

Review

Microalgal Consortia for Waste Treatment and Valuable Bioproducts

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Abstract: Microalgae have been considered a promising and sustainable candidate for wastewater treatment and valuable bioproducts, such as feedstocks for food, nutrients, and energy. However, many challenging bottlenecks, such as low biomass productivity, expensive biomass harvesting techniques, and inefficient extraction of biofuels restrict its large-scale commercial production. Symbiotic relationships between microalgae and bacteria, also known as microalgal consortia, have proven to be effective solutions for mitigating technical and economic limitations. The natural and artificial symbiotic microalgal consortia combine microorganisms with various metabolic activities, which leads to valuable biomass production and the removal of nutrients, pharmaceuticals, and personal care products (PPCP) from wastewater. Many microalgal consortia have been applied for various wastewater treatments with reduced energy costs and higher efficiency in recovering valuable resources. In this study we review the present research status and prospects of microalgal consortia, emphasizing the associated mechanism of microalgal consortia cooperative symbiosis and its studies on diverse environmental and biotechnological applications.

Keywords: microalgal consortia; symbiosis; wastewater treatment; resource recovery; biomass production; biofuel



Citation: Zhu, S.; Higa, L.; Barela, A.; Lee, C.; Chen, Y.; Du, Z.-Y. Microalgal Consortia for Waste Treatment and Valuable Bioproducts. *Energies* **2023**, *16*, 884. <https://doi.org/10.3390/en16020884>

Academic Editor: Dino Musmarra

Received: 2 December 2022

Revised: 30 December 2022

Accepted: 5 January 2023

Published: 12 January 2023



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1. Introduction

Microalgae are prokaryotic (cyanobacteria, which we include with microalgae, unless specifically stated otherwise) or eukaryotic photosynthetic phytoplanktonic microorganisms. They are the indisputable primary producers in the aquatic ecosystem and contribute approximately half of the global net primary productivity [1]. Microalgae have higher photosynthetic efficiency when it comes to converting solar energy into biomass than terrestrial plants. Additionally, microalgae can adapt to various environments, require less water, and have a smaller footprint for cultivation, which makes them an attractive and valuable candidate for commercialized production [2,3]. Most microalgae store a large amount (20–50% cell dry weight) of fixed carbon (CO₂) in the form of neutral lipids, with some strains of *Schizochytrium* sp. accumulating 77% of the dry weight of lipids [4]. Microalgae have been considered a sustainable and renewable alternative for bioenergy production coupled with pollutant removal from wastewater.

Although microalgae have been successfully applied in various commercial applications, it is challenging to maintain microalgal monocultures [5]. Furthermore, a series of challenging bottlenecks, such as costly biomass harvesting, low biomass productivity, and energy-intensive extraction methods, limit its large-scale production [6]. Several studies have explored the potential applications of microalgal consortia and their cooperative interactions, especially in the form of microalgal–bacterial symbiosis. In fact, large-scale cultivation of microalgae is often accompanied by other microbes. These microbes often conversely affect algal growth, boost the accumulation of lipids and carbohydrates,

facilitate microalgal cell wall disruption, and promote microalgal growth flocculation processes [1]. These cocultures could result in the development of robust systems that can resist a complex environment, thereby promoting the effective degradation of nutrients and improved biomass and bioenergy productivities [7,8].

Microalgal consortia, consisting of photosynthetic microalgae and heterotrophic bacteria (microalgal–bacterial consortia), or photosynthetic microorganisms (microalgal consortia), and microalgal–fungi or yeast (Figure 1), can naturally occur or be artificially generated for a unique application [5,7,9,10]. For example, many diatoms inhabit low-nutrient, open ocean water and have a close association with autotrophic N_2 -fixing bacteria (Cyanobacteria) [11]. Watanabe et al. isolated a fungal strain and four bacterial strains from the green algae *Chlorella sorokiniana* IAM C-212 slant culture and found that the fungus *Acremonium*-like hyphomycete KR21-2 and the bacterium *Microbacterium trichotecenolyticum* could promote the growth of *Chlorella*. Interestingly, the chlorophyll content was kept at a high level in the *C. sorokiniana* together with symbionts, while it declined dramatically in pure *C. sorokiniana* culture [12].

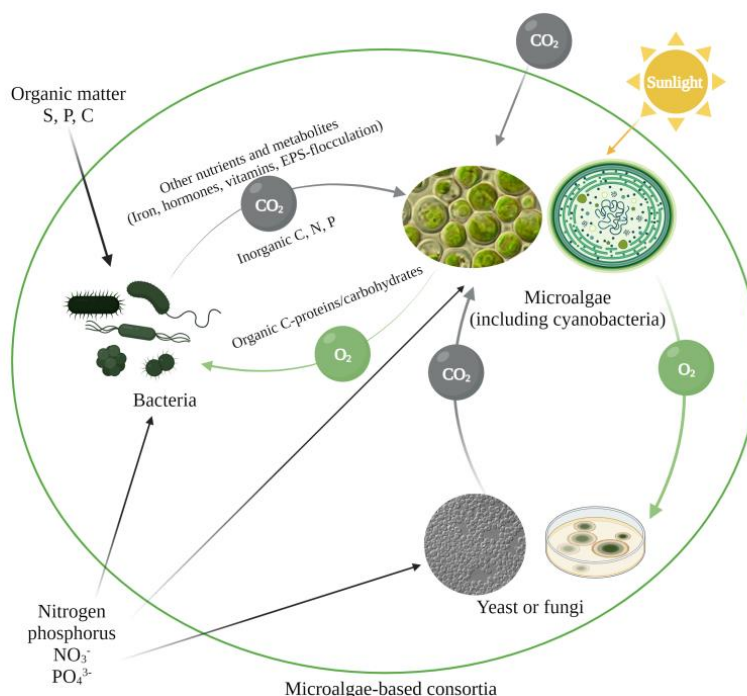


Figure 1. Schematic layout of the symbiotic principle of microalgae-based consortia. Microalgae and cyanobacteria can interact with various microorganisms, such as bacteria, yeast, and fungi. C, carbon; N, nitrogen; P, phosphorus; S, sulfur. (Modified from previous reports [5,13]).

More and more studies have illuminated that algae and bacteria synergistically affect each one's physiology, cytology, and metabolism [14,15], although bacteria have often been considered as a mere contamination of algae cultures during commercialization. In fact, Algae and bacteria have coexisted since the early stages of evolution and interacted with each other in many aspects. In nature, the development of algal blooms is often influenced by many bacteria [16–18]. Depending on the specific species and living requirements, the interactions between microalgae and other microorganisms contain a variety of biological relationships, ranging from mutualism/commensalism to competition/parasitism [19].

Many studies have elaborated on the advantages of microalgal consortia in terms of survival, nutrient removal, and biomass production against single organisms [20,21]. In fact, microalgal consortia have recently been used to enhance organics and nutrient removal efficiency from wastewater and the enrichment of microalgal biomass for biofuel and high-value-added products. Microalgal-associated bacteria or fungi were also found to improve

the sedimentation of the algae consortia, causing easier harvesting of algal biomass [9,22]. An algal–bacterial symbiosis, composed of wastewater-born filamentous blue-green algae and activated sludge (bacteria), behaved $91.0 \pm 7.0\%$ and $93.5\% \pm 2.5\%$ of nitrogen and phosphorus removal efficiencies with 5:1 (microalgae/sludge) inoculation ratios within 10 days, respectively [23]. On the contrary, the nitrogen, phosphorus, and COD removal with only microalgae or activated sludge were much lower than those microalgal consortia with both of them, indicating the importance of synergistic cooperation between microalgae and activated sludge. The highest sedimentation of microalgal biomass was achieved with the assistance of sludge by the 1:5 (microalgae/sludge) cultures. The immobilization of a microalgal bacterial consortium constituted by the genus of *Chlorella* sp., *Scenedesmus* sp., *Stichococcus* sp., *Phormidium* sp., and the actinobacteria *Rhodococcus* sp., *Kibdelosporangium aridum* onto various solid carriers (capron fibers for algae; ceramics, capon, and wood for bacteria) resulted in the formation of a stable consortium during the degradation of the industrial wastewater, thereby preventing them from being washed off. Additionally, this consortium exhibited effective removal efficiency of phenols, heavy metals (copper, nickel, zinc, manganese, and iron), and chemical oxygen demand [24]. The co-pellets produced by *Aspergillus fumigatus* in association with microalgae *Chlorella protothecoides* and *Tetraselmis suecica* have been used to purify anaerobically digested swine wastewater. It showed more than 73.9% and 55.6% removal efficiency of ammonia and phosphates, respectively [9]. The biomass production of both microalgal consortia yields 1.7- and 1.6-fold increases after 48 h of nutrient uptake.

