

INTEGRATED MICROBIAL CONSORTIUM- BASED BIOREMEDIATION OF HARMFUL ALGAL BLOOMS AND AQUACULTURE WASTEWATER: AN ECO-ENGINEERING APPROACH

**Thesis Submitted
In Partial Fulfillment of the Requirements for the
Degree of**

**MASTER OF TECHNOLOGY
in
Industrial Biotechnology**

**by
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**Under the Supervision of
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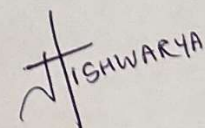
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List of Symbols, Abbreviations and Nomenclature

LIST OF SYMBOLS

Symbol Meaning

N	Nitrogen
P	Phosphorus
N ₂	Atmospheric nitrogen
CO ₂	Carbon dioxide
pH	Potential of hydrogen
SST	Sea Surface Temperature
ROS	Reactive Oxygen Species
DO	Dissolved Oxygen
TDS	Total Dissolved Solids
pCO ₂	Partial pressure of carbon dioxide
N:P	Nitrogen to phosphorus ratio
LD ₅₀	Median lethal dose
μM	Micromolar concentration
μg mL ⁻¹	Microgram per millilitre
km ²	Square kilometre
°C	Degree Celsius
h	Hour
d	Day
v/v	Volume per volume ratio
PSII	Photosystem II

LIST OF ABBREVIATIONS

Abbreviation Full Form

HABs	Harmful Algal Blooms
CyanoHABs	Cyanobacterial Harmful Algal Blooms
PME	Precision Microbiome Engineering
AMR	Antimicrobial Resistance
ARGs	Antibiotic Resistance Genes
HGT	Horizontal Gene Transfer
FAO	Food and Agriculture Organization

Abbreviation Full Form

BFT	Biofloc Technology
MBBR	Moving Bed Biofilm Reactor
AI	Artificial Intelligence
PSP	Paralytic Shellfish Poisoning
NSP	Neurotoxic Shellfish Poisoning
ASP	Amnesic Shellfish Poisoning
DSP	Diarrhetic Shellfish Poisoning
PSTs	Paralytic Shellfish Toxins
STX	Saxitoxins
CYN	Cylindrospermopsin
NOD	Nodularin
DA	Domoic Acid
OA	Ocean Acidification
DIN	Dissolved Inorganic Nitrogen
EPS	Extracellular Polymeric Substances
TDA	Tropodithietic Acid
SCFA	Short Chain Fatty Acid
SynCom	Synthetic Microbial Community
NGS	Next Generation Sequencing
CAD	Computer Aided Design
GPS	Global Positioning System
TLR	Toll Like Receptor
WHO	World Health Organization
EU	European Union
FCR	Feed Conversion Ratio
MCs	Microcystins
KNN	K-Nearest Neighbour
ROS	Reactive Oxygen Species
DNA	Deoxyribonucleic Acid
RNA	Ribonucleic Acid

NOMENCLATURE

HAB Groups and Organisms

Term	Description
Cyanobacteria	Prokaryotic photosynthetic microorganisms causing freshwater HABs
Dinoflagellates	Eukaryotic plankton associated with marine HABs
Diatoms	Silica-walled microalgae, some toxin-producing

Term	Description
Raphidophytes	Flagellated microalgae causing fish-kill blooms
Chrysophytes	Golden algae occurring mainly in freshwater
Haptophytes	Flagellated algae producing ichthyotox

ABSTRACT

Harmful algal blooms (HABs) are over growth of algae and are considered as the most rapidly intensifying ecological threat to marine and freshwater ecosystems worldwide. Although algal blooms are natural occurring phenomenon which is a result of aquatic productivity driven by toxin-producing or high biomass forming microalgae which leads to ecological, economic and public health impact. This report aims to evaluate algicidal bacteria and build a bacterial consortium which is safe and effective and acts as an eco-compatible strategy to inhibit or prevent the growth of HAB-forming species.

In this report, we assessed global HAB trends, identified causative algal species and environment and biological drivers of bloom intensification. Based on this, algicidal bacteria was selected focusing on their mechanistic pathways, modes of action, selectivity and safety for environmental application. HABs are caused by 6 major groups which are cyanobacteria (*Microcystis aeruginosa*), dinoflagellates (*Noctiluca scintillans*), diatoms (*Pseudo-nitzschia*), raphidophytes (*Heterosigma akashiwo*), haptophytes (*Phaeocystis globosa*) and some chrysophytes. Bacterial taxa such as *Pseudoalteromonas*, *Phaeobacter*, *Bacillus*, *Hahella*, and *Shewanella* shows strong algicidal activity via ROS induction, EPS degradation, extracellular enzyme production, secondary metabolite release and disruption of photosynthesis and metabolism.

