Recent Advances in the Research on the Anticyanobacterial Effects and Biodegradation Mechanisms of *Microcystis aeruginosa* with Microorganisms

Yun Kong 1,2,3,*, Yue Wang 1, Lihong Miao 4, Shuhong Mo 2, Jiake Li 2 and Xing Zheng 2

1 College of Resources and Environment, Yangtze University, Wuhan 430100, China; 2021720590@yangtzeu.edu.cn
2 State Key Laboratory of Eco-Hydraulics in Northwest Arid Region, Xi’an University of Technology, Xi’an 710048, China; moshuhong@xaut.edu.cn (S.M.); xaut_ljk@163.com (J.L.); xingzheng@xaut.edu.cn (X.Z.)
3 Key Laboratory of Water Pollution Control and Environmental Safety of Zhejiang Province, Hangzhou 310058, China
4 School of Biology and Pharmaceutical Engineering, Wuhan Polytechnic University, Wuhan 430023, China; miaowhpu@126.com
* Correspondence: ky020241@hotmail.com; Tel./Fax: +86-27-69111182

**Abstract:** Harmful algal blooms (HABs) have attracted great attention around the world due to the numerous negative effects such as algal organic matters and cyanobacterial toxins in drinking water treatments. As an economic and environmentally friendly technology, microorganisms have been widely used for pollution control and remediation, especially in the inhibition/biodegradation of the toxic cyanobacterium *Microcystis aeruginosa* in eutrophic water; moreover, some certain anticyanobacterial microorganisms can degrade microcystins at the same time. Therefore, this review aims to provide information regarding the current status of *M. aeruginosa* inhibition/biodegradation microorganisms and the acute toxicities of anticyanobacterial substances secreted by microorganisms. Based on the available literature, the anticyanobacterial modes and mechanisms, as well as the in situ application of anticyanobacterial microorganisms are elucidated in this review. This review aims to enhance understanding the anticyanobacterial microorganisms and provides a rational approach towards the future applications.

**Keywords:** *Microcystis aeruginosa*; microorganisms; biodegradation; anticyanobacterial modes; harmful cyanobacterial blooms

**1. Introduction**

Harmful cyanobacterial blooms (HCBs) caused by cyanobacteria (including *Microcystis*, *Anabaena*, *Nodularia*, *Oscillatoria*, and so on) have become a common occurrence in freshwater worldwide [1,2]. Among the blooming cyanobacteria, *Microcystis aeruginosa* is one of the most common and widespread species [3]; specifically, it is known to be a representative species due to the dominant production of microcystins [4,5]. The rapid and excessive growth of *M. aeruginosa* is harmful to drinking water treatments and aquatic ecosystems due to the release of algal organic matters and cyanobacterial toxins [6,7]. As a result, the control of HCBs in water sources is a matter of great urgency.

Many approaches have been adopted for *M. aeruginosa* removal over the past few decades [8]. Physical methods including mechanical salvage, physical aeration, and ultrasonic treatment are usually high cost and take a long time; chemical methods such as chemical oxidants are highly efficient and low-cost methods for controlling HCBs within a short time [9]. However, chemicals may lead to a secondary contamination that may lead to potential threats to the aquatic ecosystem [10,11]. Compared with the physical and chemical...
methods, biological approaches such as plant allelopathy, aquatic animals and anticyanobacterial microorganisms are considered to be an economic and environmentally friendly way for cyanobacteria inhibition/biodegradation [2,10,12]. Among these methods, anticyanobacterial microorganisms are used as efficient biological agents *M. aeruginosa* [13]; furthermore, the microcystins can be biodegraded by certain anticyanobacterial microorganisms at the same time [6,14,15].

Up to now, several review articles have been published to introduce the anticyanobacterial microorganisms including bacteria, viruses, and fungi [2,10,13,16,17]. However, the previous reviews have concentrated mainly on both the freshwater and marine cyanobacterial/algal species or diatoms. While few studies have focused on elimination and degradation of the toxic cyanobacterium *M. aeruginosa* by bacteria and fungi. Moreover, the important role of anticyanobacterial microorganisms on the key genes expression and the anticyanobacterial activities regulated by quorum sensing (QS) system hasn’t been mentioned. In order to clarify the current situation of anticyanobacterial microorganisms for *M. aeruginosa* control, the available literature on the bacteria and fungi (studies that focused on bacteriophages against *Microcystis* spp. are not included in this review) are adapted to review the current progress. In this review, anticyanobacterial substances and their acute toxicities (the half maximal effective concentration, EC$_{50}$), anticyanobacterial modes and mechanisms, as well as in situ application of anticyanobacterial microorganisms are elucidated. This review will enhance understanding the anticyanobacterial microorganisms and provide a rational attitude towards future application.

2. Anticyanobacterial Effects for *M. aeruginosa*

2.1. Anticyanobacterial Microorganisms

Over the past few decades, the isolation and identification of microorganisms with anticyanobacterial effects have attracted extensive concern. Based on the literature, a variety of anticyanobacterial microorganisms have been isolated from the natural environment, and most of them belong to the anticyanobacteria and anticyanobacterial fungi.

2.1.1. Anticyanobacteria

The high diversity of anticyanobacteria reported in the literatures is summarized in Table 1. There are more than 50 genera belonging mainly to Proteobacteria, Actinomycetes, Bacteroidetes, Firmicutes and Thermus. Proteobacteria, which is divided into five parts, is one of the most widespread and extensively studied bacteria in the microbiology field, and it is well known to effectively biodegrade cyanobacteria and diatoms in eutrophic environments [2,10]. The majority have been identified as members of *Pseudomonas* [18,19], *Aeromonas* [20,21], *Acinetobacter* [22], *Raoultella* [23], *Brevundimonas* [24], *Ochrobactrum* [25], *Halobacillus* [26], *Shewanella* [27], *Citrobacter* [28], *Stenotrophomonas* [29], *Serratia* [30] and *Hahella* [31] genera belonging to the $\gamma$-Proteobacteria class.

According to the microbial taxonomy, anticyanobacterial Actinomycetes can be classified into four major categories: *Streptomyces* sp. [32,33], *Rhodococcus* sp. [34], *Microbacterium* sp. [35] and *Arthrobacter* sp. [14]. *Streptomyces* is the most common anticyanobacterial Actinomycetes in HCBs control. A previous study confirmed that *S. grisoniobia* NT0401 shows a high anticyanobacterial activity against *M. aeruginosa* by secreting active substances [36], and the anticyanobacterial substances of amino acids (L-lysine and L-valine) [3,37], tryptamine [38] and triterpenoid saponin [35] from Actinomycetes have been identified. In addition to Actinomycetes, many other Bacteroidetes are also highly efficient at inhibiting the growth of *M. aeruginosa*, such as *Aquimarina* sp. [39], *Chryseobacterium* sp. [40,41], *Aureispira* sp. [42] and *Pedobacter* sp. [43]. Although the Bacteroidetes group has been reported to inhibit cyanobacteria, diatoms and green algae [2,10], there is no publication on the inhibition of *M. aeruginosa* by *Flavobacterium* sp. or *Cellulomonas* sp.

It is shown in Table 1 that the largest number of anticyanobacterial Firmicutes are the *Bacillus* group, accounting for 77.3% of the total number of Firmicutes, while the remaining strains are from the genera *Exiguobacterium* [44,45] and *Staphylococcus* [35].
Li et al., (2015) revealed that *Bacillus* sp. Lzh-5 releases anticyanobacterial substances to attack *M. aeruginosa*, *M. viridis*, *Chroococcus* sp., and *Oscillatoria* sp. [46]; *B. licheniformis* Sp34 can also effectively destroy the cell membrane of *M. aeruginosa* and inhibit the synthesis of microcystins [47]; moreover, the simultaneous application of *Bacillus* sp. T4 and toxin-degrading bacteria could eliminate both *Microcystis* sp. and microcystins [48]. These results demonstrate that *Bacillus* not only inhibits the growth of *M. aeruginosa* [49,50], but also inhibits the expression of microcystins synthesis gene *mcyB* [47,51] and degrades the cyanobacterial toxins [48]. Obviously, *Bacillus* has a potential application for HCBs control.

There is only one strain of *Deinococcus metallilatus* MA1002 attached to Thermus that has been reported to inhibit *M. aeruginosa* [52]. The bacterium *Deinococcus* sp. also shows an anticyanobacterial effect on the toxic dinoflagellate *Alexandrium tamarense* [53]. Except for the genera mentioned above, other genera connected with anticyanobacterial or flocculation activities also exist, including *Citrobacter* sp. [28,54] and *Sphingopyxis* sp. [55]. The above anticyanobacteria can destroy the *M. aeruginosa* cells by causing cell membrane damage, and oxidative stress and by inhibiting the gene expression from a wide range of temperatures (−20 to 121 °C) and pH (3 to 11) [5,32,33]. Not only that, the photosynthesis system of *M. aeruginosa* is also reduced [56]. To summarize, the anticyanobacteria can effectively inhibit the growth of *M. aeruginosa*, and cause an inhibition effect at a low concentration.
Table 1. Summary of anticyanobacterial microorganisms and their anticyanobacterial modes.