Several studies have reported the oil degradation potential of microbial communities dominated by phototrophic cyanobacteria such as *Microcoleus chthonoplastes*, *Phormidium corium*, *Oscillatoria salina*, *Plectonema terebrans*, and *Aphanocapsa* sp [25,26]. A stable consortium was gained by culturing the oil-tolerant phototrophic cyanobacteria genus of *Phormidium*, *Oscillatoria*, and *Chroococcus* and the oil-degrading β -proteobacterium *Burkholderia cepacia* in bioreactors. This consortium showed several advantages, including efficient total petroleum hydrocarbon removal, no soluble carbon source requirement, and good sedimentation of biosolids [27].

Concerning microalgal consortia, further studies of the interaction mechanisms help generate promising artificial microalgal consortia to apply for large-scale wastewater treatment and bioproducts. The present review is expected to enhance the understanding of the interaction mechanisms of microalgal consortia. We focus on the promising potential of microalgae-based consortia in wastewater treatment and bioproducts.

2. Mechanism of Microalgal Symbiosis

2.1. Natural Microalgal Consortia Systems

In nature, most microalgae and cyanobacteria are associated with other aerobic or anaerobic microorganisms (Table 1). Even long-term laboratory algal cultures have shown a symbiotic relationship with bacteria [28]. The lichens, which cover more than 6% of the land surface of earth, are a stable, self-supporting, mutualistic natural symbiosis between filamentous fungi and microalgae and/or a cyanobacterium [10,29]. Generally speaking, fungi consume the sugars and nutrients produced by the photosynthetic microalgae and/or cyanobacterium; in return, fungi offer protection to microalgae via retaining water, extending a larger capture region for mineral nutrients [30]. More than one-fifth of the known fungal genus is shown to be lichenized, coexisting in a close (obligate) mutualistic association with photoautotrophic microalgae and/or cyanobacteria [30]. For example, green-algal lichen (*Trebouxia* sp., *Ramalina yasudae*) showed increased tolerance to photoinhibition under drying conditions due to the association of the photobionts with the mycobionts [31]. The detailed interaction mechanisms between fungi and microalgae remain unclear. Still, it is universally accepted that the interaction between oppositely charged surfaces may prompt microalgae to attach to the fungal cell wall [9,32].

Table 1. Some examples of microalgal consortia in nature.

Microalgal Consortia in Nature	Types of Microalgal Consortia	Reference
Lichens	Microalgae–fungi	[33]
Microalgal mats or biofilms: microalgae such as diatoms, cyanobacteria, and anoxygenic phototrophic bacteria and sulfate-reducing bacteria	Microalgae–bacteria	[34]
Algal blooms	Microalgae and microalgae–bacteria	[17,35]
Diatom <i>Epithemia turgida</i> and the coccoid cyanobacteria <i>Rhopalodia gibba</i>	Microalgae–cyanobacteria	[36]
Diatom <i>Hemiaulus</i> , <i>Rhizosolenia</i> , <i>Chaetoceros</i> , and N ₂ fixing cyanobacteria <i>R. intracellularis</i> and <i>C. rhizosoleniae</i>	Microalgae–cyanobacteria	[11,37,38]
Microalgae (<i>Microcystis aeruginosa</i> , etc.) and bacteria (<i>E. coli</i> , <i>Pseudomonas</i> sp., and <i>Bacillus</i> sp., etc.): phosphorus transfer	Microalgae–bacteria	[39]
Microalgae (<i>Stichococcus</i> sp., <i>Chlorella</i> sp., and <i>S. quadricauda</i>), cyanobacteria (<i>Phormidium</i> sp., and <i>Nostoc</i> sp.), and alcanotrophic bacteria	Microalgae/Cyanobacteria–bacteria	[40]

Nitrogen-fixing cyanobacterium can transform atmospheric nitrogen into fixed nitrogen, such as ammonia, that other microorganisms could directly absorb without nitrogen-fixing ability. *Richelia intracellularis* and *Calothrix rhizosoleniae* have been proven to provide nitrogen to several diatom genera with a close symbiotic association [38].

2.2. Interaction between Microalgae and Microalgal–Bacteria Consortia

Although an axenic microalgal culture can be achieved, it is impractical to maintain an aseptic microalgal culture in a large-scale culture system, especially in outdoor open ponds. Nutrient availability, cultivation conditions, and growth phase significantly affect their relationships. Microalgal biofilms, intact or attached to solid surfaces, represent micro-ecosystems with typical photosynthetic microorganisms (green microalgae, diatoms, cyanobacteria) along with some non-photosynthetic microorganisms, especially the bacteria which are almost always present and have been proven essential for microalgal biofilm formation [10,41]. Microalgal biofilms can be found in a wide range of natural environments, including estuaries, lagoons, and sheltered sandy beaches. The majority of those microalgal biofilms secrete a sticky self-produced matrix of extracellular polymeric substance (EPS) adhering to each other and/or to a surface [34]. To some extent, the EPS matrix also acts as a storage compartment for water and other chemicals and protects the cells against harmful chemicals or the environment [34].

Little attention has been paid to the consortia formed by microalgae and other microorganisms, such as other microalgae species, cyanobacteria, fungi, and yeast. Several studies showed that heterotrophic bacteria play a ubiquitous role in algal growth and survival [42,43]. Occasionally, bacteria stimulate algal growth via supplying fixed nitrogen, releasing phytohormones and exogenous sources of thiamin (vitamin B₁), cobalamin (vitamin B₁₂), biotin (vitamin B₇), and siderophores (important chelating agents for microalgal growth under iron deficiency), while microalgae may also release organic sources, such as carbohydrates, that bacteria could utilize as an energy source [7,44–50]. The microalga *Amphidinium operculatum* was reported to exclusively gain the vitamin cobalamin from the bacteria belonging to the genus *Halomonas* living in microalgal proximity [45]. The green alga *Chlamydomonas reinhardtii* was protected from heat stress with the presence of cobalamin-producing bacteria [47]. It has also been discovered that some genus bacteria can generate antibiotics to protect microalgae against other microorganisms (mutualism/commensalism) or for algal cell lysis (parasitism, regulation of algal blooms) [51]. In addition to direct nutrient exchange, bacteria also produce AHLs (*N*-acyl-homoserine lactones) and indole-3-acetic acid (IAA), specific chemical signals, to become involved in biofilm formation and mediate collective behaviors and ecological functions between microalgae and bacteria cells, such as environmental niche formation, nutrient absorption, and reproduction [1,52].

Interactions between microorganisms in consortia are not well understood. It is widely believed that growing microorganisms in a consortium may cause both cooperative and

competitive interactions. Occasionally, some genus algicidal bacteria may generate toxic metabolites, called phycotoxins, inhibiting the growth of microalgae; in turn, some members of microalgae families (*Prasinophyceae* and *Bacillariophyceae*, etc) may produce exotoxins (such as various fatty acids, glycosides, chlorellin, terpenes, and chlorophyll α derivatives) to kill bacteria [53,54]. A similar situation also occurs in multiple algal composition consortia. For instance, when growing a microalgal consortium composed of *Pseudokirchneriella subcapitata* and *Chlorella vulgaris*, *P. subcapitata* was significantly inhibited by chlorellin, a fatty acid mixture excreted by the co-cultivated algae *C. vulgaris* [55]. Antagonistic interactions play an essential role in establishing and maintaining the microalgal consortia symbiosis [6].

3. Algal Symbiosis Enhances Stress Resilience and Tolerance

Compared to a single taxon, microalgal consortia have been proven resilient when they encounter adverse conditions and resist invasion from other microorganisms [5,56]. Table 2 shows stress resilience and tolerance enhanced in some microalgal consortia. A balanced competition within the microalgal consortia is more robust in the event of environmental flux and prevents other microorganisms from readily plundering nutrients [5,56].

Table 2. Stress resilience and tolerance enhanced in microalgal consortia.

