121889. <https://doi.org/10.1016/j.biortech.2019.121889>.
103. Yang Q, Chen L, Hu X, Zhao L, Yin P, Li Q. Toxic effect of a marine bacterium on aquatic organisms and its algicidal substances against *Phaeocystis globosa*. *PLoS ONE*. 2015;10:e0114933. <https://doi.org/10.1371/journal.pone.0114933>.
104. Rajamani S, Bauer WD, Robinson JB, Farrow JM, Pesci EC, Teplitski M, et al. The vitamin riboflavin and its derivative lumichrome activate the LasR bacterial quorum-sensing receptor. *Mol Plant-Microbe Interact*<sup>®</sup>. 2008;21:1184–92. <https://doi.org/10.1094/mpmi-21-9-1184>.
105. Natrah FMI, Kenmegne MM, Wiyoto W, Sorgeloos P, Bossier P, Defoirdt T. Effects of micro-algae commonly used in aquaculture on acyl-homoserine lactone quorum sensing. *Aquaculture*. 2011;317:53–7. <https://doi.org/10.1016/j.aquaculture.2011.04.038>.
106. Hom EFY, Aiyar P, Schaeme D, Mittag M, Sasso S. A chemical perspective on microalgal-microbial interactions. *Trends Plant Sci*. 2015;20:689–93. <https://doi.org/10.1016/j.tplants.2015.09.004>.
107. Kouzuma A, Watanabe K. Exploring the potential of algae/bacteria interactions. *Curr Opin Biotechnol*. 2015;33:125–9. <https://doi.org/10.1016/j.copbio.2015.02.007>.
108. Zhang B, Li W, Guo Y, Zhang Z, Shi W, Cui F, et al. Microalgal-bacterial consortia: from interspecies interactions to biotechnological applications. *Renew Sustain Energy Rev*. 2020;118:109563. <https://doi.org/10.1016/j.rser.2019.109563>.
109. Hu Z, Qi Y, Zhao L, Chen G. Interactions between microalgae and microorganisms for wastewater remediation and biofuel production. *Waste Biomass Valorization*. 2018;10:3907–19. <https://doi.org/10.1007/s12649-018-0325-7>.
110. Liu L, Fan H, Liu Y, Liu C, Huang X. Development of algae-bacteria granular consortia in photo-sequencing batch reactor. *Biore Technol*. 2017;232:64–71. <https://doi.org/10.1016/j.biortech.2017.02.025>.
111. Jiang L, Ji Y, Hu W, Pei H, Nie C, Ma G, et al. Adjusting irradiance to enhance growth and lipid production of *Chlorella vulgaris* cultivated with monosodium glutamate wastewater. *J Photochem Photobiol, B*. 2016;162:619–24. <https://doi.org/10.1016/j.jphotobiol.2016.07.025>.
112. Nie C, Jiang L, Hou Q, Yang Z, Yu Z, Pei H. Heuristic optimization of culture conditions for stimulating hyper-accumulation of biomass and lipid in *Golenkinia SDEC-16*. *Energies*. 2020;13:964. <https://doi.org/10.3390/en13040964>.
113. Ferro L, Colombo M, Posadas E, Funk C, Muñoz R. Elucidating the symbiotic interactions between a locally isolated microalga *Chlorella vulgaris* and its co-occurring bacterium *Rhizobium* sp. in synthetic municipal wastewater. *J Appl Phycol*. 2019;31:2299–310. <https://doi.org/10.1007/s10811-019-1741-1>.
114. Nguyen TDP, Le TVA, Show PL, Nguyen TT, Tran MH, Tran TNT, et al. Biofloculation formation of microalgae-bacteria in enhancing microalgae harvesting and nutrient removal from wastewater effluent. *Biore Technol*. 2019;272:34–9. <https://doi.org/10.1016/j.biortech.2018.09.146>.
115. Mantovani M, Marazzi F, Fornaroli R, Bellucci M, Ficara E, Mezzanotte V. Outdoor pilot-scale raceway as a microalgae-bacteria sidestream treatment in a WWTP. *Sci Total Environ*. 2020;710:135583. <https://doi.org/10.1016/j.scitotenv.2019.135583>.
116. Li H, Xing P, Wu QL. Characterization of the bacterial community composition in a hypoxic zone induced by *Microcystis* blooms in Lake Taihu, China. *FEMS Microbiol Ecol*. 2012;79:773–84. <https://doi.org/10.1111/j.1574-6941.2011.01262.x>.