| Strain Name | Target Cyanobacterium | Initial Cyanobacterial Cell Density (cells mL⁻¹) | Dosage (v/v) | Duration Time | Inhibition Rate/Removal Efficiency | Anticyanobacterial Modes | References |
|-------------|-----------------------|-------------------------------------------------|--------------|---------------|-----------------------------------|--------------------------|------------|
| **α-Proteobacteria** | | | | | | | |
| Brevibacillus laterosporus Bl-aj | M. aeruginosa | 1.0 × 10⁷ | 1.0 × 10⁸ ** | 3 d (4 d) | 72.36% (92.30%) | NA | [57] |
| Brevundimonas sp. AA06 | M. aeruginosa | FACHB-905 | NA | 4 d | 70% | NA | [24] |
| Oscillatoria sp. FJTS | M. aeruginosa | 2.0-6.0 × 10⁸ | 4.0 × 10⁷ ** | 5 d | 58.9% | indirect attack | [25] |
| Stappia sp. F2 | M. aeruginosa | FACHB-905 | 2.5 × 10⁹ | 10% | 94.9% | indirect attack | [33] |
| *R.* microtum sp. AQ_MP | M. aeruginosa | NA | 9% | 10 d | 100% | NA | [58] |
| **β-Proteobacteria** | | | | | | | |
| Alcaligenes denitrificans | M. aeruginosa | NIES 298 | 2 × 10⁵ | 0.7% | 96.4% | direct contact | [59] |
| Alcaligenes sp. H3 | wild cyanobacterium | NA | 20% | 4 d | 93% | indirect attack | [60] |
| Paucibacter aquatile DH15 | | NA | 1.0 × 10⁶ | 36h | 94.9% | combination of direct and indirect attacks | [61] |
| Achromobacter spp. LG1 | M. aeruginosa CAAT 2005-3 | 1.0 × 10⁶ | 1.0 × 10⁶ ** | 7 d | 29.0 ± 1.6-55.0 ± 3.8% | NA | [62] |
| P. aeruginosa ACB3 | M. aeruginosa FACHB-912 | 0.55-1.13 × 10⁶ | 1.0 × 10² ** | 6 d | 96.5% | indirect attack | [63] |
| P. aeruginosa UCBP-PJA14 | M. aeruginosa NIES 44 | 1.0 × 10⁵ | 1.0 × 10⁵ ** | 10 d | 73.0 ± 2.7% | NA | [64] |
| P. aeruginosa KACC10292 | T. M. aeruginosa | NIES 298 | 1.1 × 10⁵ | 10% | 96% | indirect attack | [20] |
| P. graminis A01 | M. aeruginosa FACHB-905 | 1.0 × 10⁷ | 10% | 7 d | 93.81% | NA | [65] |
| P. graminis A14 | M. aeruginosa FACHB-905 | 5.3 × 10⁶ | 15% | 7 d | 98.8% | indirect attack | [19] |
| P. putida CH-22 | M. aeruginosa FACHB-924 | 437 ± 21 * | 5% (10%) | 7 d | 82.6% | NA | [63] |
| **γ-Proteobacteria** | | | | | | | |
| *P.* syringae KACC10292 | T. M. aeruginosa | NIES 298 | 1.1 × 10³ | 10% | 96% | indirect attack | [20] |
| *Aeromonas* sp. FM | M. aeruginosa | FACHB-927 | 1.4 × 10⁷ | 2.1 × 10⁶ ** | 4 d | up to 95% | NA | [66] |
| *Aeromonas* sp. FM | | | | | | | |
| *Aeromonas* sp. FM | | | | | | | |
| *Aeromonas* sp. GLY-2107 | M. aeruginosa | NIES 9110 | 1.0 × 10⁷ | 1% | 96.5 ± 1.1% | indirect attack | [69] |
| *Aeromonas* sp. GLY-2107 | | | | | | | |
| *Aeromonas* sp. L23 | M. aeruginosa UTEX LB 2383 | 6.0 × 10⁶ | 25% | 5 d | 88 ± 1.2% | indirect attack | [21] |
| *Aeromonas* sp. NHSB | | | | | | | |
| *Aeromonas* sp. | | | | | | | |
| Strain Name          | Target Cyanobacterium | Initial Cyanobacterial Cell Density (cells mL\(^{-1}\)) | Dosage (v/v) | Duration Time | Inhibition Rate/Removal Efficiency | Anticyanobacterial Modes | References |
|----------------------|-----------------------|--------------------------------------------------------|--------------|---------------|-----------------------------------|--------------------------|------------|
| Acinetobacter sp. J25 | NA                    | NA                                                     | 10%          | 24 d          | 87.86%                            | NA                       | [71]       |
| Acinetobacter sp. CMDB-2  | M. aeruginosa FACHB-905 | 1.0 × 10^8                                             | 5%           | 3 d           | 87.5%                             | indirect attack           | [22]       |
| A. guillouiae A2       | M. aeruginosa FACHB-905 | 1.0 × 10^8                                             | 10%          | 7 d           | 91.6%                             | indirect attack           | [72]       |
| R. putida sp. R11      | M. aeruginosa FACHB-905 | NA                                                     | 15% (30%)    | 6 d           | 57.63% (93.58%)                   | NA                       | [73]       |
| R. planticola          | M. aeruginosa FACHB-905 | NA                                                     | 4% (8%)      | 9 d (3 d)     | nearly 60% (83%)                   | indirect attack           | [72]       |
| R. ornithinolytica S1  | M. aeruginosa FACHB-905 | NA                                                     | 5%           | 3 d           | 96.2%                             | indirect attack           | [23]       |
| Halobacillus sp. H9    | M. aeruginosa FACHB-905 | 2.0 × 10^7                                             | 5%           | 24 h          | 90% (93 ± 1%)                     | indirect attack           | [26]       |
| Shewanella sp. Lzh-2   | M. aeruginosa FACHB-905 | 1.0 × 10^7                                             | 10%          | 6 d           | 92.3 ± 6.8%                       | indirect attack           | [27]       |
| Sternotrophomonas maltophilia 15 | M. aeruginosa FACHB-905 | 400 *                                                  | NA           | 16 d          | ~80%                              | indirect attack           | [74]       |
| Halolo sp. K22         | M. aeruginosa FACHB-1752 | 0.01 ***                                               | 3 d           | 60%           | NA                                | indirect attack           | [31]       |
| Citrobacter sp. R1     | M. aeruginosa FACHB-905 | 1.0 × 10^7                                             | 16.7%        | 3 d           | 81.6 ± 2.2%                       | NA                       | [28]       |
| Citrobacter sp. AzoR-1 | M. aeruginosa          | 1.0 × 10^7                                             | NA           | NA            | ~95%                              | indirect attack           | [54]       |
| Enterobacter sp. NP23  | M. aeruginosa          | 1.0 × 10^8                                             | 1.0 × 10^8 **| 20 d          | ~70%                              | NA                       | [75]       |
| Shigella sp. H3        | M. aeruginosa wild cyanobacterium | NA           | 20%          | 10 d          | 78%                                | direct attack             | [60]       |
| Serratia marcescens LTH-2 | M. aeruginosa TH1     | 3.0 × 10^6                                             | 5%           | 2 d (3 d)     | 72.4% (79.0%)                     | indirect attack           | [76]       |
| S. marcescens BWL1001  | M. aeruginosa          | NA                                                     | NA           | 2 d           | 91.1%                             | indirect attack           | [30]       |
| Aquimarina salinae     | M. aeruginosa MTY01    | 1.0 × 10^5                                             | 10%          | 3 (6 d)       | 80% (100%)                        | indirect attack           | [39,77]   |
| Chryseobacterium sp.   | M. aeruginosa FACHB-905 | 6.0 × 10^6                                             | 10%          | 3 d           | up to 80%                         | direct attack             | [40]       |
| Chryseobacterium sp. H2 | M. aeruginosa FACHB-905 | NA                                                     | 10%          | 7 d           | 85.3%                             | NA                       | [79]       |
| Chryseobacterium sp. GLY-1106 | M. aeruginosa 9110   | 1.0 × 10^7                                             | NA           | 6 d           | 98.9%                             | indirect attack           | [41]       |
| Chryseobacterium sp. S7 | M. aeruginosa FACHB-905 | 718 *                                                  | 28.5%        | 7 d           | 99.32%                            | indirect attack           | [79]       |
| Aureimonas sp. CCB-Q81 | M. aeruginosa NISE 102 | NA                                                     | NA           | 3 min         | 75.39%                            | indirect attack           | [42]       |
| Pedobacter sp. Mal11-5 | M. aeruginosa NIES 843 | NA                                                     | 6.7%         | 2 d (10 d)    | exceeded 50% (75–85%)             | NA                       | [43]       |
Table 1. Cont.

| Strain Name       | Target Cyanobacterium | Initial Cyanobacterial Cell Density (cells mL⁻¹) | Dosage (v/v) | Duration Time | Inhibition Rate/Removal Efficiency | Anticyanobacterial Modes       | References |
|-------------------|-----------------------|-------------------------------------------------|--------------|---------------|-----------------------------------|---------------------------------|------------|
| *Actinomycetes*   |                        |                                                 |              |               |                                   |                                 |            |
| Streptomyces sp. NT0401 | *M. aeruginosa* PCC 7806 | NA                                              | 5%           | 5 d           | up to 85%                         | indirect attack                  | [36]       |
|                   | *M. aeruginosa* XW01   |                                                 |              |               |                                   |                                 |            |
| Streptomyces sp. L74   | *M. aeruginosa* FACHB-905 | 1.0 × 10⁶                                         | 10%          | 4 d           | 71.48 ± 5.33%                     | indirect attack                  | [33]       |
| S. neugamunensis    | *M. aeruginosa* NIES 298 | NA                                              | NA           | 7 d           | 84.5%                            | NA                              | [60]       |
| S. rameus KKU-A3    | *M. aeruginosa* KCU-13  | NA                                              | 10%          | 7 d           | 81.56%                           | NA                              | [81]       |
| S. aureantiogriseus PK1 | *M. aeruginosa* KCU-13  | ~1.5 × 10⁶                                        | 5%           | 8 d           | ~83.3%                           | indirect attack                  | [82]       |
| *Streptomyces* sp. KY-34 | *M. aeruginosa* FACHB-905 | 354.3 ± 13.8 *                                    | 3% (10%)     | 8 d           | 81.2% (99.0%)                     | indirect attack                  | [56]       |
| *Streptomyces* sp. HJC-D1 | *M. aeruginosa* FACHB-905 | 637.5 ± 32.1 *                                    | 5% (10%)     | 5 d           | 88.4 ± 2.8% (91.8 ± 1.2%)         | indirect attack                  | [32]       |
|                   | *S. globisporus* C9    |                                                 |              |               |                                   |                                 |            |
|                   | *M. aeruginosa* NIES 44 |                                                 |              |               |                                   |                                 |            |
|                   | *M. aeruginosa* NIES 90 |                                                 |              |               |                                   |                                 |            |
|                   | *M. aeruginosa* NIES 843|                                                 |              |               |                                   |                                 |            |
|                   | *M. aeruginosa* FACHB-905| 300 ± 60 *                                       | 5%           | 5 d           | 95.1 ± 1.6%                       | direct attack                    | [83]       |
|                   | *M. aeruginosa* PCC 7806|                                                 |              |               |                                   |                                 |            |
| *Actinomycetes*    |                        |                                                 |              |               |                                   |                                 |            |
| S. amritsarensis   | *M. aeruginosa* NIES 44 |                                                 |              |               |                                   |                                 |            |
|                   | *M. aeruginosa* NIES 90 |                                                 |              |               |                                   |                                 |            |
|                   | *M. aeruginosa* NIES 843|                                                 |              |               |                                   |                                 |            |
|                   | *M. aeruginosa* FACHB-905| 500 ± 100 *                                       | 5%           | 5 d (10 d)    | 81.4 ± 0.57% (80.7 ± 0.87%)       | NA                              | [5]        |
|                   | *M. aeruginosa* DCM4   |                                                 |              |               | 84.9 ± 0.3%                       |                                 |            |
|                   |                        |                                                 |              |               | 86.5 ± 2.1%                       |                                 |            |
| S. jiujiangensis DJ0074 | *M. aeruginosa* FACHB-905 | 5.0 × 10⁶                                         | 10%          | 8 d           | 90.50 ± 1.08%                     | indirect attack                  | [84]       |
| *Streptomyces* sp. U3 | *M. aeruginosa* PCC 1752| NA                                              | 5%           | 3 d           | 36.22%                           | indirect attack                  | [85]       |
| *Rhodococcus* sp. KWR2 | *M. aeruginosa* NIES 843|                                                 |              |               |                                   |                                 |            |
|                   | *M. aeruginosa* UTEX 2388| 1.72 × 10⁶                                        | 2% (filtrate) | 5 d           | 97%                              | indirect attack                  | [34]       |
|                   | *M. aeruginosa* KW     |                                                 |              |               | 94%                              |                                 |            |
|                   | *M. aeruginosa* Mi 0601|                                                 |              |               | 79%                              |                                 |            |
| *Microbacterium* sp. F3 | *M. aeruginosa* FACHB-905 | 2.5 × 10⁶                                         | 10%          | 7 d           | 84.8%                            | indirect attack                  | [35]       |
| *Arthrobacter* sp. | *M. aeruginosa*        |                                                 |              |               | 32.3 ± 13.8%                      | NA                              | [14]       |
| Strain Name                  | Target Cyanobacterium | Initial Cyanobacterial Cell Density (cells mL\(^{-1}\)) | Dosage (\(v/v\)) | Duration Time | Inhibition Rate/Removal Efficiency | Anticyanobacterial Modes | References |
|-----------------------------|-----------------------|---------------------------------------------------------|---------------------|---------------|-----------------------------------|--------------------------|------------|
| Bacillus subtilis C1        | M. aeruginosa         | 1000 *                                                  | 1%                  | 2 d           | 85%                              | NA                       | [86]       |
| B. fusiformis B5            | M. aeruginosa         | 412.3 *                                                 | 3.6 \(\times\) \(10^5\) ** | 7 d           | nearly 90%                        | indirect attack          | [87]       |
| Bacillus sp. S51107         | M. aeruginosa 9110    | 1.0 \(\times\) \(10^6\)                                | 10%                 | 6 d           | 92.51 \(\pm\) 2.79%              | indirect attack          | [88]       |
|                            | M. aeruginosa PCC 7806|                                                         |                     |               | 91.65 \(\pm\) 1.00%              |                          |            |
| Bacillus sp. AF-1           | M. aeruginosa NIES 843| 1.6 \(\times\) \(10^3\)                                | 2%                  | 3 d (6 d)     | 77% (93%)                        | indirect attack          | [51]       |
| Bacillus sp. Lzh-5          | M. aeruginosa 9110    | 1.0 \(\times\) \(10^7\)                                | 10%                 | 6 d           | 91.2 \(\pm\) 6.3%                | indirect attack          | [46]       |
| Bacillus sp. T4             | M. aeruginosa KW      | 1.0 \(\times\) \(10^8\)                                | 5%                  | 3 d           | ~100%                            | indirect attack          | [48]       |
| B. licheniformis Sp34       | M. aeruginosa DCM3    | 1.35 \(\times\) \(10^5\)                                | 5%                  | 5 d (10 d)    | 69.4 \(\pm\) 0.67 (97.1 \(\pm\) 0.86%) | indirect attack          | [47]       |
|                            | M. aeruginosa DCM4    |                                                         |                     |               | 60.8 \(\pm\) 1.63 (82.4 \(\pm\) 2.09%) |                          |            |
|                            | M. aeruginosa NIES 843|                                                         |                     |               | 78.7 \(\pm\) 5.94% (97.1 \(\pm\) 0.86%) |                          |            |
| Bacillus mycoides B16       | M. aeruginosa PCC 7806| -1.0 \(\times\) \(10^6\)                               | NA                  | 6 d           | 97%                              | NA                       | [90]       |
| Bacillus methylophilicus ZJU| M. aeruginosa         | 1.0 \(\times\) \(10^7\)                                | 16.7%               | 3 d           | 89 \(\pm\) 0.5%                  | indirect attack          | [50]       |
| Bacillus sp. Mal 11-2       | M. aeruginosa NIES 843| NA                                                      | 6.7%                | 10 d          | up to 60%                        | NA                       | [43]       |
| Bacillus sp. Mal 11-10      | M. aeruginosa NIES 843| NA                                                      |                     | 10 d          | 55–64%                          | NA                       |            |
| B. amyloliquefaciens FZB42  | M. aeruginosa NIES 843| 1.0 \(\times\) \(10^6\)                                | NA                  | 7 d           | 98.78%                          | NA                       | [91]       |
| B. amyloliquefaciens CH03   | M. aeruginosa NIES 843|                                                         |                     |               | 94.39%                          | NA                       |            |
| Bacillus sp. B50            | M. aeruginosa         | 100%                                                    |                     |               |                                  |                          |            |
|                            | M. aeruginosa FACHB-905|                                                         |                     |               |                                  |                          |            |
|                            | M. aeruginosa FACHB-1023|                                                        |                     |               |                                  |                          |            |
|                            | M. aeruginosa NIES 843|                                                         |                     |               |                                  |                          |            |
|                            | M. aeruginosa PCC 7806|                                                         |                     |               |                                  |                          |            |
|                            | M. aeruginosa CHAB-439|                                                         |                     |               |                                  |                          |            |
|                            | M. aeruginosa CHAB-456|                                                         |                     |               |                                  |                          |            |
| B. amyloliquefaciens T1     | M. aeruginosa         | 100%                                                    | 5%                  | 6 d           | 99.4%                            | indirect attack          | [92,93]    |
|                            | M. aeruginosa FACHB-905|                                                         |                     |               | 62.52%                          |                           |            |
|                            | M. aeruginosa FACHB-907|                                                         |                     |               | 100%                            |                           |            |
|                            | M. aeruginosa FACHB-908|                                                         |                     |               | 66.90%                          |                           |            |
|                            | M. aeruginosa FACHB-912|                                                         |                     |               | 71.08%                          |                           |            |
|                            | M. aeruginosa PCC 7806|                                                         |                     |               | 60.33%                          |                           |            |
| B. methylotrophicus ZJU     | M. aeruginosa         | 1.0 \(\times\) \(10^7\)                                | 16.7%               | 3 d           | 89 \(\pm\) 0.5%                  | NA                       | [50]       |
| Paenibacillus sp. Sj-73     | M. aeruginosa PCC 7806| NA                                                      | 5%                  | 7 d           | 83.97 \(\pm\) 1.60%              | indirect attack          | [95]       |
|                            | M. aeruginosa TH1701  | NA                                                      | 5% (10%)            | 7 d           | 92.10% (94.38%)                 | indirect attack          | [95]       |
| Exiguobacterium sp. h10     | M. aeruginosa PCC 7820| NA                                                      | 5%                  | 2 d (6 d)     | 43.4% (73.6%)                   | indirect attack          | [44]       |
### Table 1. Cont.