Microalgal Consortia	Effects	Reference
Microalgae (<i>Stichococcus</i> sp., <i>Chlorella</i> sp., and <i>S. quadricauda</i>), cyanobacteria (<i>Phormidium</i> sp., and <i>Nostoc</i> sp.), and alcanotrophic bacteria	High resistance to various toxicants; stimulate algae cell growth	[40]
Green algae <i>C. sorokiniana</i> and four bacteria (salicylate-degrading <i>R. basilensis</i> , phenol-degrading <i>A. haemolyticus</i> , and phenanthrene-degrading <i>P. migulae</i> and <i>S. yanoikuyae</i>)	Have an excellent tolerance to toxic compounds and could efficiently biodegrade these three pollutants (up to 85%)	[57–59]
Microalga <i>Ulothrix gigas</i> , fungi <i>Geotrichum</i> sp. and <i>Aspergillus</i> sp., and bacteria <i>Pseudomonas</i> sp. and <i>Thiobacillus</i> sp.	Survive under acidic (pH 3–5) and heavy-metal contaminated conditions	[60]
Lichen (<i>Trebouxia</i> sp., <i>R. yasudae</i>)	Increase tolerance to photoinhibition under drying conditions	[31]

Most natural cyanobacteria/microalgae and bacteria in extreme habitats, such as deserts, exist as consortia that provide robustness and extensive metabolic capabilities, thereby enabling them to generate tight relationships. Most of them can tolerate harsh and rapidly fluctuating environmental situations, intense ultraviolet radiation, and lack of water [61]. In the Antarctic sea-ice, algae and bacteria coexist to resist extreme environments, such as low temperature, low light, high UV-radiation, and even low nutrients [62]. The microalgae (*Stichococcus* sp., *Chlorella* sp., and *Scenedesmus quadricauda*) and cyanobacteria (*Phormidium* sp., and *Nostoc* sp.) in combination with alcanotrophic bacteria, originating from soils and water bodies with oil spills, were observed tolerant against increased amounts of toxicants and were able to survive on the medium containing 1% black oil. The alcanotrophic bacteria could restore the reproductivity in algae sensitive to black oil and stimulate cell growth in tolerant algae [40]. In fact, the cyanobacteria seem not to degrade petroleum compounds but more likely play an important role in biodegradation by supporting the growth and activity of the actual degraders [63]. The microalgal–bacteria consortia comprising the green algae *C. sorokiniana* and four bacteria (phenol-degrading *Acinetobacter haemolyticus*, salicylate-degrading *Ralstonia basilensis*, and phenanthrene-degrading *Pseudomonas migulae* and *Sphingomonas yanoikuyae*) have excellent tolerance to toxic compounds. They could efficiently biodegrade these three pollutants (up to 85%) [57–59].

4. Algal Symbiosis Promotes Development

As shown in Table 3, microalgal consortia usually exchange nutrients such as oxygen, vitamins, nitrogen, and carbon during coexistence, which helps to improve biomass productivity and quality [64]. The combination between *Chlorella ellipsoidea* and *Brevundimonas*

sp. was found to lengthen the exponential growth stage and caused a 50-fold increase in biomass production [28]. The bacterium genus *Pseudomonas* sp., *Bacillus* sp., *Azospirillum* sp., *Acinetobacter* sp., *Rhodococcus* sp., and the activated sludge were proposed as plant growth-promoting bacteria, which were adequate to enhance microalgae growth [65–67]. In particular, the coexistence and interactions between microalgae and bacteria have shown positive enhancement in microalgae biomass production. Bacteria affect the abundance and growth of associated microalgae and vice versa. The freshwater microalga *Chlorella* spp. showed increased growth parameters, including pigment, lipid variety and content, and cell or population size, with *Azospirillum brasilense*, a microalgae-growth-promoting bacterium [14,15]. The biomass production of a consortium containing 15 native microalgal isolates reached approximately 9.2–17.8 tons ha⁻¹ year⁻¹ using wastewater containing 85–90% carpet industry effluents with 10–15% municipal sewage as substrates [68]. The microalgal consortia of *Chlorella variabilis* and *Scenedesmus obliquus* yielded 673 mg L⁻¹ biomass using dairy wastewater as substrate with a specific growth rate of 0.75 day⁻¹ under cool-white, fluorescent light. The chlorophyll and lutein contents were also enhanced by approximately 9.3 mg L⁻¹ and 7.22 mg L⁻¹, respectively [69]. The biomass and net photosynthetic activity of a consortium of *S. obliquus* and *Candida tropicalis* were increased by 30.3% and 61%, respectively, compared with *S. obliquus* alone [70].

Table 3. The biomass production of microalgal consortia.

Microalgal Consortia	Substrate	Yield/Productivity Monoculture	Consortia	Reference
<i>C. variabilis</i> , <i>S. obliquus</i>	Dairy wastewater	NA	0.673 g L ⁻¹	[69]
<i>Haematococcus pluvialis</i> , <i>Phaffia rhodozyma</i> AS2-1557	Synthetic medium	0.62 g L ⁻¹ , 5.02 g L ⁻¹	5.70 g L ⁻¹	[71]
<i>Chlorella</i> sp., <i>Acutodesmus</i> sp., and <i>Scenedesmus</i> sp.	Municipal wastewater	NA	117.1 mg L ⁻¹ d ⁻¹	[72]
<i>Scenedesmus</i> sp. YC001, <i>Flavobacteria</i> sp., <i>Sphingobacteria</i> sp., <i>Proteobacteria</i> sp	Municipal wastewater	NA	282.6 mg L ⁻¹ d ⁻¹	[73]
<i>S. obliquus</i> , <i>C. tropicalis</i>	BG11 medium	3.5 g L ⁻¹ , NA	4.38 g L ⁻¹	[70]
<i>Spirulina platensis</i> UTEX 1926, <i>Rhodotorula glutinis</i> 2.541	Synthetic medium	0.20 g L ⁻¹ , 1.7 g L ⁻¹	3.67 g L ⁻¹	[74]
<i>Phormidium</i> sp., <i>Limnothrix</i> sp., <i>Anabaena</i> sp., <i>Westiellopsis</i> sp., <i>Fischerella</i> sp., <i>Spirogyra</i> sp.	Sewage wastewater	NA	1.07 g L ⁻¹	[75]
<i>Botryococcus</i> sp., <i>Chlorella</i> sp., <i>Cricosphaera</i> ., <i>Dunaliella</i> sp., <i>Nannochloris</i> sp., <i>Spirulina</i> sp., <i>Tetraselmis</i> sp., <i>Phaeodactylum</i> sp.	Carpet mill effluents	NA	1.47 g L ⁻¹	[68]
<i>S. obliquus</i> , <i>Acutodesmus obliquus</i> , <i>C. sorokiniana</i> and <i>C. vulgaris</i>	Bark-hydrolysate fermentation effluents	NA	139 mg L ⁻¹ d ⁻¹	[76]
MAC1 (<i>Chlorella</i> sp., <i>Nannochloropsis</i> sp., <i>Scenedesmus bijugatus</i> , <i>C. reinhardtii</i> , and <i>Oscillatoria</i>)	Municipal wastewater	NA	1.53 g L ⁻¹ , 1.04 g L ⁻¹	[77]
MAC2 (<i>Chlorella</i> sp., <i>Nannochloropsis</i> sp., <i>Scenedesmus dimorphus</i> , <i>Kirchmella</i> , and <i>Microcoleus</i>)	Municipal wastewater	NA	1.53 g L ⁻¹ , 1.04 g L ⁻¹	[77]
<i>Isochrysis galbana</i> and <i>Ambrosiozyma cicatricosa</i>	Synthetic medium with seawater	1.17 g L ⁻¹ , 0.17 g L ⁻¹	1.32 g L ⁻¹	[78]
<i>C. vulgaris</i> var. <i>vulgaris</i> TISTR 8261 and <i>Trichosporonoides spathulata</i>	Crude glycerol-based medium	0.75 g L ⁻¹ , 10.23 g L ⁻¹	11.85 g L ⁻¹	[79]

NA: not available.

5. Applications of Microalgal Consortia for Waste Treatment

5.1. Wastewater Treatment

Increasing anthropogenic activities have caused excessive disposal of wastes into water bodies, thus destroying water quality and aquatic ecosystems. Those wastewaters, including agricultural, industrial, and municipal wastewater, are an unbalanced mixture of organic and inorganic compounds causing eutrophication and deterioration of aquatic ecosystems. The main task of wastewater purification is to effectively reduce the proportion of nutrients and chemical oxygen demand (COD) before reusing or returning that wastewater to the environment. Conventional aerobic activated sludge or anaerobic wastewater treatment processes have economic and technical restrictions due to their high energy requirements and lower nutrient removal efficiency [80,81]. For example, an aeration procedure may occupy 45–75% of the energy consumption of wastewater treatment [82].