117. Toyama T, Hanaoka T, Yamada K, Suzuki K, Tanaka Y, Morikawa M, et al. Enhanced production of biomass and lipids by *Euglena gracilis* via co-culturing with a microalga growth-promoting bacterium, *Emticia* sp. EG3. *Biotechnol Biofuels* 2019;12. <https://doi.org/10.1186/s13068-019-1544-2>
118. Ji X, Jiang M, Zhang J, Jiang X, Zheng Z. The interactions of algae-bacteria symbiotic system and its effects on nutrients removal from synthetic wastewater. *Biore Technol*. 2018;247:44–50. <https://doi.org/10.1016/j.biortech.2017.09.074>.
119. Huo S, Kong M, Zhu F, Qian J, Huang D, Chen P, et al. Co-culture of *Chlorella* and wastewater-borne bacteria in vinegar production wastewater: enhancement of nutrients removal and influence of algal biomass generation. *Algal Res*. 2020;45:101744. <https://doi.org/10.1016/j.algal.2019.101744>.
120. O'Neil JM, Davis TW, Burford MA, Gobler CJ. The rise of harmful cyanobacteria blooms: the potential roles of eutrophication and climate change. *Harmful Algae*. 2012;14:313–34. <https://doi.org/10.1016/j.hal.2011.10.027>.
121. Kumsiri B, Pekkoh J, Pathom-aree W, Lumyong S, Pumas C. Synergistic effect of co-culture of microalga and *actinomyces* in diluted chicken manure digestate for lipid production. *Algal Res*. 2018;33:239–47. <https://doi.org/10.1016/j.algal.2018.05.020>.

122. Orandi S, Lewis DM. Biosorption of heavy metals in a photo-rotating biological contactor-a batch process study. *Appl Microbiol Biotechnol*. 2012;97:5113–23. <https://doi.org/10.1007/s00253-012-4316-5>.
123. Barreiro-Vescovo S, González-Fernández C, de Godos I. Characterization of communities in a microalgae-bacteria system treating domestic wastewater reveals dominance of phototrophic and pigmented bacteria. *Algal Res*. 2021;59:102447. <https://doi.org/10.1016/j.algal.2021.102447>.
124. Parakh SK, Praveen P, Loh K-C, Tong YW. Wastewater treatment and microbial community dynamics in a sequencing batch reactor operating under photosynthetic aeration. *Chemosphere*. 2019;215:893–903. <https://doi.org/10.1016/j.chemosphere.2018.10.085>.
125. Cirri E, Pohnert G. Algae-bacteria interactions that balance the planktonic microbiome. *New Phytol*. 2019;223:100–6. <https://doi.org/10.1111/nph.15765>.
126. Arias DM, Uggetti E, García-Galán MJ, García J. Cultivation and selection of cyanobacteria in a closed photobioreactor used for secondary effluent and digestate treatment. *Sci Total Environ*. 2017;587–588:157–67. <https://doi.org/10.1016/j.scitotenv.2017.02.097>.
127. Wang X, Li Z, Su J, Tian Y, Ning X, Hong H, et al. Lysis of a red-tide causing alga, *Alexandrium tamarense*, caused by bacteria from its phycosphere. *Biol Control*. 2010;52:123–30. <https://doi.org/10.1016/j.biocntr.2009.10.004>.
128. Liu H, Zhou Y, Xiao W, Ji L, Cao X, Song C. Shifting nutrient-mediated interactions between algae and bacteria in a microcosm: evidence from alkaline phosphatase assay. *Microbiol Res*. 2012;167:292–8. <https://doi.org/10.1016/j.micres.2011.10.005>.
129. Luo L, Lin X, Zeng F, Luo S, Chen Z, Tian G. Performance of a novel photobioreactor for nutrient removal from piggery biogas slurry: operation parameters, microbial diversity and nutrient recovery potential. *Biores Technol*. 2019;272:421–32. <https://doi.org/10.1016/j.biortech.2018.10.057>.
130. Zhang B, Wang L, Riddicka B, Li R, Able J, Boakye-Boaten N, et al. Sustainable production of algal biomass and biofuels using swine wastewater in North Carolina. *US Sustainability*. 2016;8:477. <https://doi.org/10.3390/su8050477>.
131. Sutapa BM, Dhruvi A, Gopa RB. Pharmacological, pharmaceutical, cosmetic and diagnostic applications of sulfated polysaccharides from marine algae and bacteria. *Afr J Pharm Pharmacol*. 2017;11:68–77. <https://doi.org/10.5897/ajpp2016.4695>.
132. Hamed I. The evolution and versatility of microalgal biotechnology: a review. *Comprehens Rev Food Sci Food Safety*. 2016;15:1104–23. <https://doi.org/10.1111/1541-4337.12227>.