| Strain Name                      | Target Cyanobacterium | Initial Cyanobacterial Cell Density (cells mL$^{-1}$) | Dosage (v/v) | Duration Time | Inhibition Rate/Removal Efficiency | Anticyanobacterial Modes | References |
|----------------------------------|-----------------------|------------------------------------------------------|--------------|---------------|-----------------------------------|---------------------------|------------|
| **Firmicutes**                   |                        |                                                      |              |               |                                   |                           |            |
| Exiguobacterium sp. A27         | M. aeruginosa PCC 7806 | $1.0 \times 10^7$                                   | 10%          | 2 d           | $64.4 \pm 10.3\%$                  | indirect attack           | [96]       |
| Exiguobacterium indicum EI9     | M. aeruginosa FACHB-905| $4.4 \times 10^5$                                   | 1.1 $\times 10^8$ ** | NA            | NA                                 |                           |            |
| Staphylococcus sp. F1           | M. aeruginosa FACHB-905| $2.5 \times 10^6$                                   | 10%          | 7 d           | 96.0%                              | indirect attack           | [35]       |
| **Thermus**                     |                        |                                                      |              |               |                                   |                           |            |
| Deinococcus metallilatus MA1002 | M. aeruginosa PCC 7806 | $6.0 \times 10^6$                                   | 10%          | 3 d           | up to 80%                          | indirect attack           | [52]       |
| **Ascomycota**                  |                        |                                                      |              |               |                                   |                           |            |
| Trichoderma citrinoviride       | M. aeruginosa          | $3.2 \times 10^4$                                   | 10%          | 2 d           | 100%                               |                           | [6]        |
| Aspergillus niger 7806F3        | M. aeruginosa PCC 7820 | $5.0 \times 10^7$                                   | 10%          | 4 d           | up to 80%                          | indirect attack           | [15]       |
| Penicillium chrysogenum          | M. aeruginosa          | $3.85%$                                              | 6 d           |              | 69.56%                             |                           |            |
| Aureobasidium pullulans KKUY070 | M. aeruginosa DRCK1    | $5.0 \times 10^6$                                   | 1.2 $\times 10^6$ ** | 1 d (3 d) | 84% (100%)                         |                           | [98]       |
| **Basidiomycetes**              |                        |                                                      |              |               |                                   |                           |            |
| Loparia spadice                  | M. aeruginosa FACHB-912| $798 \pm 13$ *                                       | NA           | 39 h          | 100%                               |                           | [99]       |
| Phanerochaete chrysosporium      | M. aeruginosa          | about $1.57 \times 10^7$                             | 500 ***      | NA            | $88.6 \pm 0.52\%$                  |                           | [100,101] |
| Irpex lacteus T2b                | M. aeruginosa          | 646.25$\pm$19.11 *                                  | 30 h         |              | 96.82%                             |                           |            |
| Trametes hirsuta T24             | M. aeruginosa PCC 7806 | 705.19$\pm$15.45 *                                  | 39 h         |              | 60.19%                             |                           |            |
| T. versicolor F21a               | M. aeruginosa          | 701.33$\pm$13.30 *                                  | 30 h         |              | 100%                               |                           |            |
| Bjerkandera adusta T1            | M. aeruginosa          | 656.28$\pm$26.78 *                                  | 39 h         |              | 98.35%                             |                           |            |
| Phellinus noxius HN-1            | M. aeruginosa NIES 843 | 656.28$\pm$26.78 *                                  | NA           |              | NA                                 |                           |            |
| Trichaptum abietinum 1302BG      | M. aeruginosa FACHB-918| 750 *                                                | NA           | 2 d           | 100%                               | direct attack             |            |
| M. aeruginosa FACHB-918          | 1300 *                 | NA                                                   | 36 h         |              | 100%                               |                           |            |

NA means the date is not available, not mentioned, or unclear. An asterisk (*) stands for the Chl a concentration, µg L$^{-1}$; Two asterisks (**) represent the cell concentrations of anti-cyanobacterial microorganisms, cfu mL$^{-1}$; Three asterisks (***) represent the dry cell weight concentrations of the anti-cyanobacterial microorganisms, mg L$^{-1}$. 
2.1.2. Anticyanobacterial Fungi

Compared with the studies of anticyanobacteria, the research and application of fungi for eliminating or inhibiting *M. aeruginosa* cells has not received much attention until 2010 [105,106]. Only Ascomycetes and Basidiomycetes have been found to have the anticyanobacterial effects against *M. aeruginosa*. It has been reported that the fungus *Trichaptum abietinum* 1302BG can eliminate four cyanobacteria directly including *M. aeruginosa* FACH-918 and *M. aeruginosa* PCC 7806 in 48 h [106]. Some other fungi such as *Trichoderma citrinoviride* [6], *Penicillium chrysogenum* [97], *Aureobasidium pullulans* KKYU070 [98], *Lopharia spadicea* [99], *Phanerochaete chrysosporium* [100,101], *Ir pep lacteus* T2b [102], *Tremetes versicolor* F21a [107] and *Bjerkandera adusta* T1 [103] also show good inhibitory activities against *M. aeruginosa*. It has been stated that *T. citrinoviride* and *A. pullulans* have highly specific anticyanobacterial effects towards *Microcystis* spp. while they have an insignificant effects on the green algae or diatoms [6,98]; furthermore, the biodegradation of *M. aeruginosa* cells may be due to the excretion of the lytic enzyme (N-β-acetylglucosaminidas) [98], which can degrade the peptidoglycan from the cyanobacterial cell wall. The extracellular enzymes of cellulose, β-glucosidase, protease, and laccase from *T. versicolor* F21a have also been proven to be responsible for the degradation of *Microcystis* spp. [107,108].

On the contrary, the *M. aeruginosa* cells are damaged in a short time under the treatment of *T. abietinum* 1302BG, *I. lacteus* T2b or *T. hirsuta* T24, and the anticyanobacterial process occurs “cell to cell” through the following steps: (1) the fungus comes into physical contact with the surface of the cyanobacterial cells; (2) cyanobacterial cells are encompassed with mycelia, which destroy the cyanobacterial cell wall and membrane; and (3) the nucleic acids and other substances of cyanobacteria cells are released [17]. Fungi have the natural ability to destroy *Microcystis* cells by secreting anticyanobacterial substances or through “cell to cell” contact. Apart from the growth inhibition and cell lysis of *M. aeruginosa*, some fungi are able to remove microcystins [6,98,106], and the removal mechanism is related to the adsorption/biodegradation of fungus or the inhibition expression of microcystins synthesis gene [15].

2.2. Anticyanobacterial Substances

The metabolic activities of microorganisms are diverse, some of the secretory substances have anticyanobacterial or algicidal activities. However, due to the complexity of separation and purification, only part of the anticyanobacterial substances have been identified [2,10]. On the basis of the relative literatures and types of compounds, the isolated substances can be classified into five major categories: alkaloids, protein/amino acids, fatty acid/cyclic peptides/peptide derivates, enzymes and others (Table 2). The alkaloids are not only secreted by bacteria such as *Aeromonas* sp. [67,69], *Pseudomonas* sp. [66], *Bacillus* sp. [88,91] and *Streptomyces* sp. [38,84], but are also produced by the fungus *Phellinus* sp. [104]. For example, the anticyanobacterial compound isolated from *A. guillouiae* A2 has been identified as 4-hydroxyphenethyamine (C8H11NO), with the EC50 of 22.5 ± 1.9 mg L−1 in 72 h [72]; the prodigiosin can be produced by both *S. marcescens* LTH-2 and *Hahella* sp. KA22, while it shows higher anticyanobacterial effect against *M. aeruginosa* FACHB 905 (EC50 of 0.16 mg L−1) compared to *M. aeruginosa* FACHB-1752 (EC50 of 5.87 mg L−1) [31,109], demonstrating the different EC50 of prodigiosin is probably related to the cyanobacteria species. For the cyclic peptides, the hexahydropyrrolo[1,2-a]pyrazine-1,4-dione (cyclo[Gly-Pro]) can also be secreted by *Stenotrophomonas* sp. [29], *Bacillus* sp. [46] and *Sheuanaella* sp. [27], the EC50 against *M. aeruginosa* 9110 is from 5.7 to 5.9 mg L−1.

The diketopiperazine substances produced by bacteria have been recognized as having anticyanobacterial activities for *M. aeruginosa*. The EC50 of value of cyclo(4-OH-Pro-Leu) (7-hydroxy-3-isobutyl-hexahydro-pyrrolo[1,2-a]pyrazine-1,4-dione) and cyclo(Pro-Leu) (hexahydro-3-(2-methylpropyl)-pyrrolo[1,2-a]pyrazine-1,4-dione) isolated from *Chryseobacterium* sp. GLY-1106 against *M. aeruginosa* is 1.26 and 2.70 mg L−1, respectively [41]. Another diketopiperazine 3-benzyl-piperazine-2,5-dione (cyclo[Gly-Phe]) was firstly reported by Guo et al., (2016) [69], who showed that cyclo(Gly-Phe) has weaker anticyanobacterial activ-
ity (EC\textsubscript{50,24h} of 4.72 mg L\textsuperscript{-1}) compared with cyclo(Pro-Phe) (EC\textsubscript{50,24h} of 1.85 mg L\textsuperscript{-1}) \cite{88}. Diketopiperazine substances with similar structures often exhibit distinct biological properties. After short-term exposure to \textit{M. aeruginosa}, cyclo(4-OH-Pro-Leu) interrupts the flux of electron transport in the photosynthetic system and cyclo(Pro-Leu) inhibits the antioxidant enzyme activities of \textit{M. aeruginosa} \cite{41}, whereas 3-isopropyl-hexahydropyrrolo[1,2-a]pyrazine-1,4-dione (cyclo[Pro-Val]) causes significant damage to cyanobacterial cell membranes \cite{46}.