5.1.1. High-Value Products

Numerous studies have shown that microalgal consortia (especially the microalgal–bacterial consortia) in wastewater treatment presented higher biodegradation efficiency of complex substrates and resource recovery with high resistance to environmental condition oscillations [13,83–85]. The complex interactions between microalgae and bacteria in wastewater treatment are not yet fully understood. Generally speaking, photosynthetic microalgae could effectively absorb and utilize nutrients, including phosphorus, nitrogen, and organic matter from municipal wastewater, into their biomass as cell constituents and release exogenous oxygen to realize the requirements of most aerobic bacteria. In return, most of the heterotrophic bacteria could also oxidize organic carbon and release CO₂, which microalgae could consume as an autotrophic carbon source, thereby improving the purification efficiency of wastewater (Figure 1) [7,86–88]. Meanwhile, numerous studies have reported that high-value-added products, including pigments, nutraceuticals, and lipids, as well as animal feeds and gas biofuels, such as CH₄ and H₂, could be gained concomitantly with wastewater treatment by microalgal consortia processes depending on the type of wastewater treated and the culture conditions (Figure 2) [56,89–92]. Additionally, the concept of an algal bio-refinery with wastewater treatment allows for the increased utilization of microalgal biomass when applied to biofuel production as well as allowing for long-term economic viability and the reduction in residuary wastes associated with wastewater treatment [93]. During microalgal–bacterial consortia wastewater treatment processes, it was observed that bacteria release EPS that mediate their aggregation with various microalgae [1,22,94].

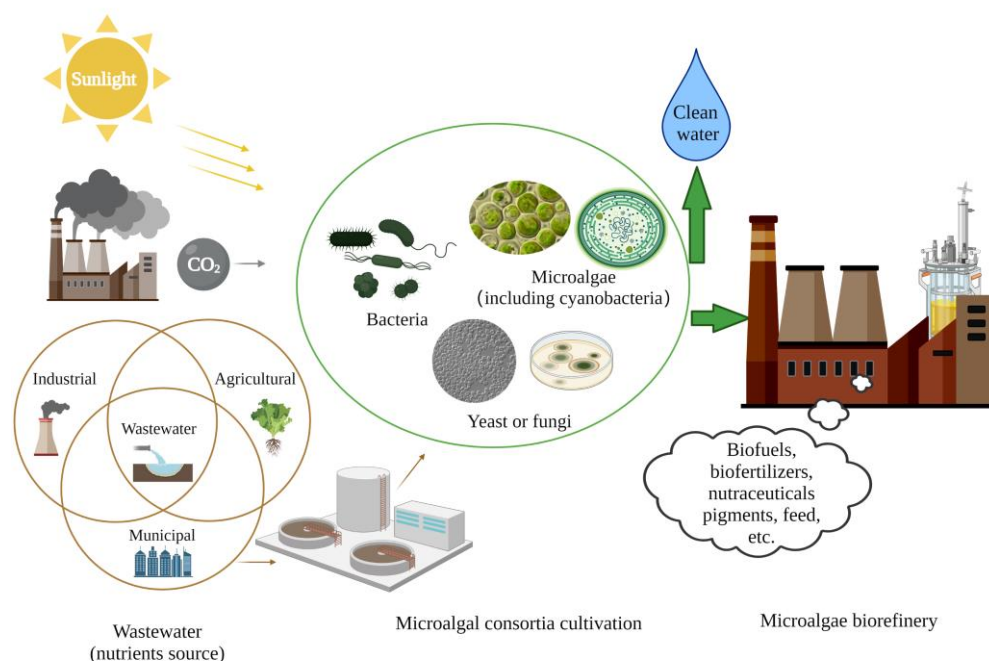


Figure 2. Microalgal consortia in wastewater treatment. Microalgal consortia (center) can be used to treat various wastewater (left) for clean water and valuable products, such as biofuels, biofertilizers, nutraceuticals, pigments, and feed (right).

5.1.2. Nutrient Removal

Several studies regarding the nutrient removal efficiency of microalgal consortia under various cultivation conditions are shown in Table 4. It was reported that the *C. vulgaris*–*A. brasilense* consortia immobilized in alginate significantly removed ammonium and soluble phosphorus ions from synthetic wastewater [65]. A microalgal–bacterial consortium of *C. vulgaris* and *Bacillus licheniformis* showed apparent removal rates of total nitrogen, ammonium, orthophosphate phosphate, and soluble COD of 88.82%, 84.98%, 84.87%, and 82.25%

on the treatment of municipal water, respectively. Meanwhile, pollutants such as protein substances which are difficult to degrade in natural water, were efficiently degraded along with the nutrient removal process [95]. The co-immobilization consortium of microalga *C. vulgaris* and bacterium *Pseudomonas putida* showed similar removal results of both nutrients and COD than each axenic culture, indicating their mutualistic association [96,97]. In another report, 78% of $\text{NH}_4\text{-N}$ removal efficiency was achieved with an alga *C. vulgaris*/bacterium *B. licheniformis* cell density ratio of 1:1, compared with 63% in the single algal system under the same conditions.

Table 4. Nutrient removal efficiency of microalgal consortia in wastewater treatment.

Microalgae	Bacteria/Fungi	Culture Method	Time (d)	COD Ci	R	Nitrogen Ci	R	Phosphorus Ci	R	References
<i>C. reinhardtii</i> <i>C. vulgaris</i>	NA	Semi-batch	2	45	86	110	97.8	25	92.8	[98]
Blue-green algae	Activated sludge	Batch	8–10	369.7	95.8	47.6	91	8.6	93.5	[23]
<i>Scenedesmus</i> sp. YC001	<i>Flavobacteria</i> <i>Sphingobacteria</i> <i>Proteobacteria</i>	Batch	14	295.5	92.3	40.6	95.8	7.7	98.1	[73]
<i>C. sorokiniana</i>	<i>Pseudomonas</i> H4	Batch	0.25	352 ^a	46	28.3 ^a	71	9.8 ^a	72.8	[99]
<i>C. vulgaris</i>	<i>P. putida</i>	Continuous	1	1159.2	94.2	49.23	96.6	12.83	86.9	[97]
<i>C. vulgaris</i>	<i>P. putida</i>	Batch	2	1159.2	97	49.23	100	12.83	100	[97]
<i>Navicula</i> sp., <i>Nitzschia</i> sp. and <i>Stigeoclonium</i> sp.	Wastewaterborne bacteria	Continuous	10	593	91	71.2	99	15.3	49	[100]
<i>Leptolyngbya</i> sp., <i>Ochromonas</i> sp., and <i>Poteroochromonas</i>	Wastewaterborne bacteria	Batch	14	2650	92.8	48	78.1	5	99	[101]
<i>C. vulgaris</i>	<i>Planktothrix isothrix</i>	Batch	9	NA	NA	79.3	43.9–81.5	7.5	98.4–100	[21]
<i>P. subcapitata</i>	<i>Synechocystis salina</i>	Batch	7	NA	NA	45	72	10	91.8	[102]
<i>M. aeruginosa</i>	<i>S. salina</i>	Batch	7	NA	NA	45	77.7	10	97.2	[102]
<i>C. vulgaris</i>	<i>S. salina</i>	Batch	7	NA	NA	45	84.5	10	85.9	[102]
Chlorophyta sp.	<i>Rhodocyblaceae</i> sp.	Batch	120	600	95	50	99	10	42	[103]
<i>Lyngbya</i> sp., <i>Chlorella</i> sp., <i>Calothrix</i> sp., <i>Ulothrix</i> sp.	-	Batch	14	2150	88.2	83.7	83.3	3.1	97.7	[75]
<i>C. reinhardtii</i> , <i>S. rubescens</i> and <i>C. vulgaris</i>	-	Batch	5–14	NA	NA	52.8–98.7	41.2–100	3.9–11.5	12.2–100	[104]
<i>Chlorella</i> and <i>Phormidium</i>	-	Batch	12	2940	79.9	75	86.7	200	83	[105]
<i>C. protothecoides</i>	<i>A. fumigatus</i>	Batch	2	NA	NA	164.3	73.7	38.7	55.6	[9]
<i>T. suecica</i>	<i>A. fumigatus</i>	Batch	2	NA	NA	168.8	62.1	45	57.8	[9]

Ci: initial concentration (mg L^{-1}); R: removal efficiency (%); NA: not available; a: estimate from the available data.

Interestingly, the removal efficiency of $\text{NH}_4\text{-N}$ rose to 86% by adjusting the pH from acidic (pH 3.5) to neutral [50]. Too high or low pH can affect the growth of algae and bacteria through direct cellular damage and by altering the availability of nutrients [106–108]. Therefore, pH may be a vital factor determining the application of algal–bacteria consortia in wastewater treatment processes, as CO_2 generation and consumption by bacteria and algae lead to an imbalance of pH in the cocultured system. Several other environmental factors, such as dissolved oxygen, light condition, initial inoculums ratios, temperature, etc., significantly affect nutrient removal efficiency [23,50,69,73]. For example, a well-balanced microbial consortium consisting of microalgae (*Scenedesmus* sp. YC001) and bacteria (*Flavobacteria*, *Sphingobacteria*, and *Proteobacteria*) showed the most efficient nutrient removals (92.3% COD, 95.8% TN, 98.1% TP), and the highest dry cell weight and lipid productivity ($282.6 \text{ mg L}^{-1} \text{ day}^{-1}$, $71.4 \text{ mg L}^{-1} \text{ day}^{-1}$) via two-phase photoperiodic operation (12:60 h light–dark cycle followed by 12:12 h cycle) in wastewater treatment, respectively [73].