133. Scaglioni PT, Pagnussatt FA, Lemos AC, Nicolli CP, del Ponte EM, Badiale-Furlong E. *Nannochloropsis* sp. and *Spirulina* sp. as a source of antifungal compounds to mitigate contamination by *Fusarium graminearum* species complex. *Current Microbiol*. 2019;76:930–8. <https://doi.org/10.1007/s00284-019-01663-2>.
134. Yang K, Chen Q, Zhang D, Zhang H, Lei X, Chen Z, et al. The algicidal mechanism of prodigiosin from *Hahella* sp. KA22 against *Microcystis aeruginosa*. *Scientific Reports* 2017;7. <https://doi.org/10.1038/s41598-017-08132-5>.
135. Park JBK, Craggs RJ, Shilton AN. Recycling algae to improve species control and harvest efficiency from a high rate algal pond. *Water Res*. 2011;45:6637–49. <https://doi.org/10.1016/j.watres.2011.09.042>.
136. Okoro V, Azimov U, Munoz J, Hernandez HH, Phan AN. Microalgae cultivation and harvesting: growth performance and use of flocculants - a review. *Renew Sustain Energy Rev*. 2019;115:109364. <https://doi.org/10.1016/j.rser.2019.109364>.
137. Zullaikah S, Utomo AT, Yasmin M, Ong LK, Ju YH. Ecofuel conversion technology of inedible lipid feedstocks to renewable fuel. *Adv Eco-Fuels Sustain Environ* 2019;237–76. <https://doi.org/10.1016/b978-0-08-102728-8.00009-7>.
138. Kim T-H, Lee K, Oh B-R, Lee M-E, Seo M, Li S, et al. A novel process for the coproduction of biojet fuel and high-value polyunsaturated fatty acid esters from heterotrophic microalgae *Schizochytrium* sp. ABC101. *Renewable Energy*. 2021;165:481–90. <https://doi.org/10.1016/j.renene.2020.09.116>.
139. Yao L, Gerde JA, Lee S-L, Wang T, Harrata KA. Microalgae lipid characterization. *J Agric Food Chem*. 2015;63:1773–87. <https://doi.org/10.1021/jf5050603>.
140. Chen X, Hu Z, Qi Y, Song C, Chen G. The interactions of algae-activated sludge symbiotic system and its effects on wastewater treatment and lipid accumulation. *Biores Technol*. 2019;292:122017. <https://doi.org/10.1016/j.biortech.2019.12.2017>.
141. Siddiki SKYA, Mofijur M, Kumar PS, Ahmed SF, Inayat A, Kusumo F, et al. Microalgae biomass as a sustainable source for biofuel, biochemical and biobased value-added products: an integrated biorefinery concept. *Fuel*. 2022;307:121782. <https://doi.org/10.1016/j.fuel.2021.121782>.
142. Tighiri HO, Erkuert EA. Biotreatment of landfill leachate by microalgae-bacteria consortium in sequencing batch mode and product utilization. *Biores Technol*. 2019;286:121396. <https://doi.org/10.1016/j.biortech.2019.12.1396>.
143. Majee SB, Avlani D, Biswas GR. Pharmacological, pharmaceutical, cosmetic and diagnostic applications of sulfated polysaccharides from marine algae and bacteria. *Afr J Pharm Pharmacol*. 2017;5:68–77. <https://doi.org/10.5897/AJPP2016.4695>.
144. Yaakob MA, Mohamed RMSR, Al-Gheethi A, Aswathnarayana Gokare R, Ambati RR. Influence of nitrogen and phosphorus on microalgal growth, biomass, lipid, and fatty acid production: an overview. *Cells*. 2021;10:393. <https://doi.org/10.3390/cells10020393>.
145. Zarrinmehar MJ, Farhadian O, Heyrati FP, Keramat J, Koutra E, Kornaros M, et al. Effect of nitrogen concentration on the growth rate and biochemical composition of the microalgae, *Isochrysis galbana*. *Egypt J Aquat Res*. 2020;46:153–8. <https://doi.org/10.1016/j.ejar.2019.11.003>.
146. Maltsev Y, Maltseva K. Fatty acids of microalgae: diversity and applications. *Rev Environ Sci Bio/Technol*. 2021;20:515–47. <https://doi.org/10.1007/s11157-021-09571-3>.
147. Ramos-Romero S, Torrella JR, Pagès T, Viscor G, Torres JL. Edible microalgae and their bioactive compounds in the prevention and treatment of metabolic alterations. *Nutrients*. 2021;13:563. <https://doi.org/10.3390/nu13020563>.