Previous studies have indicated that amino acids have powerful anticyanobacterial effects against \textit{Microcystis} spp. at concentrations between 0.6 and 5.0 mg L\textsuperscript{-1} \cite{11,110,111}, and the inhibition effect of L-lysine against \textit{Microcystis} sp. is remarkable \cite{110}. Moreover, the eutrophic lake with the dominant species of cyanobacterium \textit{M. aeruginosa} is selectively controlled by lysine \cite{111}. The amino acids and proteins have commonly been identified and reported as the anticyanobacterial substances for \textit{M. aeruginosa}. Two amino acids (L-lysine and L-phenylalanine) are purified from \textit{B. amyloliquefaciens} T1 that have an inhibition effect against \textit{M. aeruginosa} FACHB-905 \cite{94}; the L-valine, which shows a better anticyanobacterial activity than L-lysine, is also isolated from \textit{S. jiujiangensis} JXJ 0074 \cite{37}. It is interesting that the anticyanobacterial efficiency of tryptamine and tryptoline on \textit{M. aeruginosa} FACHB-905 is 80 ± 1% and 100 ± 2%, respectively, but the growth of \textit{M. aeruginosa} is recovered as tryptamine (tryptoline) and is completely used or degraded by microorganisms \cite{38}. Therefore, the persistence of amino acids should be further considered when they are used for eutrophication control \cite{112}.
Table 2. Anticyanobacterial substances and their EC$_{50}$ on *M. aeruginosa*.

| Anticyanobacterial Substances | Strain Name | Target Cyanobacterium | Initial Cyanobacterial Cell Density (cells mL$^{-1}$) | EC$_{50}$ (mg L$^{-1}$) | References |
|-------------------------------|-------------|------------------------|-----------------------------------------------------|------------------------|------------|
| Harmane (1-methyl-β-caroline) | *Pseudomonas* sp. K44-1 | *M. aeruginosa* NIES 299 | NA | NA | [66] |
| prodigiosin (C$_{20}$H$_{25}$N$_{3}$O) | *S. marcescens* LTH-2 | *M. aeruginosa* TH1 | 3.0 $\times$ 10$^{6}$ | 0.048 $\pm$ 0.004 (24 h) | [76,109] |
|                               | NA | *M. aeruginosa* TH2 | 0.089 $\pm$ 0.011 (24 h) | 0.25 (24 h)/0.16 (72 h) |
|                               | *Habella* sp. KA22 | *M. aeruginosa* FACHB-1752 | NA | 5.87 (72 h) | [31] |
| 2-(3, 4-dihydroxy2-methoxyphenyl)-1,3-benzodioxole-5-carbaldehyde | *Phellinus noxius* HN-1 | *M. aeruginosa* NIES 843 | 656.28 $\pm$ 26.78 * | 20.6 (72 h) | [104] |
| 3, 4-dihydroxybenzalacetone(C$_{10}$H$_{10}$O$_{3}$) | *Bacillus amyloliquefaciens* FZB42 | *M. aeruginosa* NIES 843 | 1.0 $\times$ 10$^{6}$ | 4.13 (96 h) | [91] |
| Tryptamine (C$_{11}$H$_{12}$N$_{2}$) | *Streptomyces eurocidicus* JXJ-0089 | NA | NA | 3.00 $\pm$ 0.09 (72 h) | [38] |
| Tryptoline (C$_{11}$H$_{12}$N$_{2}$) | *Bacillus* sp. S51107 | *M. aeruginosa* 9110 | 1.0 $\times$ 10$^{7}$ | 1.10 (24 h) | [69] |
| 3-methylindole | *Aeromonas* sp. GLY-2107 | *M. aeruginosa* 9110 | 1.0 $\times$ 10$^{7}$ | 6.55 (24 h) | [88] |
| indole-3-carboxaldehyde | *Bacillus* sp. S51107 | *M. aeruginosa* 9110 | 1.0 $\times$ 10$^{6}$ | 6.42 (72 h) | [84] |
| 2′-deoxyadenosine (C$_{10}$H$_{10}$N$_{2}$O$_{3}$) | *Streptomyces jiujiangensis* JXJ 0074 | *M. aeruginosa* FACHB-905 | 5.0 $\times$ 10$^{6}$ | 53.75 (72 h) | [41] |
| adenosine | *Shewanella* sp. Lzh-2 | *M. aeruginosa* 9110 | 1.0 $\times$ 10$^{7}$ | 12.5 | [27] |
| 2,3-indolinedione | *Acinetobacter guillouiae* A2 | *M. aeruginosa* FACHB-905 | $\sim$1.0 $\times$ 10$^{6}$ | 22.5 $\pm$ 1.9 (72 h) | [72] |
| 4-hydroxyphenethylamine (C$_{9}$H$_{11}$NO) | *Acinetobacter guillouiae* F6 | *M. aeruginosa* 9110 | NA | 5.9 (24 h) | [29] |
| cyclo(Gly-Pro) | *Stenotrophomonas* sp. F6 | *M. aeruginosa* 9110 | 1.0 $\times$ 10$^{6}$ | 1.85 (24 h) | [88] |
| cyclo(PRO-Phe) | *Bacillus* sp. S51107 | *M. aeruginosa* 9110 | 1.0 $\times$ 10$^{6}$ | 1.26 (24 h) | [41] |
| cyclo(4-OH-PRO-Leu) (C$_{11}$H$_{18}$N$_{2}$O$_{3}$) | *Chryseobacterium* sp. GLY-1106 | *M. aeruginosa* 9110 | 1.0 $\times$ 10$^{7}$ | 2.70 (24 h) | [41] |
| cyclo(Gly-Pro) | *Bacillus* sp. Lzh-5 | *M. aeruginosa* 9110 | 1.0 $\times$ 10$^{7}$ | 5.7 (24 h) | [46] |
| cyclo(Gly-Pro) | *Shewanella* sp. Lzh-2 | *M. aeruginosa* 9110 | 1.0 $\times$ 10$^{7}$ | 19.4 (24 h) | [27] |
| cyclo(Gly-Phe) | *Aeromonas* sp. GLY-2107 | *M. aeruginosa* 9110 | 1.0 $\times$ 10$^{7}$ | 4.72 (24 h) | [69] |
| trans-3-indoleacrylic acid | *Rhodococcus* sp. p52 | *M. aeruginosa* | 7.3 $\times$ 10$^{6}$ | NA | [113] |
| DL-pipecolic acid | *L-pyroglutamic acid* | NA | NA | NA | |
Table 2. Cont.

| Anticyanobacterial Substances | Strain Name             | Target Cyanobacterium | Initial Cyanobacterial Cell Density (cells ml.\(^{-1}\)) | EC\(_{50}\) (mg L.\(^{-1}\)) | References |
|-------------------------------|-------------------------|-----------------------|----------------------------------------------------------|-----------------------------|------------|
| Fusaricidins                  | *Paenibacillus polymyxa E681* | *M. aeruginosa*       | 2.37 ± 0.15 × 10\(^7\)                                   | NA                         | [3]        |
| Protein                       | *Raoultella planticola*                                         | *M. aeruginosa*       | NA                                                       | NA                         | [70]       |
| L-lysine and L-phenylalanine  | *Bacillus amyloliquefaciens T1*                                | *M. aeruginosa*       | 1.0 × 10\(^6\)                                          | NA                         | [94]       |
| L-valine                      | *Streptomyces fujianensis JXJ 0074*                            | *M. aeruginosa*       | 5.0 × 10\(^6\)                                          | NA                         | [37]       |
| L-lysine                      | *Streptomyces phaeofaciens S-9*                                | *M. aeruginosa*       | NA                                                       | NA                         | [114]      |
| L-lysine                      | *Aeromonas* sp. FM                                                | *M. aeruginosa*       | NA                                                       | NA                         | [115]      |
| Enzyme                        | *Streptomycetes neymagawaensis*                                 | *M. aeruginosa*       | NA                                                       | NA                         | [80]       |
| L-amino acid oxidase          | *Aquimarina spongiae*                                            | *M. aeruginosa*       | NA                                                       | NA                         | [77]       |
| Microcystinase A              | *Sphingopyxis* sp. C1                                            | *M. aeruginosa*       | 3.75 × 10\(^6\)                                        | NA                         | [55]       |
| Active flocculating substance | *Halobacillus* sp. H9                                            | *M. aeruginosa* PCC 7806 | 2.0 × 10\(^7\)                                         | NA                         | [26]       |
| Clavulanate                   | *Aeromonas* sp. FM                                                | *M. aeruginosa*       | NA                                                       | NA                         | [115]      |
| Biosurfactant                 | *Bacillus subtilis* C1                                            | *M. aeruginosa*       | 1000 *                                                   | NA                         | [86]       |
| Lumichrome                    | *Aeromonas* veronii A134                                         | *M. aeruginosa* MGK   | NA                                                       | NA                         | [116]      |
| Triterpenoid saponin          | *Streptomyces* sp. L74                                           | *M. aeruginosa*       | 1 × 10\(^6\)                                            | NA                         | [33]       |
| Hydroquinone                  | *Stenotrophomonas* sp. F6                                        | *M. aeruginosa* 9110  | 0.96 (24 h)                                             | NA                         | [29]       |
| Nanaomycin A methyl ester     | *Streptomyces halstedii YIM 001*                                 | *M. aeruginosa*       | −1.0 × 10\(^6\)                                         | 2.97 (72 h)                | [117]      |

NA means the date is not available, not mentioned or unclear; An asterisk (*) stands for the Chl a concentration, µg L.\(^{-1}\).
3. Anticyanobacterial Modes and Mechanisms

3.1. Anticyanobacterial Modes

In general, the anticyanobacterial modes by microorganisms are divided into direct attack (bacterial and cyanobacterial cell contact) and indirect attack (the release of anticyanobacterial substances) (Figure 1) \[10,32,72,118\]. To date, although anticyanobacteria can directly kill several different kinds of cyanobacteria, only few has been reported. A wide range of cyanobacteria including \textit{M. aeruginosa}, \textit{M. wese}, \textit{A. viridis}, \textit{A. flos-aquae}, \textit{Exiguobacterium tenuis}, \textit{Nostoc punctiforme} and \textit{Spirulina maxima} are lysed by \textit{B. cereus} DC22 with the direct attack mode, as well as chlorophyceae (\textit{Chlorella ellipsoidea} and \textit{Selenastrum capricornutum}) \[89\]. In addition to \textit{B. cereus}, other anticyanobacteria that destroy \textit{M. aeruginosa} with direct attack have also been reported. For example, the anticyanobacterial modes of \textit{Aeromonas bestiarum} HYD0802-MK36 \[20\], \textit{Chryseobacterium sp.} \[40\], \textit{Streptomyces globisporus} G9 \[83\], \textit{Alcaligenes denitrificans} \[59\], and \textit{Shigella} sp. H3 \[60\] on \textit{M. aeruginosa} are regarded as direct attack, and a number of cyst-like cells are formed in cyanobacteria during the direct attack \[10\]. It is speculated that the cyanobacterial cell walls are partially destroyed at the contact point with the anticyanobacteria, and the formation of cyst-like cells is a potential defense system against anticyanobacteria \[2,10\].

![Figure 1. Anticyanobacterial modes of microorganisms against \textit{M. aeruginosa}.](image)

The indirect attack mode has been observed in the numerous metabolites from most of the reported anticyanobacterial microorganisms, and the anticyanobacterial characteristics of these bacteria seem to be unique to \textit{M. aeruginosa}. Up to now, the genus \textit{Acinetobacter} \[22,72,119\] and \textit{Exiguobacterium} \[44,45,96\], which firstly attach to \textit{M. aeruginosa} and then cause serious damage to the cyanobacterial cell structure and morphology, are recognized as degrading \textit{M. aeruginosa} by producing anticyanobacterial substances. Nevertheless, some anticyanobacteria can inhibit or kill green alga and cyanobacteria with an indirect attack simultaneously. For instance, \textit{B. amyloliquefaciens} FZB42 can efficiently eliminate \textit{M. aeruginosa}, \textit{Anabaena} sp., \textit{A. flos-aquae} and \textit{Nostoc} sp. by secreting bacilysin \[91\]. In line with this genus, \textit{B. amyloliquefaciens} T1 produces amino acids to inhibit the growth of four \textit{Microcystis} spp., but not of \textit{Anabaena flos-aquae} or \textit{Chlorella pyrenoidosa} \[49,94\]; \textit{S. amritsarenensis} HG-16 kills \textit{A. flos-aquae}, \textit{Phormidium} sp. and five \textit{Microcystis} spp. by secreting active substances, but has a small inhibitory effect on \textit{C. vulgaris} and a promoting effect on \textit{Oscillatoria} sp. \[5\]. Along with this, the anticyanobacterial modes of \textit{Aquimarina salinaria} on green algae and cyanobacterium, which is a direct attack on \textit{C. vulgaris} 211-31 and an indirect attack on \textit{M. aeruginosa} MTY01, is quite different \[39\]. Furthermore, a recent study firstly demonstrated that \textit{Paucibacter aquatile} DH15 inhibits \textit{M. aeruginosa} by both direct and indirect attacks \[61\], which would be interesting and could shed further light on the anticyanobacterial modes by microorganisms.
3.2. Anticyanobacterial Mechanisms

Currently, the anticyanobacterial mechanisms of microorganisms against *M. aeruginosa* are mainly dependent on the attack modes, and these mechanisms are revealed with the changes in the photosynthesis system, antioxidant enzymes system, gene expression and QS system (Figure 2).