Compared with the single microalgae for wastewater treatment, researchers have found that multiple algal composition systems can make up for the deficiency of a single algal species through synergistic cooperation. Shi et al. found that two green algae species consortia (*C. vulgaris* and *Scenedesmus rubescens*) could remove phosphate, ammonium, and nitrate to less than 10% of the initial concentration with the immobilization of those two mi-

coalgae on a twin-layer system, thereby comparing well with single alginate-immobilized microalgae [109]. Twelve native microalgae consortia showed removal rates ranging from 74.34 to 91.07% of NO_3^- -N and 60.37 to 79.27% of PO_4^{3-} -P, respectively [110]. Although the multiple microalgal consortia may have a higher removal efficiency of nutrients and could enhance the resistance to various environments, allelopathic competition may exist between different microalgae. The allelochemical chlorellin produced by *C. vulgaris* has inhibitory effects on *P. subcapitata* [55]. Therefore, in order to generate efficient multiple microalgal consortia, it is necessary to understand the interaction mechanism between different microalgae.

5.2. Pharmaceuticals

Pharmaceuticals and personal care products (PPCPs) contain various chemicals, including prescription and non-prescription drugs, illegal drugs, veterinary drugs, cosmetics, etc. [111]. PPCP release into the aquatic environment is unavoidable (marine, rivers, estuaries, lakes, and underground water) due to their wide application. The increasing number of PPCPs found in the atmosphere has raised concerns due to their negative impact on ecosystems and unknown effects on human health [112]. Conventional activated sludge processes [113], advanced oxidation [114], adsorption [115], and membrane separation [116] were commonly used for PPCPs removal from wastewater. However, those methods have their disadvantages.

Microalgae-based remediation, especially the microalgal–bacterial photobioreactor, is an emerging and ecofriendly way to remove PPCPs with greater opportunities for industrial application. A consortium of *C. vulgaris* and *S. obliquus* synergistically and efficiently biotransformed ibuprofen and triclosan [117]. A revolving algal biofilm (RAB) reactor was successfully applied to remove five model PPCP compounds from a waterbody, including ibuprofen, oxybenzone, triclosan, bisphenol A and N, and N-diethyl-3-methylbenzamide (DEET), with 70% to 100% removal efficiencies [118]. The removal of PPCPs was mainly attributed to the degradation by the algae. Meanwhile, the removal efficiencies of nutrients by RAB reactors were not affected by exposure to PPCPs. The multivariate microbial community structure in algal biofilm enhanced the PPCP removal efficiency of the RAB reactor as different microorganisms degrade particular PPCP compounds. Several examples of microalgal consortia for PPCP treatment are summarized in Table 5.

Table 5. Microalgal consortia for PPCP treatment.

Microalgal Consortia	Target Pharmaceutical	Removal Efficiency	Reference
<i>C. vulgaris</i> and <i>S. obliquus</i>	Ibuprofen	Approximately 60%	[117]
<i>C. vulgaris</i> , <i>Pseudonabaena acicularis</i> , <i>Scenedesmus acutus</i> , and activated sludge	Ibuprofen, naproxen, salicylic acid, triclosan and propylparaben	94%, 52%, 98%, 100%, and 100%, respectively.	[119]
<i>Anabaena cylindrica</i> , <i>Chlorococcus</i> , <i>S. platensis</i> , <i>Chlorella</i> , <i>S. quadricauda</i> , and <i>Anaebena</i>	Estrone, 17 β -estradiol, 17 α -ethinylestradiol	83.9%, 91.2%, and 86.8%, respectively.	[120]
<i>C. vulgaris</i> and heterotrophic microorganisms	Tetracycline	69%	[121]
Green algae, diatom and cyanobacteria assemblages (RAB reactors)	Ibuprofen, oxybenzone, triclosan, bisphenol A and N, N-diethyl-3-methylbenzamide (DEET)	70%–100%	[118]
<i>Chlorella</i> sp., and four Gram negative bacteria: <i>Pseudomonas</i> sp., <i>Raoultella ornithinolytica</i> , <i>Pseudomonas aeruginosa</i> , <i>Stenotrophomonas</i> sp	Acetaminophen, aspirin, ketoprofen, salicylic acid	80–100%, 100%, 20–98%, 80–100%, respectively.	[122]
<i>S. obliquus</i> , <i>Chlamydomonas mexicana</i> , <i>C. vulgaris</i> , <i>Ourococcus multisporus</i> , <i>Micractinium resseri</i>	Enrofloxacin	26%	[123]

6. Application of Microalgal Consortia in Biofuels

The energy crisis, increasing fossil fuel prices, and environmental pollution have spurred global attention to seek alternative renewable energy sources, such as bioethanol, biogas, and biodiesel derived from fats and oils by fatty acid methyl transesterification [124].

Currently, commercial crops, such as palm, rapeseed, and soybean, provide the most widely available forms of biofuel [125,126]. However, there are several limitations to this mode of biofuel production as these crops have significant land requirements and are in high demand as a food source. Microalgae are becoming a popular alternative to terrestrial plants and commercial food crops due to their increased photosynthetic rate, oil production, rapid growth rate, carbon sequestration, reduced land, and space requirements, and biomass production [127,128].

Microalgal biomass contains a large quantity of biodegradable compounds, including carbohydrates, lipids, and proteins. Carbohydrates and lipids are major energy storage locations in microalgae and can be used to synthesize a range of biofuels (Figure 3) [129–131]. Overall, algae are easy to cultivate and can grow almost anywhere and only require an aquatic environment, sunlight, and a few simple nutrients [125,126]. Coupled with other organisms, algae consortia provide a pathway to finding usable renewable resources. Table 6 shows some examples of microalgal consortia for biofuel production.

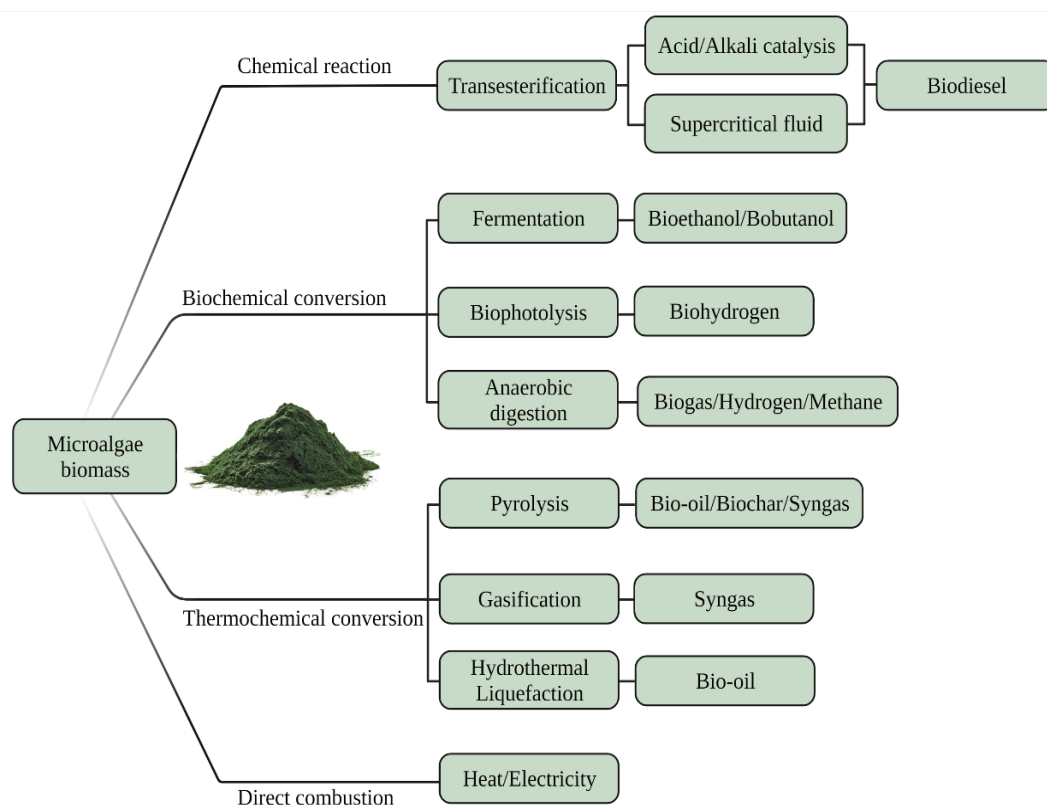


Figure 3. Bioenergy production based on the biomass from microalgal consortia.