Algicidal bacteria can be considered as an emergent mitigation strategy offering a promising, environmentally compatible solution. This work supports the solution of Algicidal bacteria, which can be used as a consortium by evaluating their safety level, selective targeting of HABs and microbial control potential which will help in future field-deployable HAB management.

In parallel, PME-oriented strategies for aquaculture wastewater treatment, especially probiotics, synbiotics, synthetic microbial communities (SynComs), biofloc systems, and omics-guided bioremediation platforms were analyzed for their role in wastewater treatment. Their relevance extends beyond nutrient removal alone. In many cases, the same interventions are discussed in relation to host immune support, microbial community stabilization, and suppression of resistant or opportunistic pathogens. Taken together, this work suggests that carefully assembled and field-deployable microbial consortia could support a more integrated management framework, one that addresses HAB control, wastewater remediation, and AMR mitigation within aquaculture ecosystems without treating those issues as separate engineering targets.

Keywords: harmful algal blooms (HABs); algicidal bacteria; bacterial consortia; precision microbiome engineering; aquaculture wastewater bioremediation; antimicrobial resistance; antibiotic resistance genes; synthetic microbial communities; biofloc systems

CHAPTER 1

INTRODUCTION TO HARMFUL ALGAL BLOOMS (HABs)

Algal blooms are natural occurring phenomenon which are found in marine or freshwater system and are usually harmless and form part of normal aquatic productivity, but some species can grow excessively in favoured environmental conditions and produce potent toxin that harms ecological balance. These Harmful algal blooms are environmental threats, driven by nutrient enrichment, global warming, altered hydrological dynamics and adaptive traits of HABs. In past two decades, Toxin-producing Algae which are present in lakes, rivers and oceans grow excessively and forms algal blooms that are toxic for the water bodies, environment and human health. In the recent decades, their frequency, intensity and geographic extent have been increased significantly. Hence, Harmful Algal Blooms (HABs) are causing the most pressing ecological and public health challenges in the 21st century. Global HAB frequency and severity has been increased significantly across different region. Many incidences have been reported from North America, Europe, China, India and coastal regions of South America and Africa have revealed that HABs events have been nearly doubled in occurrence causing harm to aquatic ecosystem.



Fig. 1 Harmful Algal Bloom formations (HABs) on the Achencovil river. (A) & (B) showing unusual colouration of water at different intensities of light (Binoy et al., 2020).

HABs have the tendency to rapidly proliferate, often with the help of nutrients and favourable temperature. Some of the factors involved in their excessive growth in both fresh and marine water is nutrient over-enrichment from agricultural sites, untreated sewages (Eutrophication) and industrial wastage. In Freshwater system, Phosphorus (P) is the primary nutrient, while in marine environments, Nitrogen (N) plays a major role to promote rapid growth of HABs and they also have the ability to fix atmospheric nitrogen (N₂) for their enrichment, which is a major ecological disadvantage for marine environment. Amongst the other factors that play a major role is climatic conditions. Rising Global temperature also fuels the growth of HABs and enhance their metabolism. Warmer water leads to thermal stratification, reducing mixing of water and leading to nutrient accumulation on surface, where HABs thrives.

These HABs produce potent biotoxins which leads to bioaccumulation in food chain and contaminated water, cause oxygen depletion (Hypoxia) which can lead to mass fish kills and disrupt aquatic ecosystem across the world. HABs are classified into two – Planktonic and Benthic HABs. Planktonic HABs are those which floats in the water, whereas Benthic HABs attaches to bottom of the water bodies forming a visible mat.

Addressing this challenge effectively demands a solution that targets the root causes of HABs and their ecological consequences. By focusing on combining nutrient-input control, early warning systems, ecological improvement, and innovative biological interventions, like using algicidal bacteria as a mitigation strategy, can help in targeting bloom suppression. These interventions can ensure long-term environmental safety after evaluating the results of rigorous laboratory testing and risk assessment to safeguard non-targeted organisms. As this effective measure requires an adaptive management framework, such as policies and risk evaluation based on environmental feedback, monitoring data, and climate-induced changes, so that these methods can be field-deployed and bring changes in real-world conditions to maintain the ecological balance of the ecosystem.