![Figure 2. Anticyanobacterial mechanisms of microorganisms against *M. aeruginosa*](image)

3.2.1. Effects of Anticyanobacterial Microorganisms on Photosynthesis

Photosynthesis, which converts solar energy into chemical energy through the photosynthesis system (PS) II and PS I, is the principal mode of energy metabolism in cyanobacteria [120]. Anticyanobacterial microorganisms can significantly affect the photosynthesis of *M. aeruginosa* cells in several ways, including decreasing the chlorophyll *a* (Chl *a*) contents and photosynthetic pigments [56], and the disruption of the electron transport pathway in PS [23,93]. Chl *a* is one of the important components of cyanobacterial pigments. It is markedly decreased in *M. aeruginosa* under the exposure of anticyanobacteria such as *P. aeruginosa* [18,63], *Streptomyces* sp. [33,36], *Exiguobacterium* sp. [44,45], and so on. For the photosynthetic pigments, phycocyanobilin (PC), allophycocyanin (APC) and phycoerythrin (PE) are major indicators of cyanobacterial photosynthetic efficiency and are essential apparatus for light harvesting [61], and the addition of an anticyanobacterium results in a significant decrease in the PC, APC and PE by disrupting the synthesis of an photosynthetic pigments [56]. In addition, the expressions of *pcA* and *apcA* genes for PC and APC synthesis in *M. aeruginosa* are down-regulated by *Paenibacillus* aquatile DH15, which shows an inhibition effect on active chlorophyll [61]. It has been noted that the Chl *a* decrease is closely related to the reduction in photosynthetic pigments, and the cyanobacterial membrane is sensitive and easily damaged by anticyanobacterium [56].

The variations of cyanobacterial energy kinetics have also been evaluated by Chl fluorescence parameters, such as the maximum photochemical quantum yield of PS II (Fv/Fm), the effective quantum yield (Φe), and the maximum electron transport rate (ETRmax) [41,95]. With the addition of fermentation filtrate (5%, v/v) of *Paenibacillus* sp. SJ-73, the Fv/Fm values of *M. aeruginosa* PCC7806 and *M. aeruginosa* TH1701 dramatically decline from 0.52 and 0.29 to 0 [95]; similarly, it is only 0.08 (14.3% of the initial value) for *M. aeruginosa* FACHB-905 after being treated for 24 h by the fermentation filtrate (5%, v/v) of *Raoultella* sp. S1 [23]. Besides, the Φe and ETRmax of *M. aeruginosa* 9110 following the treatment of *Chryseobacterium* sp. GLY-1106 decrease gradually with time [41]; the ETRmax values of *M. aeruginosa* are also depressed significantly under the stress of *Raoultella* sp.
3.2.2. Effects of Anticyanobacterial Microorganisms on Antioxidant Enzymes System

The oxidative damage of the cyanobacterial cells can occur under different environmental stress conditions, and it will result in an increase in reactive oxygen species (ROS), which includes the superoxide anion radical, hydrogen peroxide and hydroxyl radicals [51,61]; while excess ROS often leads to oxidative stress, lipid peroxidation, and DNA damage [56,121]. The enzymatic antioxidants (such as catalase (CAT), superoxide dismutase (SOD), peroxidase (POD), and so on) and non-enzymatic antioxidants (such as ascorbic acid (AsA) and glutathione (GSH)) are responsible for removing the overproduction of ROS [2,31,41]. For instance, *Streptomyces eurocicus* [X]-0089 inhibits the growth of cyanobacterial cells in various ways, including promoting ROS production (e.g., $O_2•^−$), inhibiting the antioxidant synthesis, removing chlorophyll and destroying cell walls [38].

The ROS of cyanobacteria increases excessively by either the direct attack or indirect attack of anticyanobacterial microorganisms. The $O_2•^−$ content in *M. aeruginosa* cells is induced largely by 4 µg mL$^{-1}$ 3, 4-dihydroxybenzalacetone (DBL) secreted from *Phellinus nxis* HN-1 and increased from 0.360 ± 0.001 to 0.400 ± 0.001 µg g$^{-3}$ [104]. The ROS level of *M. aeruginosa* NIES 843 treated with *Bacillus* sp. AF-1 (cell-free filtrate) was lower than that of the control at the first 48 h but much higher at 72 h, indicating that some evasive mechanisms were taken to prevent the ROS accumulation in cyanobacterial cells at the initial stage [51]. Similar variations of ROS have been observed in *M. aeruginosa* KW after being treated with *Pauicibacter aquatile* DH15, and the malondialdehyde (MDA) content and SOD activity related to remove ROS also increased at first and then decreased [61]; the MDA content, CAT and POD activity of *M. aeruginosa* FACHB-905 also increased quickly when fermentation liquid (5%, v/v) of *P. aeruginosa* [18] and *P. chrysosporium* was added quickly [101]; moreover, the responses of *M. aeruginosa* FACHB-905 cells to *Streptomyces* sp. KY-34 and *Streptomyces* sp. HJC-D1 following a similar pattern with the increases of CAT, SOD and POD, and the MDA further increased during the incubation time [56,121]. Although the antioxidants increased immediately to relieve the damage caused by anticyanobacteria, the cyanobacterial cell membrane may have decompose due to the accumulation of MDA [18,67,121].

For the non-enzymatic antioxidants, the variation of GSH is opposite to that of the antioxidant activity. The *Bacillus licheniformis* Sp34 induces more GSH production in *M. aeruginosa* at first to clear ROS, but the GSH content is much lower at 20 h (compared with the control) [47]. Such a phenomenon is also obtained in the anticyanobacterial process of *Raoultella* sp. S1 [23]. The prodigiosin from *Hahella* sp. KA22 also leads to the variation of GSH content, while the GSH content decreases slightly after exposure for 36 h [31]. These results demonstrate that the ROS levels and MDA contents decrease under prolonged exposure to anticyanobacteria [31,33,65]; in addition, the non-enzymatic antioxidants also play a critical role in protecting the cyanobacterial cells from oxidative damage under anticyanobacterial stress [23].

3.2.3. Effects of Anticyanobacterial Microorganisms on Gene Expression

The relative transcriptional level of some critical genes in cyanobacteria can be dramatically changed by anticyanobacterial microorganisms and substances, including genes related to the synthesis of photosystem reaction center proteins (*PsaA, psaB, psbA1* and *psbD1*) [47,57], peptidoglycan synthesis (*glmS*), membrane proteins (*ftsH*), antioxidantase (*prx*) [100], heat-shock proteins (*grpE*) [100], fatty acids (*fabZ*) [100], cyanotoxin microcystins (*mcyA, mcyB, mcyC* and *mcyD*) [83,97], the functions of cell division (*ftsZ*) [93], CO$_2$ fixation (*rbcL*) [61], and DNA repair (*ftsH* and *recA*) [2,5]. Researchers have reported that the tran-
scription expressions of genes $ftsZ$, $psbA1$, and $glmS$ are decreased by DBL that is isolated from $P. noxius$ HN-1 [104] and bacilysin that secreted from $B. amylovorans$ FZB42 [91]. The expressions of gene $ftsZ$ and $psbA$ are also significantly inhibited by $Bacillus$ sp. B50 [93], and the transcriptions of photosynthesis-related genes ($psaB$ and $psbD1$) and CO$_2$ fixation gene ($rbcL$) are inhibited by $B. licheniformis$ Sp34 [47], indicating that the metabolisms of $M. aeruginosa$ are destroyed. Other studies on transcriptomic analysis have demonstrated that the principal subunits of the reaction center ($PsaA$ and $PsaB$) and other subunits ($PsaC$, $PsaE$, $PsaD$, $PsaF$ and $PsaL$) are significantly down-regulated by $B. laterosporus$ Bl-zj [57]. It is similar in the case of $S. globisorus$ G9, $S. amritsarensis$ and $Raoultella$ sp. S1, which suppresses the expression of $psbA1$, $psbD1$ or $rbcL$ [5,23,83]. The reduction in photosynthesis-related gene transcripts might result in an interruption in the electron transport chain and may finally affect the CO$_2$ fixation process [61].

Gene such as $ncyB$ that are involved in microcystins synthesis are also inhibited by $Penicillium$ spp. [97], the white-rot fungi $P. chrysosporium$ [100,101] and $P. noxius$ HN-1 [104]; moreover, both directly attack the anticyanobacterium ($S. globisorus$ G9) [83] and indirectly attack anticyanobacteria (including $S. amritsarensis$ HG-16 and $Bacillus$ sp. AF-1) could inhibit microcystins synthesis [5,51]. However, the inhibiting ability of $Bacillus$ sp. AF-1 has not been confirmed with microcystins measurements [5].

### 3.2.4. Regulating the Anticyanobacterial Activity by QS System

QS system is the regulator control system for microorganisms that sense the cell density of their own species and make themselves to coordinate gene expression and physiological accommodation on a community scale [122,123]. It is a cell-to-cell communication that relies on the signal molecules [124], and the accumulated QS signals can bind to the cognate receptors and regulate biological activities and cellular functions [69,125]. Previous studies have shown that microbial behaviors such as the secondary metabolites, cell motility and antibiotic resistance are all influenced by QS [122,123]; in addition, QS signals that contribute to the interactions between planktonic microalgae and bacteria are summarized as the N-acyl-homoserine lactones (AHLs) [69], the 2-alkyl-4-quinolones (AQs) [123], long-chain fatty acids and fatty acid methyl esters (autoinducer-2, AI-2) and dihydroxypentanedione furanone derivatives [12]. It is agreed that most of the anticyanobacterial activities by Gram-negative bacteria (such as $Pseudomonas$ sp., $Acinetobacter$ sp., etc.) are the consequence of bacterial-cyanobacterial QS rather than bacterium-cyanobacteria interactions [12,124]. Some species of $Serratia$ sp. [109] and $Hahella$ sp. [31] can produce prodigiosin to inhibit $M. aeruginosa$, and the prodigiosin production is regulated by $LuxI$ and $LuxR$, which are the crucial genes of AHLs [126]. The QS signal molecule (C4-HSL), which belongs to the classic AHL-based $LuxIR$-type QS system of Gram-negative bacteria, is responsible for the synthetic process of the anticyanobacterial compound (3-methylindole) from $Aeromonas$ sp. GLY-2107 [69]. During the anticyanobacterial process, the QS systems of Gram-negative bacteria produce AHLs signaling molecules, which are synthesized by the basic regulatory protein of $LuxI$ [69,88,126].

In contrast, a wide range of the Gram-positive anticyanobacteria (such as $Streptomyces$ sp., $Bacillus$ sp., etc.) generally use AI-2 as the signal molecules in QS systems [125]. The anticyanobacterium $S. xianmenensis$ Lzh-2 exhibits QS behavior, and the $LuxS$ gene is crucial for the AI-2 type QS system; obviously, the anticyanobacterial activity of $S. xianmenensis$ Lzh-2 is regulated through the $LuxS$/AI-2 QS system by inducing the production of anticyanobacterial compounds 2, 3-indolinedione and cyclo(Gly-Pro) [126]. The AI-2 type QS behavior is present in $Bacillus$ sp. [127]. Genomic analysis of $B. subtilis$ JA has indicated the existence of the $LuxS$ gene that regulates the pheromone biosynthesis, and the high-molecular-weight anticyanobacterial compounds (>3 kDa) produced by $Bacillus$ sp. S51107 have been proven to be primarily regulated by the $Npr-R-NprX$-type (AI-2) QS system [88]. As a consequence, the AI-2 QS system has been considered as a possible strategy to regulate the behavior of the anticyanobacterial effects of Gram-positive bacteria.
QS behavior has been reported in recent years, there is still an improved understanding of
the interaction between cyanobacteria and anticyanobacterial microorganisms.