Table 6. Microalgal consortia for biofuel production.

Microalgal Consortia	Type of Substrate	Biofuels	References
<i>Scenedesmus</i> sp., <i>Chlorella</i> sp., and activated sludge bacteria	Piggery waste	0.36–0.79 L g ⁻¹ biogas, 0.18–0.44 L g ⁻¹ CH ₄ , 245 ± 19 ppm (v/v) H ₂ S	[132]
<i>Scenedesmus</i> sp., <i>Keratococcus</i> sp., <i>Oscillatoria</i> sp.	Synthetic medium	45 mL H ₂ g ⁻¹ VS, 432 mL CH ₄ g ⁻¹ VS	[90]
<i>Chlamydomonas</i> sp. MACC-549 and hydrogenase-deficient <i>E. coli</i>	Synthetic medium	1196.06 ± 4.42 μL H ₂ L ⁻¹	[133]
<i>C. reinhardtii</i> cc124 and hydrogenase-deficient <i>E. coli</i>	Synthetic medium	5800.54 ± 65.73 μL H ₂ L ⁻¹	[133]
<i>Navicula</i> sp., <i>Nitzschia</i> sp., <i>Stigeoclonium</i> sp., and wastewaterborne bacteria	Municipal wastewater	348 mL CH ₄ g ⁻¹ VS and 56 mL CH ₄ g ⁻¹ VS d ⁻¹	[100]

Table 6. Cont.

Microalgal Consortia	Type of Substrate	Biofuels	References
<i>C. vulgaris</i> , <i>Chloroflexi</i> , <i>Alphaproteobacteria</i> , <i>Betaproteobacteria</i> , <i>Gammaproteobacteria</i> , <i>Deltaproteobacteria</i> , <i>Planctomycea</i>	Municipal wastewater	271.34 ± 6.65 mL CH ₄ g ⁻¹ VS	[134]
<i>Chlorella</i> sp., <i>Phormidium</i> sp.	Rural wastewaters	0.79 m ³ kg CH ₄ VS ⁻¹	[105]
<i>Scenedesmus</i> sp., <i>Chlorella</i> sp.	Urban wastewater	307 mL biogas g ⁻¹ VS	[135]
<i>C. vulgaris</i> , <i>S. obliquus</i> and <i>C. reinhardtii</i>	Piggery wastewater	171 mL CH ₄ g COD ⁻¹	[136]
<i>S. platensis</i> and alkaliphilic H ₂ S-oxidizing bacterial consortium	Anaerobic effluents	0.21–0.27 L CH ₄ g ⁻¹ VS	[137]
<i>Chlorella</i> sp., <i>Scenedesmus</i> sp., and aerobic granular sludge (predominant genera <i>Xanthomonadaceae</i> and <i>Rhodobacteraceae</i>)	Municipal wastewater	Maximum biodiesel yield of 66.21 ± 1.08 mg g ⁻¹ suspended solids with large quantities of polyunsaturated fatty acid methyl ester	[138]
<i>Ulothrix</i> sp., <i>Klebsormidium</i> sp., and anaerobic sludge	Aquaculture wastewater	226 mL CH ₄ g ⁻¹ VS	[139]

VS: volatile solid.

6.1. Biodiesel

Biodiesel is recognized as an ideal recyclable energy carrier. Biodiesel has a reduced emission of carbon monoxide, hydrocarbons, sulfur, aromatic compounds, and particulate matter while performing equally to petroleum diesel [125,127]. The combustion and production of biodiesel in place of nonrenewable diesel reduces greenhouse gas emissions by 41% and yields 93% more energy than the energy invested in its conversion [140]. Additionally, biodiesel has a higher flashpoint, which makes it safer to handle. It has a higher lubricity and is biodegradable [127]. Conventional biodiesel is produced from animal fats or vegetable oils, and this method is unable to meet the growing fuel demands [4,141]. Using microalgae as an alternative oil source in place of animal fats and plant oils in biodiesel production can be a more sustainable solution [125]. Algae contain one of the most energy-dense renewable components in nature, known as triacylglycerols (TAGs), making them an ideal feedstock for biodiesel [127,142]. TAGs can be converted into fatty acid methyl esters via transesterification, which are the main components of biodiesel. In this process, TAGs react with a solvent, usually methanol, to produce the fatty acid methyl esters and glycerol as a byproduct [142–144]. Microalgae are primarily known to produce and accumulate these lipids within their cells and have relatively more significant amounts than terrestrial plants [129,145]. Lipid production in microalgae can be further increased by initiating a stress response through nutrient deprivation, pH changes, and salinity changes [145,146].

Using microalgae as an alternative oil source for biodiesel has its limitations. The low efficiency of conventional microalgae cultivation procedures limits the large-scale production of microalgae biodiesel. To combat this inefficiency, microalgae consortia can be used to improve microalgal culture growth and promote the uptake and conversion of nutrients from wastewater. This can greatly reduce the production cost of environmentally friendly technologies, especially by combining wastewater treatment with biodiesel production. Under nitrogen- or phosphorus-limited conditions, the microalgae accumulated a high lipid content (up to 64% dry cell weight) which could be used for biodiesel production [147–149].

The consortium of the oil-rich microalga *Chlorella pyrenoidosa* and a high-efficient heterotrophic ammonia-oxidizing *Kluyvera* sp. bacterium FN5 showed 91% of the degradation rate of NH₃-N with 0.35g/L and 39.0% of the microalgae biomass and lipid content. The lipids had a satisfactory potential for biodiesel production with 43.9% of the saturated fatty acids, 37.1% of the monounsaturated fatty acids, and 19.0% of the polyunsaturated fatty acids, respectively [150]. A *Leptolyngbya*-based microbial consortium produced exceptional biomass containing approximately 13% lipids (*w/w*) on a dry weight basis when raisin or winery wastewater was used as a substrate. The ratio between saturated and

monounsaturated fatty acids reached approximately 85%, making this consortium suitable for biodiesel production [101]. The *C. sorokiniana* CY-1 co-cultivated with *Pseudomonas* sp. Yielded desirable properties, thus potentially generating high-quality biodiesel [67].

6.2. Biohydrogen

Although biohydrogen is still in the early stages of development, it has drawn significant research attention in recent years and shows potential as a method for producing sustainable hydrogen gas [3,151,152]. However, hydrogen production techniques, such as coal gasification, biomass gasification/pyrolysis, and electrolysis and thermolysis of water, require a significant amount of energy and release pollutants into the environment. In microalgae specifically, maximizing the process of biophotolysis will be a vital step in increasing hydrogen yields [151].

6.2.1. Biohydrogen Production in Algae

Microalgal biohydrogen production occurs in two stages. During the first stage, carbohydrates and lipids produced during photosynthesis are acquired and used as a feedstock for anaerobic digesters in the second stage. During the second stage, anaerobic digestion is utilized to convert carbohydrates and lipids into biohydrogen gas [153]. The most efficient species for this process should be able to quickly metabolize hydrogen at a high rate while keeping stable intracellular conditions to limit the depletion of available glycogen. *Desertifilum* sp. IPPAS B-1220 is shown to be effective in producing hydrogen (Kossalbayev et al., 2020). Many studies have also tested the potential benefits of adding DCMU (3-(3,4-dichlorophenyl)-1,1-dimethylurea) and have found positive results. In light conditions, DCMU is a photosynthesis inhibitor. When added to cyanobacteria, it will increase hydrogen output. When combined with *Desertifilum*, hydrogen production was increased by 1.5 times [154]. *Chlorella* sp. KLA59, a green alga species, has also displayed favorable characteristics for hydrogen production [155]. *C. reinhardtii* is another green alga as a popular option for biohydrogen production [154,156]. These algae, along with *Pseudomonas* sp. can improve hydrogen production. *Pseudomonas* sp. has a high oxygen consumption rate, controlling the amount of oxygen present in the hydrogenase process [156]. When *C. reinhardtii* and *Pseudomonas* sp. are cultured together, the accumulated hydrogen amounts are $\sim 120 \text{ mL L}^{-1} \text{ H}_2$, higher than the pure algae alone [156].

6.2.2. Biohydrogen Production in Algal Consortia

The hydrogenase enzyme activity, which is highly sensitive to oxygen, is the main influencing factor of biohydrogen production by microalgae [133,157,158]. As oxygen is the potent inhibitor of hydrogenase, a strict anaerobic environment is necessary for efficient hydrogen production by microalgae, although algae almost exclusively live in a complex ecosystem interacting with multiple micro- or macroorganisms. Due to oxygen elimination by highly efficient bacterial respiration, the green photoheterotrophic microalga–bacteria consortia can improve biohydrogen production [159]. The most common microalgal–bacterial consortia are often composed of the unicellular green microalga *C. reinhardtii* and various genera of bacterial symbionts, including *Leifsonia*, *Rhodococcus*, *Brevundimonas*, and *Escherichia*. [133].