In parallel, rapid expansion of aquaculture has further intensified concerns associated with eutrophication and microbial imbalance in aquatic environments. Global aquaculture production reached 94.4 million tonnes in 2022, accounting for over 50% of the total aquatic food supply. According to the Food and Agriculture Organization (FAO), this is further expected to exceed 140 million tonnes by 2050, representing the fastest-growing food production sector in the world.¹⁻⁴ Increased demand for animal protein is being met with the rapid intensification of aquaculture practices globally.^{5,6} This has significantly enhanced aquaculture productivity, but it has also introduced several environmental and public health challenges due to higher stocking densities, shorter production cycles, and excessive reliance on chemotherapeutic agents. This dual-natured environmental burden is now in turn threatening the long-term viability of this sector.^{7,8} One major problem that arises from excessive nitrogen and phosphorus content linked to fish waste and leftover feeds is eutrophication,

which may cause anoxia and proliferation of algae.⁹ On the other hand, the widespread use of prophylactic treatment and antibiotics in aquaculture has made aquatic habitats breeding grounds for antibiotic resistance genes (ARGs) and organisms with antimicrobial resistance (AMR).^{10–12}

Under such conditions, precision microbiome engineering (PME) has become a feasible solution from an interdisciplinary perspective for addressing fish health issues by applying developments in microbiology, multi-omics, and synthetic biology to construct and manipulate the microbiota towards specific objectives.¹³ PME is comprised of strategies such as classical probiotics, heat-inactivated paraprobiotics, metabolite-rich postbiotics, prebiotic-probiotic synbiotics, and precisely designed SynComs, which can modulate microbial communities in both fish guts and production water, simultaneously enhancing nutrient removal and reducing the load of pathogenic and resistant microorganisms.^{5,14,15} A comprehensive review that addresses PME's dual functionality and defines it as a novel convergent paradigm remains lacking. In parallel, bioremediation strategies have also evolved to support this convergence. Advanced technologies such as biofloc technology (BFT), moving bed biofilm reactor (MBBR) are efficiently reducing the loads of nitrogen, phosphorus, and organic carbon in aquaculture effluents to a level that is comparable with municipal wastewater treatments.^{16–21} The application of multi-omics tools (metagenomics, metatranscriptomics, metabolomics) and artificial intelligence (AI) for real-time effluent quality prediction has further enhanced the precision and scalability of these approaches.^{22,23}

Most of the existing studies focus either on host-associated microbiome manipulation for the improvement of fish health or on environmental bioremediation to enhance water quality. Addressing this gap is therefore essential for developing sustainable aquaculture systems. This report aims to combine the evidence from environmental biotechnology and aquaculture production science to examine the role of PME for its dual functionality in wastewater purification as well as in mitigating AMR. Through the integration of current research findings and new approaches in methodology, this report redefines PME as a holistic concept that forms the basis of sustainable development in aquaculture ecosystems.

Therefore, integrating algicidal bacterial systems with precision microbiome engineering offers a promising systems-level approach for developing safe, selective, and field-deployable strategies against HABs. Such integrated microbial frameworks may help achieve long-term ecological sustainability while minimizing environmental risks associated with conventional bloom control method.

CHAPTER 2

RELATED WORKS

Literature Review

Rapidly reproducing algae causes large widespread Harmful algal bloom (HABs) which has long term effects on aquatic animals and environment, Human health and their countries economy. These HABs are produced by toxin-releasing species such as dinoflagellates, cyanobacteria & diatoms, all leading to reduced oxygen levels, impedes food webs and cause contaminated water supplies. Though these blooms are a natural phenomenon however their increased frequency, intensity and spatial extent in current times have led to serious concern worldwide.

The escalating frequency of HABs is a clear reflection of aquatic imbalance, mediated by various factors such as climate change, hydrological variations, nutrient enrichment (Levels of nitrogen and phosphorus) and anthropogenic activities. Remote sensing, satellite imaging, continuous monitoring provided scientist with important insights into the temporal and spatial dynamics of these events.

Analysis of these trends is crucial for predicting future bloom and development of the new technology for better management of HABs.

This chapter encompasses the review of the existing literature on the causative agents, abundance and intensity of Harmful algal blooms across the various geographies of the world. It encapsulates records from Global and region-specific studies and signifies the formation of HABs, the causative species and the conditions which favor their growth.