4. Application and Prospective
4.1. Application of Anticyanobacterial Microorganisms

In consideration of the drawbacks of physical and chemical methods, the biological
control of HCBs is of great importance for the aquatic ecological environment. In particu-
lar, the application of anticyanobacterial microorganisms (bacteria and fungi) or their
anticyanobacterial substances is regarded as the most suitable approach due to the eco-
nomical and environment-friendly performance. It is well known that it is difficult for
microorganisms to exist persistently in the aquatic environment [128]. To overcome this
limitation, microbial immobilized technology using different porous matrices for enhanc-
ing the cyanobacterial removal efficiency has been attempted. For example, a biological
treatment system equipped with coconut packing carriers has been established to enrich
anticyanobacteria. The results indicate that the average anticyanobacterial efficiency of
87.69 ± 2.44% is obtained and 13 genera anticyanobacteria, which account for 10.17% of
the total bacteria, are responsible for the removal of HCBs [129]. As the Brevundimonas sp.
AA06 is immobilized using polyvinyl alcohol-sodium alginate beads and B. methylotroph-
icus ZJU is immobilized with Fe3O4 nanoparticles, the inhibition effects are much better
than freely suspended cells [24,50]; meanwhile, the extracellular polymeric substances
produced by P. aeruginosa ZJU1 are made as bioflocculants, and the removal efficiency of
M. aeruginosa reached 100 ± 0.07% in 5 min at the dosage of 2.75 g/L bioflocculant [130].
These strategies demonstrating the “indirect attack” of microorganisms could be immobi-
лизized by multi-functional systems and their anticyanobacterial products could be further
enriched. Taking full account of the uncertainties of using anticyanobacterial microorgan-
isms to control/eliminate HCBs in natural waters, the “direct attack” microorganisms may
be as ineffective as “indirect attack” microorganisms in actual applications.

In situ eutrophication controls have also been carried out in other research. It was
found that the Chl a removal efficiency reached 99.2% when the anticyanobacterium
B. cereus N-1 was immobilized with a floating carrier for natural eutrophication water [48];
the wild cyanobacteria from a shallow eutrophic pond were significantly controlled by
adding solid B. amyloliquefaciens T1 agent at the concentration of 0.5 mg L−1 (or above) [49].
Taking the recycling utilization of the industrial waste product into account, approximately
80.0% of the M. aeruginosa and 48.1% of the microcystin-LR were removed by the biosorbent,
which originated from the Escherichia coli biomass [131]. Apart from the persistent existence
of microorganisms, anticyanobacterial effects are concerned with environmental conditions
and nutrient concentrations [132]. As the previous study indicates, the yeast Candida utilis
F87, which converts the nitrogen and phosphorus into microbial protein, can inhibit the
growth of M. aeruginosa by nutrient competition [133]. Therefore, the issue of nutrient
competition in cyanobacterial control using microorganisms is a crucial consideration.
Based on the current collection of literature, the anticyanobacterial microorganisms have a
potential application for HCBs control in the natural environment.

4.2. Summary and Prospective

Interactions between cyanobacteria and microorganisms are considered to be an inte-
gral part of the geochemical cycle. However, with the spatial and temporal heterogeneity,
these interactions can be modulated in various ways, and highly efficient anticyanobacterial
strategies in the eutrophic environment can be obtained from microorganisms. Plentiful
studies have reported on ecological interactions between anticyanobacteria and cyanobac-
terium M. aeruginosa, which are focused on the anticyanobacterial microorganisms, sub-
stances, modes and mechanisms. Although the anticyanobacterial approach by microor-
ganisms seems to be safe and effective, it is still appreciated that there are limitations and
challenges in field applications. A drawback of this approach is that anticyanobacterial
microorganisms must be chosen carefully to secrete specific anticyanobacterial compounds
and the dosage of the microorganism inoculum or microbial agent is of great importance. On the other hand, the abiotic and biotic factors of the natural environment may have a remarkable influence on the distribution of cyanobacteria and the cyanobacterial response to anticyanobacterial substances.

Besides the target specificity, the complicating factors in realistic eutrophic environment research are the complexity of consortia with multiple species and the unsustainability of anticyanobacteria. It is delightful to see that the studies for HCBs control in situ have contributed to a better understanding of the role of anticyanobacterial microorganisms, especially the multiple regulations for microcysts. Further investigations should be focused on the simultaneous removal of nitrogen, phosphorus and microcysts by mixed microbial community, and the understanding of the cell-to-cell communication and the defense mechanisms of QS systems. Besides, more insights are needed for the specific genes encoding photosystem synthesis, peptidoglycan synthesis, membrane proteins, cyanotoxin microcysts, DNA repair and so on.

**Author Contributions:** Conceptualization, Y.K., L.M. and J.L.; investigation, Y.W., S.M. and X.Z.; writing—original draft preparation, Y.K., Y.W. and L.M.; writing—review and editing, J.L., S.M. and X.Z. All authors have read and agreed to the published version of the manuscript.

**Funding:** This study was financially supported by grants from the Open Research Fund Program of State Key Laboratory of Eco-hydraulics in Northwest Arid Region, Xi’an University of Technology (No. 2021FKT-8), the Key Laboratory of Water Pollution Control and Environmental Safety of Zhejiang Province (No. 2018SZJSHKF06) and the Natural Science Foundation of Jiangsu Province (No. BK20150165).

**Institutional Review Board Statement:** Not applicable.

**Informed Consent Statement:** Not applicable.

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

**References**

1. Harke, M.J.; Steffen, M.M.; Gobler, C.J.; Otten, T.G.; Wilhelm, S.; Wood, S.A.; Paerl, H.W. A review of the global ecology, genomics, and biogeography of the toxic cyanobacterium, *Microcystis* spp. Harmful Algae 2016, 54, 4–20. [CrossRef] [PubMed]

2. Yang, C.; Hou, X.; Wu, D.; Chang, W.; Zhang, X.; Dai, X.; Du, H.; Zhang, X.; Igarashi, Y.; Luo, F. The characteristics and algicidal mechanisms of cyanobactericidal bacteria, a review. World J. Microbiol. Biotechnol. 2020, 36, 188. [CrossRef]

3. Ko, S.-R.; Lee, Y.-K.; Srivastava, A.; Park, S.-H.; Ahn, C.-Y.; Oh, H.-M. The Selective Inhibitory Activity of a Fusaricidin Derivative on a Bloom-Forming Cyanobacterium, *Microcystis* sp. Microbiol. Biotechnol. 2019, 29, 59–65. [CrossRef]

4. Han, S.-I.; Kim, S.; Choi, K.Y.; Lee, C.; Park, Y.; Choi, Y.-E. Control of a toxic cyanobacterial bloom species, *Microcystis aeruginosa*, using the peptide HPA3NT3-A2. Environ. Sci. Pollut. Res. 2019, 26, 32255–32265. [CrossRef] [PubMed]

5. Yu, Y.; Zeng, Y.; Li, J.; Yang, C.; Zhang, X.; Luo, F.; Dai, X. An algicidal *Streptomyces amritsarensis* strain against *Microcystis aeruginosa* strongly inhibits microcystin synthesis simultaneously. Sci. Total Environ. 2018, 650, 34–43. [CrossRef]

6. Mohamed, Z.A.; Hashem, M.; Alamri, S.A. Growth inhibition of the cyanobacterium *Microcystis aeruginosa* and degradation of its microcystin toxins by the fungus *Trichoderma citrinoviride*. Toxicon 2014, 86, 51–58. [CrossRef] [PubMed]

7. Goslan, E.H.; Seigle, C.; Purcell, D.; Henderson, R.; Parsons, S.A.; Jefferson, B.; Judd, S.J. Carbonaceous and nitrogenous disinfection by-product formation from algal organic matter. Chemosphere 2016, 170, 1–9. [CrossRef]

8. Xin, H.; Yang, S.; Tang, Y.; Wu, M.; Deng, Y.; Xu, B.; Gao, N. Mechanisms and performance of calcium peroxide-enhanced Fe(ii) coagulation for treatment of *Microcystis aeruginosa*-laden water. Environ. Sci. Water Res. Technol. 2020, 6, 1272–1285. [CrossRef]

9. Chen, Z.; Li, J.; Chen, M.; Koh, K.Y.; Du, Z.; Gin, K.Y.-H.; He, Y.; Ong, C.N.; Chen, J.P. *Microcystis aeruginosa* removal by peroxides of hydrogen peroxide, peroxymonosulfate and peroxydisulfate without additional activators. Water Res. 2021, 201, 117263. [CrossRef]

10. Wang, M.; Chen, S.; Zhou, W.; Yuan, W.; Wang, D. Algal cell lysis by bacteria: A review and comparison to conventional methods. Algal Res. 2020, 46, 101794. [CrossRef]

11. Matthijs, H.C.P.; Jančula, D.; Visser, P.M.; Maršílek, B. Existing and emerging cyanocidal compounds: New perspectives for cyanobacterial bloom mitigation. Aquat. Ecol. 2016, 50, 443–460. [CrossRef]

12. Demuez, M.; González-Fernández, C.; Ballesteros, M. Algicidal microorganisms and secreted algicides: New tools to induce microalgal cell disruption. Biotechnol. Adv. 2015, 33, 1615–1625. [CrossRef] [PubMed]

13. Sun, R.; Sun, P.; Zhang, J.; Esquivel-Elizondo, S.; Wu, Y. Microorganisms-based methods for harmful algal blooms control: A review. Bioresour. Technol. 2018, 248, 12–20. [CrossRef] [PubMed]
14. Benegas, G.R.S.; Bernal, S.P.E.; de Oliveira, V.M.; Passarini, M.R.Z. Antimicrobial activity against Microcystis aeruginosa and degradation of microcystin-LR by bacteria isolated from Antarctica. *Environ. Sci. Pollut. Res.* 2021, 28, 52381–52391. [CrossRef] [PubMed]

15. Li, Y.; Wu, X.; Jiang, X.; Liu, L.; Wang, H. Algalicidal activity of *Aspergillus niger* induced by calcium ion as signal molecule on *Microcystis aeruginosa*. *Algal Res.* 2021, 60, 102536. [CrossRef]

16. Meyer, N.; Bigalke, A.; Kaulfuß, A.; Pohnert, G. Strategies and ecological roles of algalicidal bacteria. *FEMS Microbiol. Rev.* 2017, 41, 880–899. [CrossRef]

17. Mohamed, Z.A.; Hashem, M.; Alamri, S.; Campos, A.; Vasconcelos, V. Fungal biodegradation and removal of cyanobacteria and microalgae: Potential applications and research needs. *Environ. Sci. Pollut. Res.* 2021, 28, 37041–37050. [CrossRef]

18. Zhou, S.; Yin, H.; Tang, S.; Peng, H.; Yin, D.; Yang, Y.; Liu, Z.; Dang, Z. Physiological responses of *Microcystis aeruginosa* against the algalicidal bacterium *Pseudomonas aeruginosa*. *Ecotoxicol. Environ. Saf.* 2016, 127, 214–221. [CrossRef]

19. Zhang, H.; Yu, Z.; Huang, Q.; Xiao, X.; Wang, X.; Zhang, F.; Wang, X.; Liu, Y.; Hu, C. Isolation, identification and characterization of phytoplanктон-lytic bacterium CH-22 against *Microcystis aeruginosa*. *Linnmologica* 2011, 41, 70–77. [CrossRef]

20. Park, B.S.; Park, C.-S.; Shin, Y.; Yoon, S.; Han, M.-S.; Kang, Y.-H. Different Algicidal Modes of the Two Bacteria HYD0802-MK36 and *Pseudomonas syringae* KACC10292 against Harmful Cyanobacteria *Microcystis aeruginosa*. *Toxins* 2022, 14, 128. [CrossRef]

21. Das Nishu, S.; Kang, Y.; Han, I.; Jung, T.Y.; Lee, T.K. Nutritional status regulates algicidal activity of *Aeromonas* sp. L23 against cyanobacteria and green algae. *PLoS ONE* 2019, 14, e0213370. [CrossRef]

22. Li, H.; Ai, H.; Kang, L.; Sun, X.; He, Q. Simultaneous *Microcystis* Algicidal and Microcystin Degrading Capability by a Single *Acinetobacter* Bacterial Strain. *Environ. Sci. Technol.* 2016, 50, 11903–11911. [CrossRef] [PubMed]

23. Li, D.; Kang, X.; Chu, L.; Wang, Y.; Song, X.; Zhao, X.; Cao, X. Algicidal mechanism of *Raoultella ornithinolytica* against *Microcystis aeruginosa*: Antioxidant response, photosynthetic system damage and microcystin degradation. *Environ. Pollut.* 2021, 287, 117644. [CrossRef] [PubMed]

24. Zhang, H.; Wang, Y.; Huang, J.; Fan, Q.; Wei, J.; Wang, F.; Jia, Z.; Xiang, W.; Liang, W. Inhibition of *Microcystis aeruginosa* using *Brevundimonas* sp. AA06 immobilized in polyvinyl alcohol-sodium alginate beads. *Desalination Water Treat.* 2018, 111, 192–200. [CrossRef]

25. Mu, R.; He, Y.; Liu, S.; Wang, X.; Fan, Z. The Algicidal Characteristics of One Algae-Lysing FDT5 Bacterium on *Microcystis aeruginosa*. *Geormicrobiol. J.* 2009, 26, 516–521. [CrossRef]

26. Zhang, D.; Ye, Q.; Zhang, F.; Shao, X.; Fan, Y.; Zhu, X.; Li, Y.; Yao, L.; Tian, Y.; Zheng, T.; et al. Flocculating properties and potential of *Halobacillus* sp. strain H9 for the mitigation of *Microcystis aeruginosa* blooms. *Chemosphere* 2018, 218, 138–146. [CrossRef]