Compared to bacterial and algal monocultures, most consortia showed enhanced H_2 production yield, rate, and duration. When hydrogenase-deficient *Escherichia coli* was used as a symbiotic bacterium, the *Chlamydomonas* sp. MACC-549 and *C. reinhardtii* cc124 generated the highest hydrogen yields with $1196.06 \pm 4.42 \text{ } \mu\text{L H}_2 \text{ L}^{-1}$ and $5800.54 \pm 65.73 \text{ } \mu\text{L H}_2 \text{ L}^{-1}$, respectively [133]. The yield of hydrogen was 14 times greater, and the growth rate was 26% higher, when the transgenic *C. reinhardtii* strain CC849 strain (lba), was co-cultured with the *Bradyrhizobium japonicum* in Tris-acetate-phosphate (TAP) or TAP-sulfur media, compared with the cultivation of the algae alone under the same conditions [160]. In the future, genetic manipulation techniques can be utilized to potentially increase hydrogen production by microalgal consortia even further [3,161].

Furthermore, many studies have reported that algae strains were used as the organic carbon source utilized by the symbiotic bacterial strains, which ultimately produce hydrogen. Lipid-extracted algal residues have also been found to be an effective substrate in the process of hydrogen fermentation [162]. The starch of *C. reinhardtii* and *Dunaliella tertiolecta* was degraded to lactic acid by *Lactobacillus amylovorus*, which was used as an electron donor for hydrogen production of the photosynthetic bacterium *Rhodobium marinum* A-501 [163,164]. The relationship between *Dunaliella* as a biomass substrate and hyper-thermophilic archaeon *Thermococcus eurythermalis* A501 has been studied using dark fermentation techniques and proved to be an efficient H₂ production mode [162]. Hydrogen, methane, fatty acids, and alcohol are all products of dark fermentation. Additionally, the fatty acids and alcohols produced during dark fermentation reduce carbon dioxide by making electrons and hydrogen available [165]. Together, *Dunaliella primolecta* and *D. tertiolecta* improved hydrogen production compared with previous studies under these conditions [162].

6.3. Bioethanol and Biogas

The microalgae oil can be used for biodiesel, while the residual biomass containing a high carbohydrate content can be fermented into bioethanol and biogas, such as methane and hydrogen sulfide [106]. Carbohydrates are an essential source of energy for most life forms, and algae are able to accumulate high amounts of carbohydrates throughout their lifecycle [142]. These sugars are a carbon source for specific bacteria or yeast, which produce ethanol under anaerobic conditions [130,131]. Similar to lipid production, applying different environmental stress on algae can increase carbohydrate content by altering biochemical pathways [166,167]. Those new energy sources present a promising opportunity to reduce the world's dependence on fossil fuels.

For instance, a native microalgae consortium, comprised of 79% *Scenedesmus* sp., 19% *Keratococcus* sp., 2% *Oscillatoria* sp., and other undetermined species, generated hydrogen and methane at approximately 45 mL H₂ g VS⁻¹ and 432 mL CH₄ g VS⁻¹ under the treatment of thermal-acidic hydrolysis [90]. The high methane yield and production rates (348 mL CH₄ g⁻¹ VS and 56 mL CH₄ g⁻¹ VS d⁻¹) were obtained at 10 d of the hydraulic retention time using a granular microalgal–bacterial system in a high-rate algal pond [100]. Choudhary et al. revealed that the microalgal consortia PA6 containing the dominated microalgal genus *Chlorella* and *Phormidium* was rich in protein (45%) followed by lipids (31%) and carbohydrates (10%) with 0.79 m³ kg VS⁻¹ of theoretical methane potential [105]. This suggests the PA6 microalgal consortia have promising prospects for biogas production.

An advanced micro-bio-loop (AMBL) system, which incorporated producers, consumers, and decomposers (microalgae, anaerobic, and aerobic bacteria) has shaped an independent and sustainable cycling micro-eco-chain. The micro-eco-chain is more energy-efficient, sustainable, and environmentally friendly in producing biogas than the conventional biogas production system (CBPS) [168]. Theoretically, with the addition of sunlight, the AMBL system can create a continuous stream of biogas without requiring any additional external input or generating any internal output to its surroundings. Through the use of the AMBL system, preprocessing and the subsequent treatment of biogas residues can be omitted.

7. Applications of Microalgal Consortia for Value-Added Bioproducts

Microalgal consortia produce a wide variety of products that are useful in several different industries. As shown in Figure 4, algal biomass is commonly used around the world in animal feed ingredients, soil fertilizer, or human nutritional supplementation [169–171]. Table 7 summarizes some examples of microalgal consortia for bioproducts. For instance, a recent study revealed that the protein composition of the *C. variabilis* and *S. obliquus* consortia was higher than the carbohydrate and lipid composition under all wavelengths of light, suggesting their potential application as a protein source for animal feed or an ingredient for nutrient products [69]. Another study demonstrated that the microalgal–

bacterial consortium created in wastewater was effective in both pollutant removal and biomass production, as the biomass produced was composed of nearly 22% crude protein and 70% fatty acids [172]. Su et al. reported a collection of 12 algae–microbial consortia and identified consortia with enhanced essential amino acid content and omega-3 fatty acid composition after mixotrophic cultivation, making it a potential source for animal and/or human supplementation [173]. Moreover, microalgal metabolites are of huge biotechnological potential and are often used for various natural and sustainable pharmaceutical products [174,175].

Table 7. Microalgal consortia in bioproduction.

Microalgal Consortia	Bioproducts	Effects/ Productivity	Reference
MC1 consortia (<i>Chlorella</i> , <i>Scenedesmus</i> , <i>Chlorococcum</i> , <i>Chroococcus</i>)	Biofertilizer	Enhanced plant growth and yield; 7.4–33% increase in plant dry weight and up to 10% in spike weight	[176,177]
MC2 consortia (<i>Phormidium</i> , <i>Anabaena</i> , <i>Westiellopsis</i> , <i>Fischerella</i> , <i>Spirogyra</i>)			
<i>A. oscillarioides</i> CR3, <i>B. diminuta</i> PR7, and <i>O. anthropi</i> PR10	Biofertilizer	Increased nitrogen, phosphorus, and potassium (NPK) content and improved rice yield by 21.2%	[178]
<i>S. platensis</i> , <i>P. stutzeri</i>	Biofertilizer	Enhanced plant growth and yield in onion; 31.5% increase in total net return per hectare	[179]
<i>S. obliquus</i> , <i>A. obliquus</i> , <i>C. sorokiniana</i> and <i>C. vulgaris</i>	Pigments	25.8 mg L ⁻¹ of total chlorophyll and 5.9 mg L ⁻¹ of carotenoids	[76]
<i>C. variabilis</i> , <i>S. obliquus</i>	Pigments	7.22 mg g ⁻¹ of lutein	[69]
<i>H. pluvialis</i> , <i>P. rhodozyma</i> AS2–1557	Pigments	Consortia: 12.95 mg L ⁻¹ of astaxanthin; monoculture: 3.68 mg L ⁻¹ , 1.09 mg L ⁻¹ , respectively	[71]
<i>S. obliquus</i> , <i>C. tropicalis</i>	Pigments	14 µg mL ⁻¹ of chlorophyll a	[70]
MAC1 (<i>Chlorella</i> sp., <i>Nannochloropsis</i> sp., <i>S. bijugatus</i> , <i>C. reinhardtii</i> , and <i>Oscillatoria</i>)	Pigments	19.17–25.17 µg mL ⁻¹ of chlorophyll	[77]
MAC2 (<i>Chlorella</i> sp., <i>Nannochloropsis</i> sp., <i>S. dimorphus</i> , <i>Kirchnella</i> , and <i>Microcoleus</i>)			
<i>Desmodesmus</i> sp. CHX1, <i>Paenibacillus</i> , <i>Thiopseudomonas</i> , and <i>Pseudomonas</i>	Animal feed	21.80% and 69.78% of crude protein and fatty acids	[172]
AC1 (<i>Chlorella</i> , <i>Paludisphaera</i>), AC4 (<i>Chlorella</i> , <i>Colpoda</i> , <i>Synechocystis</i> , <i>Planctomycetota</i> SM1A02), AC5 (<i>Chlorella</i> , <i>Colpoda</i> , <i>Nuclearia</i> , <i>Synechocystis</i>), AC6 (<i>Tetrademus</i> , <i>Colpoda</i> , undetectable composition of prokaryotes). AC11 (<i>Chlorella</i> , <i>Cyclidium</i> , <i>Synechocystis</i> , <i>Planctomycetota</i> SM1A02)	Animal feed, human supplementation	Average protein content of 393 ± 83 g kg ⁻¹ DM, average polyunsaturated fatty acid content of 25.6 ± 7.3% of total lipids	[173]
<i>C. vulgaris</i> LEB106 and <i>Agaricus blazei</i> LPB03	Exopolysaccharides	Consortia: 5.17 g L ⁻¹ ; monoculture: 0.95 g L ⁻¹ , 4 g L ⁻¹ , respectively	[180]
<i>C. vulgaris</i> LEB106 and <i>Trametes versicolor</i> CC124	Exopolysaccharides	Consortia: 7.10 g L ⁻¹ ; monoculture: 0.95 g L ⁻¹ , 4.95 g L ⁻¹ , respectively	[180]
<i>C. vulgaris</i> var. <i>vulgaris</i> TISTR 8261 and <i>T. spathulata</i>	Lipid	47% lipid content; contain higher saturated fatty acids (palmitic acid and stearic acid)	[79]
<i>C. sorokiniana</i> CY-1, <i>Pseudomonas</i> sp.	Lipid	Consortia: 23.37 mg L ⁻¹ d ⁻¹ , monoculture: 15.1 mg L ⁻¹ d ⁻¹ , NA	[67]
<i>Scenedesmus</i> sp. YC001, <i>Flavobacteria</i> sp., <i>Sphingobacteria</i> sp., <i>Proteobacteria</i>	Lipid	71.4 mg L ⁻¹ d ⁻¹	[73]
<i>S. obliquus</i> , <i>C. tropicalis</i>	Lipid	97.8 mg L ⁻¹ d ⁻¹	[70]
<i>S. platensis</i> UTEX 1926, <i>R. glutinis</i> 2.541	Lipid	Consortia: 467 mg L ⁻¹ ; monoculture: 13 mg L ⁻¹ , 135 mg L ⁻¹ , respectively	[74]