2.1 Global Intensification of Harmful Algal Blooms Over the Past Two Decades

Over the past two decades, over 200 phytoplankton taxa have been identified as HAB-forming. A global mapping study (2003–2020) found that 31.47 million km² of coastal ocean area experienced algal blooms—about 24.2% of global land area or 8.6% of global ocean area (Dai et al., 2023). Bloom frequency has increased by 4.6% since 2016, largely due to climate change, indicating that HAB-prone regions are rapidly expanding worldwide.

Large lakes globally show a significant rise in bloom frequency at ~1.8% per year, totalling a 36% increase in the past 20 years. Subtropical lakes exhibit the strongest intensification (2.3% annually), followed by tropical lakes (1.4% annually). Smaller lakes (<1000 km²) show 3.3% annual bloom frequency, compared to ~2.3% in larger lakes (Feng et al., 2024).

Regionally, HABs show distinct patterns in intensity and dominant taxa. In India, coastal HABs have risen sharply since 1950, with Cyanobacteria, Dinoflagellates, and Diatoms dominating during 1998–2010. Indian freshwater systems show a $16.1\% \pm 14.0\%$ rise in HAB frequency over the past two decades. Chinese lakes show a comparable increase of $7.1\% \pm 9.2\%$ over the same period (Feng et al., 2024).

A recent study analyzing sediments from 80 Canadian lakes found that HABs increased sevenfold in the 1960s compared to pre-1960 levels. In North America, long-term satellite data show a 2–3% annual rise in bloom occurrence in large lakes, especially the Great Lakes and major reservoirs. Lake Erie's Cyanobacteria blooms, for instance, have doubled in intensity since the early 2000s due to phosphorus runoff and warming waters.

In Africa and South America, although data are limited, satellite observations indicate a 1–1.5% annual increase in HABs across equatorial and subtropical lakes (Feng et al., 2024).

Overall, these studies highlight a global yet regionally varied intensification of harmful algal blooms driven by nutrient loading, climate change, and hydrological shifts.

2.2 Factors contributing to the intensification of HABs and why they are worse now?

Some of the underlying factors include biological mechanisms of bloom formation like rapid reproduction, colony formation, and competitive interactions, usually similar across ocean basins but the frequency, intensity, and species composition of HABs vary considerably among regions. The reason of this difference is nutrient availability, hydrological regimes, climate-induced changes, and human activities.

2.3 Climate warming and stratification –

Rising Sea surfaces Temperature (SST) being one of the major factors intensifying HABs globally, contributing to increased growth rates and thermal tolerance of thermophilic phytoplankton species, especially Nitrogen-fixing cyanobacteria and Dinoflagellates. Globally, warming trends of expansion of HABs have been linked to shifts in bloom timing and prolonged growth periods, suggesting that thermal adaptation and selection of causative species of HABs under higher SST plays a major role in increased frequency of HABs over the years especially from 2010-2024 (Q. Zheng et al., 2024).

Stratification is a phenomenon, when enhanced creates a surface layer which reduces vertical nutrient mixing. This condition helps HABs in exploiting surface layers, while rich nutrients water remains isolated deeply. One of the studies proved that the seasonal intensification of HABs have indicated a direct relationship with stratification strength in Arabian Sea.

2.4 Nutrient Enrichment: Nitrogen Fixation and Phosphorus Consumption

Nutrient enrichment, especially Nitrogen and Phosphorus acts as a significant player in enhancing the intensity, frequency and spatial extent of HABs globally. Several studies have showed a steady rise in dissolved inorganic nitrogen (4–8 μM) and phosphate (0.3–1.2 μM) concentrations in coastal waters of Asia, Europe, and North America, correlating with elevated HAB occurrences.

Nitrogen-fixing Cyanobacteria has played a pivotal role in intensification of HABs event over the past two decades, especially in nitrogen-limited coastal and open-ocean systems. Species such as *Trichodesmium*, *Dolichospermum*, and *Nodularia* can convert atmospheric N_2 into bioavailable forms, effectively overcoming the difficulty of nitrogen limitation that would reduce the phytoplankton growth.

Before 2010, Phosphorus has been the limiting nutrient in coastal and ocean waters for the growth of HABs, but availability of phosphorus has become a critical factor in the past two decades. Enhanced phosphate from the agricultural fertilizers and industrial discharge has increased the N:P ratio, which became sufficient for the proliferation of Dinoflagellates and Raphidophytes.