27. Li, Z.; Lin, S.; Liu, X.; Tan, J.; Pan, J.; Yang, H. A freshwater bacterial strain, *Shewanella* sp. Lzh-2, isolated from Lake Taihu and its two algicidal active substances, hexahydropyrrolo[1,2-a]pyrazine-1,4-dione and 2,3-indolinedione. *Appl. Microbiol. Biotechnol.* 2014, 98, 4737–4748. [CrossRef]

28. Sun, P.; Esquivel-Elizondo, S.; Zhao, Y.; Wu, Y. Glucose triggers the cytotoxicity of *Citrobacter* sp. R1 against *Microcystis aeruginosa*. *Sci. Total Environ.* 2017, 603–604, 18–25. [CrossRef]

29. Lin, S.; Geng, M.; Liu, X.; Tan, J.; Yang, H. On the control of *Microcystis aeruginosa* and *Synechococcus* species using an algicidal bacterium, *Stenotrophomonas F6*, and its algicidal compounds cyclo-(Gly-Pro) and hydroquinone. *J. Appl. Phycol.* 2015, 28, 345–355. [CrossRef]

30. Liu, W.; Yang, J.; Tian, Y.; Zhou, X.; Wang, S.; Zhu, J.; Sun, D.; Liu, C. An in situ extraction fermentation strategy for enhancing prodigiosin production from *Serratia marcescens* BWL1001 and its application to inhibiting the growth of *Microcystis aeruginosa*. *Biochem. Eng. J.* 2020, 166, 107836. [CrossRef]

31. Yang, K.; Chen, Q.; Zhang, D.; Zhang, H.; Lei, X.; Chen, Z.; Li, Y.; Hong, Y.; Ma, X.; Zheng, W.; et al. The algicidal mechanism of prodigiosin from *Halhella* sp. KA22 against *Microcystis aeruginosa*. *Sci. Rep.* 2017, 7, 7750. [CrossRef] [PubMed]

32. Kong, Y.; Wang, Q.; Chen, Y.; Xu, X.; Zhu, L.; Yao, H.; Pan, H. Anticyanobacterial process and action mechanism of *Streptomyces* sp. HJC-D1 on *Microcystis aeruginosa*. *Environ. Prog. Sustain. Energy* 2020, 39, e13392. [CrossRef]

33. Luo, J.; Wang, Y.; Tang, S.; Liang, J.; Lin, W.; Luo, L. Isolation and Identification of Algicidal Compound from *Streptomyces* and Algicidal Mechanism to *Microcystis aeruginosa*. *PLoS ONE* 2013, 8, e67444. [CrossRef] [PubMed]

34. Lee, Y.-K.; Ahn, C.-Y.; Kim, H.-S.; Oh, H.-M. Cyanobactericidal effect of *Rhodococcus* sp. isolated from eutrophic lake on *Microcystis* sp. *Biotechnol. Lett.* 2010, 32, 1673–1678. [CrossRef]

35. Chen, H.; Fu, L.; Luo, L.; Lu, J.; White, W.L.; Hu, Z. Induction and Resuscitation of the Viable but Nonculturable State in a Cyanobacteria-Lysing Bacterium Isolated from Cyanobacterial Bloom. *Microb. Ecol.* 2011, 63, 64–73. [CrossRef]

36. Hua, X.-H.; Li, J.-H.; Li, J.-J.; Zhang, L.-H.; Cui, Y. Selective inhibition of the cyanobacterium, *Microcystis*, by a *Streptomyces* sp. *Biotechnol. Lett.* 2009, 31, 1531–1535. [CrossRef]

37. Zhang, B.-H.; Chen, W.; Li, H.-Q.; Yang, J.-Y.; Zha, D.-M.; Duan, Y.-Q.; Hozzein, N.W.; Xiao, M.; Gao, R.; Li, W.-J. L-valine, an antialgal amino acid from *Streptomyces jiujiangensis* JX]0074. *Appl. Microbiol. Biotechnol.* 2016, 100, 4627–4636. [CrossRef]

38. Zhang, B.-H.; Ding, Z.-G.; Li, H.-Q.; Mou, X.-Z.; Zhang, Y.-Q.; Yang, J.-Y.; Zhou, E.-M.; Li, W.-J. Algicidal Activity of *Streptomyces eurodicus* JX]-0089 *Metabolites* and Their Effects on *Microcystis* Physiology. *Appl. Environ. Microbiol.* 2016, 82, 5132–5143. [CrossRef]
40. Zhang, C.; Massey, I.Y.; Liu, Y.; Huang, F.; Gao, R.; Ding, M.; Xiang, L.; He, C.; Li, Y.; et al. Identification and characterization of a novel indigenous algicidal bacterium Chryseobacterium species against Microcystis aeruginosa. J. Toxicol. Environ. Heal. Part A 2019, 82, 845–853. [CrossRef]

41. Guo, X.; Liu, X.; Pan, J.; Yang, H. Synergistic algicidal effect and mechanism of two diketopiperazines produced by Chryseobacterium sp. strain GLY-1106 on the harmful bloom-forming Microcystis aeruginosa. Sci. Rep. 2015, 5, 14720. [CrossRef] [PubMed]

42. Furusawa, G.; Iwamoto, K. Removal of Microcystis aeruginosa cells using the dead cells of a marine filamentous bacterium, Aureocapsa sp. CCB-QB1. PeerJ 2022, 10, e12867. [CrossRef] [PubMed]

43. Li, Y.; Hongyi, W.; Komatsu, M.; Ishibashi, K.; Jinsan, L.; Ito, T.; Yoshikawa, T.; Maeda, H. Isolation and characterization of a novel bacteriophage specific to Microcystis aeruginosa. Appl. Microbiol. Biotechnol. 2014, 99, 981–990. [CrossRef]

44. Li, Y.; Liu, L.; Xu, Y.; Li, P.; Zhang, K.; Jiang, X.; Zheng, T.; Wang, H. Stress of algicidal substances from a bacterium Exiguobacterium sp. h10 on Microcystis aeruginosa. Lett. Appl. Microbiol. 2016, 64, 57–65. [CrossRef]

45. Liu, J.; Yang, C.; Chi, Y.; Wu, D.; Dai, X.; Zhang, X.; Igarashi, Y.; Luo, F. Algicald characterization and mechanism of Bacillus licheniformis Sp34 against Microcystis aeruginosa in Dianchi Lake. J. Basic Microbiol. 2018, 59, 206–214. [CrossRef]

46. Lu, Z.; Geng, M.; Yang, H. Algicald activity of Bacillus sp. Lzh-5 and its algicald compounds against Microcystis aeruginosa. Appl. Microbiol. Biotechnol. 2014, 99, 107–114. [CrossRef] [PubMed]

47. Li, Y.; Kong, Y.; Gao, S.; Miao, L.; Zou, P.; Xu, B.; Zeng, C.; Zhang, X. Bacillus myloliiqueficiens T1 as a potential control agent for cyanobacteria. J. Appl. Physiol. 2018, 127, 1213–1221. [CrossRef] [PubMed]

48. Liu, P.; Hui, C.; Wang, S.; Khan, R.A.; Zhang, Q.; Zhao, Y.-H. Enhancement of algicald properties of immobilized Bacillus methylotrophicus ZJU by coating with magnetic Fe3O4 nanoparticles and wheat bran. J. Hazard. Mater. 2015, 301, 65–73. [CrossRef]

49. Sun, P.; Hu, C.; Wang, S.; Khan, R.A.; Zhang, Q.; Zhao, Y.-H. Enhancement of algicald properties of immobilized Bacillus methylotrophicus ZJU by coating with magnetic Fe3O4 nanoparticles and wheat bran. J. Hazard. Mater. 2015, 301, 65–73. [CrossRef]

50. Xuan, H.; Dai, X.; Li, J.; Zhang, X.; Yang, C.; Luo, F. A Bacillus sp. strain with antagonistic activity against Fusarium graminearum kills Microcystis aeruginosa selectively. Sci. Total Environ. 2017, 583, 214–221. [CrossRef] [PubMed]

51. Kim, W.; Kim, M.; Hong, M.; Park, W. Killing effect of deinoxanthins on cyanobloom-forming Microcystis aeruginosa: Eco-friendly production and specific activity of deinoxanthins. Environ. Res. 2021, 200, 114555. [CrossRef] [PubMed]

52. Li, Y.; Zhu, H.; Lei, X.; Zhang, H.; Cai, G.; Chen, Z.; Fu, L.; Xu, H.; Zheng, T. The death mechanism of the harmful algal bloom species Alexandrium tamarense induced by algicald bacterium Deinococcus sp. Y35. Front. Microbiol. 2015, 6, 992. [CrossRef] [PubMed]

53. Xu, L.; Huo, M.; Sun, C.; Cui, X.; Zhou, D.; Crittenden, J.C.; Yang, W. Bioreosources inner-recycling between bioflocculation of Microcystis aeruginosa and its reutilization as a substrate for bioflocculant production. Sci. Rep. 2017, 7, 43784. [CrossRef]

54. Liu, H.; Guo, X.; Liu, L.; Yan, M.; Li, J.; Hou, S.; Wan, J.; Feng, L. Simultaneous Microcystin Degradation and Microcystis aeruginosa Inhibition with the Single Enzyme Microcystinase A. Environ. Sci. Technol. 2020, 54, 8811–8820. [CrossRef] [PubMed]

55. Kong, Y.; Zou, P.; Yang, Q.; Xu, X.; Miao, L.; Zhu, L. Physiological responses of Microcystis aeruginosa under the stress of antialgal actinomycetes. J. Hazard. Mater. 2013, 262, 274–280. [CrossRef]

56. Zhang, Y.; Chen, D.; Zhang, N.; Li, F.; Luo, X.; Li, Q.; Li, C.; Huang, X. Transcriptional Analysis of Microcystis aeruginosa Co-Cultured with Algicald Bacteria Brevibacillus laterosporus. Int. J. Environ. Res. Public Health 2021, 18, 8615. [CrossRef] [PubMed]

57. Ai, M.; Purohit, H.J.; Qureshi, A. Genomic insight for algicald activity in Rhizobium strain AQ_MP. Arch. Microbiol. 2021, 203, 5193–5203. [CrossRef]

58. Pathmalal, M.M.; Zenchiro, K.; Shin-ichi, N. Algicald effect of the bacterium Alcaligenes denitrificans on Microcystis spp. Aquatic. Microb. Ecol. 2000, 22, 111–117.

59. Xue, G.; Wang, X.; Xu, C.; Song, B.; Chen, H. Removal of harmful algae by Shigella sp. H3 and Alcaligenes sp. H5: Algicald pathways and characteristics. Environ. Technol. 2021. [CrossRef]

60. Van Le, V.; Ko, S.-R.; Kang, M.; Lee, S.-A.; Oh, H.-M.; Ahn, C.-Y. Algicald of Pseudomonas aeruginosa by attachment and non-attachment effects. Environ. Pollut. 2022, 302, 119079. [CrossRef]

61. Crettaz-Minaglia, M.; Fallico, M.; Aranda, O.; Juarez, I.; Pezzoni, M.; Costa, C. Effect of temperature on microcystin-LR removal and lysis activity on Microcystis aeruginosa(cyanobacteria) by an indigenous bacterium belonging to the genus Achromobacter. Environ. Sci. Pollut. Res. 2020, 27, 44427–44439. [CrossRef]

62. Wang, X.; Xie, M.; Wu, W.; Shi, L.; Luo, L.; Li, P. Differential sensitivity of colonial and unicellular Microcystis strains to an algicald bacterium Pseudomonas aeruginosa. J. Plankton Res. 2013, 35, 1172–1176. [CrossRef]

63. Kang, Y.-H.; Park, C.-S.; Han, M.-S. Pseudomonas aeruginosa UCBBP-PA14 a useful bacterium capable of lysing Microcystis aeruginosa cells and degrading microcystins. J. Appl. Physiol. 2012, 24, 1517–1525. [CrossRef]
93. Shao, J.; Jiang, Y.; Wang, Z.; Peng, L.; Luo, S.; Gu, J.; Li, R. Interactions between algicidal bacteria and the cyanobacterium \textit{Microcystis aeruginosa}: Lytic characteristics and physiological responses in the cyanobacteria. \textit{Int. J. Environ. Sci. Technol.} 2013, \textit{11}, 469–476. [CrossRef]

94. Xu, B.; Miao, L.; Yu, J.; Ji, L.; Lu, H.; Yang, J.; Gao, S.; Kong, Y. Isolation and identification of amino acids secreted by \textit{Bacillus amyloliquifaciens} T1 with anti-cyanobacterial effect against cyanobacterium \textit{Microcystis aeruginosa}. \textit{Desalination Water Treat.} 2021, \textit{231}, 329–339. [CrossRef]