148. Levasseur W, Perré P, Pozzobon V. A review of high value-added molecules production by microalgae in light of the classification. *Biotechnol Adv*. 2020;41:107545. <https://doi.org/10.1016/j.biotechadv.2020.107545>.
149. Rasouli Z, Valverde-Pérez B, D'Este M, De Francis D, Angelidaki I. Nutrient recovery from industrial wastewater as single cell protein by a co-culture of green microalgae and methanotrophs. *Biochem Eng J*. 2018;134:129–35. <https://doi.org/10.1016/j.bej.2018.03.010>.
150. Aditya L, Mahlia TMI, Nguyen LN, Vu HP, Nghiem LD. Microalgae-bacteria consortium for wastewater treatment and biomass production. *Sci Total Environ*. 2022;838:155871. <https://doi.org/10.1016/j.scitotenv.2022.155871>.
151. Abd El-Hack ME, Abdel-Moneim A-ME, Shehata AM, Mesalam NM, Salem HM, El-Saadony MT, et al. Microalgae applications in poultry feed. *Handbook of Food and Feed from Microalgae* 2023:435–50. <https://doi.org/10.1016/b978-0-323-99196-4.00008-5>.
152. Torregrosa-Crespo J, Montero Z, Fuentes J, Reig García-Galbís M, Garbayo I, Vilchez C, et al. Exploring the valuable carotenoids for the large-scale production by marine microorganisms. *Mar Drugs*. 2018;16:203. <https://doi.org/10.3390/md16060203>.
153. Sakarika M, Spanoghe J, Sui Y, Wambacq E, Grunert O, Haesaert G, et al. Purple non-sulphur bacteria and plant production: benefits for fertilization, stress resistance and the environment. *Microb Biotechnol*. 2019;13:1336–65. <https://doi.org/10.1111/1751-7915.13474>.
154. Show P, Tang M, Nagarajan D, Ling T, Ooi C-W, Chang J-S. A holistic approach to managing microalgae for biofuel applications. *Int J Mol Sci*. 2017;18:215. <https://doi.org/10.3390/ijms18010215>.
155. Santos CA, Ferreira ME, Lopes da Silva T, Gouveia L, Novais JM, Reis A. A symbiotic gas exchange between bioreactors enhances microalgal biomass and lipid productivities: taking advantage of complementary nutritional modes. *J Industr Microbiol Biotechnol*. 2010;38:909–17. <https://doi.org/10.1007/s10295-010-0860-0>.
156. Zhang Y, Zheng L, Wang S, Zhao Y, Xu X, Han B, et al. Quorum sensing bacteria in the phycosphere of HAB microalgae and their ecological functions related to cross-kingdom interactions. *Int J Environ Res Public Health*. 2021;19:163. <https://doi.org/10.3390/ijerph19010163>.
157. González-Camejo J, Aparicio S, Ruano MV, Borrás L, Barat R, Ferrer J. Effect of ambient temperature variations on an indigenous microalgae-nitrifying bacteria culture dominated by *Chlorella*. *Biores Technol*. 2019;290:121788. <https://doi.org/10.1016/j.biortech.2019.12.1788>.

158. Li S, Chu Y, Xie P, Xie Y, Chang H, Ho SH. Insights into the microalgae-bacteria consortia treating swine wastewater: symbiotic mechanism and resistance genes analysis. *Biores Technol.* 2022;1(349):126892. <https://doi.org/10.1016/j.biortech.2022.126892>.
159. Liu H, Yang Y, Sun H, Zhao L, Liu Y. Effect of tetracycline on microbial community structure associated with enhanced biological N&P removal in sequencing batch reactor. *Biores Technol.* 2018;1(256):414–20. <https://doi.org/10.1016/j.biortech.2018.02.051>.
160. da Silva Rodrigues DA, da Cunha CC, Freitas MG, de Barros AL, e Castro PB, Pereira AR, de Queiroz Silva S, da Fonseca Santiago A, Afonso RJ. Biodegradation of sulfamethoxazole by microalgae-bacteria consortium in wastewater treatment plant effluents. *Sci Total Environ.* 2020;20(749):141441. <https://doi.org/10.1016/j.scitotenv.2020.141441>.
161. Zambrano J, García-Encina PA, Hernández F, Botero-Coy AM, Jiménez JJ, Irusta-Mata R. Kinetics of the removal mechanisms of veterinary antibiotics in synthetic wastewater using microalgae-bacteria consortia. *Environ Technol Innov.* 2023;29:103031. <https://doi.org/10.1016/j.eti.2023.103031>.

### **Publisher's Note**

Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.