NA: not available.

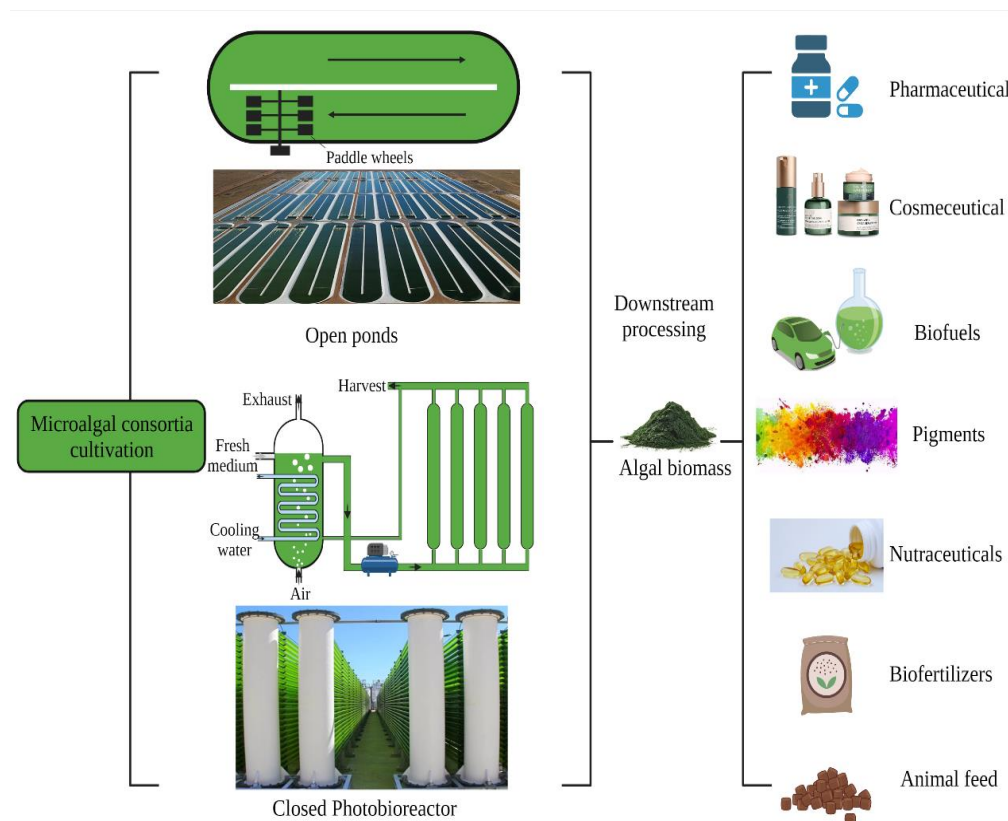


Figure 4. Microalgal consortia cultivation and its potential uses in various industries. Various cultivation systems for microalgal consortia (left) to produce biomass for diverse bioproducts, including pharmaceuticals, cosmeceuticals, biofuels, pigments, nutraceuticals, biofertilizers, and animal feed.

Microalgal biomass contains large quantities of nitrogen, and significantly, many cyanobacteria can fix atmospheric nitrogen. Therefore, such microalgal biomass could serve as biofertilizer after a series of treatments. For example, the wastewater-grown microalgal consortia biomass, produced by the unicellular microalgae consortia MC1 (*Chlorella*, *Scenedesmus*, *Chlorococcum*, *Chroococcus*) and the filamentous microalgae MC2 (*Phormidium*, *Anabaena*, *Westiellopsis*, *Fischerella*, *Spirogyra*), was used as a biofertilizer. Both consortia enhanced the wheat crop (*Triticum aestivum* L. HD2967) productivity and yield, compared with the recommended dose of NPK fertilizers [176]. Similar results were obtained in rice using the consortia of *Anabaena oscillarioides* CR3, *Brevundimonas diminuta* PR7, and *Ochrobactrum anthropi* PR10 [178]. More recently, a study has shown that the application of co-inoculants *Spirulina platensis* and *Pseudomonas stutzeri* enhanced the growth and productivity of onions (*Allium cepa* L.) [179]. Sears and Prithiviraj reported cyanobacteria-based consorcial inoculants named TerraDerm for fertilizing desert soil [181]. These examples provide promising, low-cost, and sustainable biofertilizers for agricultural production using wastewater-grown microalgal consortia biomass.

8. Conclusions and Perspective

Microalgal consortia systems possess more robust contaminant tolerance than single microorganism systems. The present studies have shown that the symbiotic interaction of microbial consortia could result in better survival, nutrient removal, and biomass production compared with processes employing only one phototrophic or heterotrophic microorganism. One of the major limitations of microalgal consortia exploitation is the requirement for cost-effective biomass harvesting techniques [182]. Selection and biometry of the dominant microalgal species in the microalgal consortia with a natural tendency to settle down is an easy way to reduce the production cost of harvesting or separating the microalgal consortia biomass [23,182,183]. From a biotechnological perspective, an

excellent microalgal consortium should be robust, self-sustainable, reproducible, profitable, and versatile in substrate production [5]. Therefore, it is essential to select particular microalgal consortia capable of growing in different wastewaters based on the specific characteristics of the wastewater, improving water quality, and simultaneously producing feedstock for biofuels such as biodiesel, bioethanol, and biomethane. Moreover, further study of the interaction between microalgae and other microorganisms will allow us to generate artificial microalgal consortia for different economic and biological requirements.

Author Contributions: Conceptualization, Z.-Y.D., S.Z. and Y.C.; methodology, Z.-Y.D. and S.Z.; writing—original draft preparation, S.Z., L.H. and C.L.; writing—review and editing, S.Z., L.H., A.B., Y.C. and Z.-Y.D.; supervision, Z.-Y.D. and Y.C.; project administration, Z.-Y.D.; funding acquisition, Z.-Y.D. All authors have read and agreed to the published version of the manuscript.

Funding: This research was funded by USDA National Institute of Food and Agriculture grant number HAW05047-H and National Science Foundation grant number 2121410.

Acknowledgments: Z.D. gratefully acknowledges the USDA National Institute of Food and Agriculture (HATCH project HAW05047-H), College of Tropical Agriculture and Human Resources, University of Hawaii at Manoa (MBBE-2303491), and the National Science Foundation grant number 2121410. C.L. is supported by the Undergraduate Research Opportunities Program at UHM (24680-QWER); L.H. is supported by the NSF grant 2121410. S.Z. and Y.C. also thank the National Key Research and Development Program of China (2018YFD1000500) and China Agriculture Research System (CARS-11-HNCYH).

Conflicts of Interest: The authors declare no conflict of interest.

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