95. Wang, S.; Yang, S.; Zuo, J.; Hu, C.; Song, L.; Gan, N.; Chen, S. Simultaneous Removal of the Freshwater Bloom-Forming Cyanobacterium \textit{Microcystis} and Cyanotoxin Microcystins via Combined Use of Algicidal Bacterial Filtrate and the Microcystin-Degrading Enzymatic Agent, MrA. \textit{Microorganisms} 2021, \textit{9}, 1594. [CrossRef]

96. Tian, C.; Liu, X.; Tan, J.; Lin, S.; Li, D.; Yang, H. Isolation, identification and characterization of an algicidal bacterium from Lake Taihu and preliminary studies on its algicidal compounds. \textit{J. Environ. Sci.} 2012, \textit{24}, 1823–1831. [CrossRef]

97. Han, S.; Zhou, Q.; Lilje, O.; Xu, W.; Zhu, Y.; van Ogtrop, F. Inhibition mechanism of \textit{Penicillium chrysogenum} on \textit{Microcystis aeruginosa} in aquaculture water. \textit{J. Clean. Prod.} 2021, \textit{292}, 126829. [CrossRef]

98. Mohamed, Z.A.; Alamri, S.; Hashem, M.; Mostafa, Y. Growth inhibition of \textit{Microcystis aeruginosa} and adsorption of microcystin toxin by the yeast \textit{Aureobasidium pullulans}, with no effect on microalgae. \textit{Environ. Sci. Pollut. Res.} 2020, \textit{27}, 38038–38046. [CrossRef]

99. Wang, Q.; Su, M.; Zhu, W.; Li, X.; Jia, Y.; Guo, P.; Chen, Z.; Jiang, W.; Tian, X. Growth inhibition of \textit{Microcystis aeruginosa} by white-rot fungus \textit{Lopharia spadicae}. \textit{Water Sci. Technol.} 2010, \textit{62}, 317–323. [CrossRef]

100. Zeng, G.; Gao, P.; Wang, J.; Zhang, J.; Zhang, M.; Sun, D. Algicidal Molecular Mechanism and Toxicological Degradation of \textit{Microcystis aeruginosa} by \textit{Penicillium chrysogenum}. \textit{Microorganisms} 2021, \textit{9}, 2311. [CrossRef]

101. Zeng, G.; Zhang, M.; Gao, P.; Wang, J.; Sun, D. Algicidal Efficiency and Genotoxic Effects of \textit{Planorhochaete chrysosporium} against \textit{Microcystis aeruginosa}. \textit{Int. J. Environ. Sci. Technol.} 2020, \textit{17}, 4029. [CrossRef] [PubMed]

102. Han, G.; Feng, X.; Jia, Y.; Wang, C.; He, X.; Zhou, Q.; Tian, X. Isolation and evaluation of terrestrial fungi with algicidal ability from Zijin Mountain, Nanjing, China. \textit{J. Microbiol.} 2011, \textit{49}, 562–567. [CrossRef] [PubMed]

103. Han, G.; Ma, H.; Ren, S.; Gao, X.; He, X.; Zhu, S.; Deng, R.; Zhang, S. Insights into the mechanism of cyanobacteria removal by the algicidal fungus \textit{Bjerkandera adusta} and \textit{Trametes versicolor}. \textit{Microbiol. Open} 2020, \textit{9}, e1042. [CrossRef] [PubMed]

104. Jin, P.; Wang, H.; Liu, W.; Zhang, S.; Lin, C.; Zheng, F.; Miao, W. Bactericidal metabolites from \textit{Pseudomonas noxius} HN-1 against \textit{Microcystis} aeruginosa. \textit{Sci. Rep.} 2017, \textit{7}, 3132. [CrossRef] [PubMed]

105. Jia, Y.; Wang, Q.; Chen, Z.; Jiang, W.; Zhang, P.; Tian, X. Inhibition of phytoplankton species by co-culture with a fungus. \textit{Ecol. Eng.} 2010, \textit{36}, 1389–1391. [CrossRef]

106. Jia, Y.; Han, G.; Wang, Y.; Guo, P.; Jiang, W.; Li, X.; Tian, X. The efficacy and mechanisms of fungal suppression of freshwater harmful algal bloom species. \textit{J. Hazard. Mater.} 2010, \textit{183}, 176–181. [CrossRef]

107. Du, J.; Pu, G.; Shao, C.; Cheng, S.; Cai, J.; Zhou, L.; Jia, Y.; Tian, X. Potential of extracellular enzymes from \textit{Trametes versicolor} F21a in \textit{Microcystis} spp. degradation. \textit{Mater. Sci. Eng. C} 2014, \textit{48}, 138–144. [CrossRef] [PubMed]

108. Dai, W.; Chen, X.; Wang, X.; Xu, Z.; Gao, X.; Jiang, C.; Deng, R.; Han, G. The Algicidal Fungus \textit{Trametes versicolor} F21a Eliminating Blue Algae via Genes Encoding Degradation Enzymes and Metabolic Pathways Revealed by Transcriptomic Analysis. \textit{Front. Microbiol.} 2018, \textit{9}, 826. [CrossRef]

109. Wei, J.; Xie, X.; Huang, F.; Xiang, L.; Wang, Y.; Han, T.; Massey, I.Y.; Liang, G.; Pu, Y.; Yang, F. Simultaneous \textit{Microcystis} algicidal and microcystin synthesis inhibition by a red pigment prodigiosin. \textit{Environ. Pollut.} 2019, \textit{256}, 113444. [CrossRef]

110. Annett, H.; Kunimitsu, K.M.W.M. Selective control of \textit{Microcystis} using an amino acid-a laboratory assay. \textit{J. Appl. Phycol.} 2002, \textit{14}, 85–89. [CrossRef]

111. Kaya, K.; Liu, Y.-D.; Shen, Y.-W.; Xiao, B.-D.; Sano, T. Selective control of toxic \textit{Microcystis} water blooms using lysine and malonic acid: An enclosure experiment. \textit{Environ. Toxicol.} 2005, \textit{20}, 170–178. [CrossRef] [PubMed]

112. Tian, L.; Chen, M.; Ren, C.; Wang, Y.; Li, L. Anticyanobacterial effect of l-lysine on \textit{Microcystis aeruginosa}. \textit{RSC Adv.} 2018, \textit{8}, 21606–21612. [CrossRef] [PubMed]

113. Wang, M.-H. Algicidal Activity of a Dibenzofururan-Degradator \textit{Rhodococcus} sp. \textit{J. Microbiol. Biotechnol.} 2013, \textit{23}, 260–266. [CrossRef]

114. Yamamoto, Y.; Kouchiwa, T.; Hodoki, Y.; Hotta, K.; Uchida, H.; Harada, K.-I. Distribution and identification of actinomycetes lysing cyanobacteria in a eutrophic lake. \textit{J. Appl. Phycol.} 1998, \textit{10}, 391–397. [CrossRef]

115. Liu, Y.-M. Inhibition of \textit{Microcystis aeruginosa} by the Extracellular Substances from an \textit{Aeromonas} sp. \textit{J. Microbiol. Biotechnol.} 2013, \textit{23}, 1304–1307. [CrossRef]

116. Weiss, G.; Kovalerchick, D.; Lieman-Hurwitz, J.; Murik, O.; De Philippis, R.; Carmeli, S.; Sukenik, A.; Kaplan, A. Increased algicidal activity of \textit{Aeromonas veronii} in response to \textit{Microcystis aeruginosa}: Interspecies crosstalk and secondary metabolites synergism. \textit{Environ. Microbiol.} 2019, \textit{21}, 1140–1150. [CrossRef]

117. Feng, Y.; Chang, X.; Zhao, L.; Li, X.; Li, W.; Jiang, Y. Nanaomycin A methyl ester, an actinomycete metabolite: Algicidal activity and the physiological response of \textit{Microcystis aeruginosa}. \textit{Ecol. Eng.} 2013, \textit{53}, 306–312. [CrossRef]

118. Gerphagnon, M.; Macarthur, D.; Latour, D.; Gachon, C.; Van Ogtrop, F.; Gleason, F.H.; Sime-Ngando, T. Microbial players involved in the decline of filamentous and colonial cyanobacterial blooms with a focus on fungal parasitism. \textit{Environ. Microbiol.} 2015, \textit{17}, 2573–2587. [CrossRef]

119. Su, J.F.; Shao, S.C.; Huang, T.L.; Ma, F.; Lu, J.S.; Zhang, K. Algicidal effects and denitrification activities of \textit{Acinetobacter} sp. J25 against \textit{Microcystis aeruginosa}. \textit{J. Environ. Chem. Eng.} 2016, \textit{4}, 1002–1007. [CrossRef]
120. Chen, Y.-D.; Zhu, Y.; Xin, J.-P.; Zhao, C.; Tian, R.-N. Succinic acid inhibits photosynthesis of *Microcystis aeruginosa* via damaging PSII oxygen-evolving complex and reaction center. *Environ. Sci. Pollut. Res.* 2021, 28, 58470–58479. [CrossRef]

121. Kong, Y.; Xu, X.; Zhu, L. Cyanobactericidal Effect of *Streptomyces* sp. HJC-D1 on *Microcystis aeruginosa*. *PLoS ONE* 2013, 8, e57654. [CrossRef] [PubMed]

122. Zhai, C.; Zhang, P.; Shen, F.; Zhou, C.; Liu, C. Does *Microcystis aeruginosa* have quorum sensing? *FEMS Microbiol. Lett.* 2012, 336, 38–44. [CrossRef] [PubMed]

123. Reading, N.C.; Sperandio, V. Quorum sensing: The many languages of bacteria. *FEMS Microbiol. Lett.* 2006, 254, 1–11. [CrossRef] [PubMed]

124. Zhang, Y.; Zheng, L.; Wang, S.; Zhao, Y.; Xu, X.; Han, B.; Hu, T. 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. [CrossRef] [PubMed]

125. Dow, L. How Do Quorum-Sensing Signals Mediate Algae–Bacteria Interactions? *Microorganisms* 2021, 9, 1391. [CrossRef]

126. Liu, J.; Liu, K.; Zhao, Z.; Wang, Z.; Wang, F.; Xin, Y.; Qu, J.; Song, F.; Li, Z. The LuxS/AI-2 Quorum-Sensing System Regulates the Algicidal Activity of *Shewanella xianenensis* Lzh-2. *Front. Microbiol.* 2022, 12. [CrossRef]

127. Zhang, S.-J.; Du, X.-P.; Zhu, J.-M.; Meng, C.-X.; Zhou, J.; Zuo, P. The complete genome sequence of the algicidal bacterium *Bacillus subtilis* strain JA and the use of quorum sensing to evaluate its antialgal ability. *Biotechnol. Rep.* 2020, 25, e00421. [CrossRef] [PubMed]

128. Dziallas, C.; Grossart, H.-P. Temperature and biotic factors influence bacterial communities associated with the cyanobacterium *Microcystis* sp. *Environ. Microbiol.* 2011, 13, 1632–1641. [CrossRef]

129. He, L.; Lin, Z.; Wang, Y.; He, X.; Zhou, J.; Guan, M.; Zhou, J. Facilitating harmful algae removal in fresh water via joint effects of multi-species algicidal bacteria. *J. Hazard. Mater.* 2020, 403, 123662. [CrossRef]

130. Sun, P.; Lin, H.; Wang, G.; Lu, L.-L.; Zhao, Y.-H. Preparation of a new-style composite containing a key bioflocculant produced by *Pseudomonas aeruginosa* ZJU1 and its flocculating effect on harmful algal blooms. *J. Hazard. Mater.* 2014, 284, 215–221. [CrossRef]

131. Kim, H.S.; Park, Y.H.; Kim, S.; Choi, Y.-E. Application of a polyethylenimine-modified polyacrylonitrile-biomass waste composite fiber sorbent for the removal of a harmful cyanobacterial species from an aqueous solution. *Environ. Res.* 2020, 190, 109997. [CrossRef] [PubMed]

132. Paerl, H.W.; Gardner, W.S.; Havens, K.E.; Joyner, A.R.; McCarthy, M.J.; Newell, S.; Qin, B.; Scott, J.T. Mitigating cyanobacterial harmful algal blooms in aquatic ecosystems impacted by climate change and anthropogenic nutrients. *Harmful Algae* 2016, 54, 213–222. [CrossRef] [PubMed]

133. Kong, Y.; Xu, X.; Zhu, L.; Miao, L. Control of the Harmful Alga *Microcystis aeruginosa* and Absorption of Nitrogen and Phosphorus by *Candida utilis*. *Appl. Biochem. Biotechnol.* 2012, 169, 88–99. [CrossRef] [PubMed]