2.6 CO_2 and pH effects

Rising CO_2 and ocean acidification act as co-stressors enhancing HAB growth and toxicity which further increase the eutrophication. Elevated pCO_2 alters carbon use and competition, with several dinoflagellates and toxic diatoms showing higher growth and toxin production (Tatters et al., 2012, 2013).

2.7 Rapid reproduction and colony formation

HABs intensify through rapid growth and colony formation leading to a very high population. Under favourable conditions, populations expand quickly, chains and colonies reduce grazing, enhance dispersal, and improve nutrient capture which leads to rapid growth.

Colony structure and size shift with nutrients, predators, hydrology, and temperature, increasing bloom resilience (Rigby & Selander, 2021; Stenow et al., 2024). Mucilage also supports bacteria–algae interactions that promote aggregation. These traits allow HABs to persist in stratified, low-mixing waters.

2.8 Self-defence and competitive mechanisms

Bloom dominance is reinforced by toxin production, cyst formation, and chemical signalling. Toxins decrease grazers and competitors, with levels shaped by nutrients, temperature, pH, and biotic interactions thereby increasing the bloom occurrence.

Cyst seed banks (e.g., *Alexandrium*) enable long-term survival and recurrent blooms, influenced by warming and sediment dynamics. Allelochemicals and microbial partners can trigger cyst formation or alter toxin pathways. Combined with nutrient and climate pressures, these strategies support HAB persistence and impact.

2.9 Human and Animal Health Impacts of Harmful Algal Blooms

Toxins accumulate in water and seafood cause human illnesses such as PSP, NSP, ASP, and DSP. Exposure to these toxins leads to neurological or gastrointestinal symptoms, sometimes severe reactions.

Wildlife and livestock suffer hepatotoxic, neurotoxic, or nephrotoxic effects which leads to mass mortality through contaminated water or prey. Chronic cyanotoxin exposure is linked to organ damage and potential carcinogenicity in mammal that is increasing day by day.

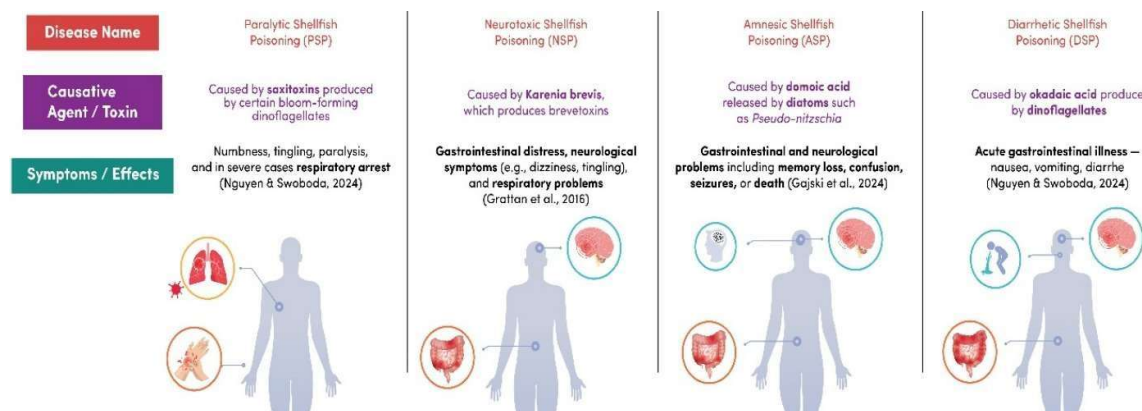


Fig. 2: Overview of Symptoms

2.10 Cyanobacteria

Cyanobacteria (blue-green algae) are prokaryotic photoautotrophs responsible for 60–70% of inland HABs. Their frequency, duration, and global extent have risen sharply over the past two decades due to nutrient enrichment, warming, and hydrological change. Tropical lakes now show 2–3× higher cyanobacterial abundance post-2010. CyanoHABs appear as planktonic toxin-producing scums or as benthic blooms increasingly common in rivers.

Key bloom-forming genera include *Microcystis*, *Dolichospermum*, *Aphanizomenon*, *Raphidiopsis*, *Nodularia*, *Planktothrix*, *Pseudanabaena*, and *Trichodesmium*. Examples include *Microcystis aeruginosa* forming >80% of phytoplankton biomass in Tamil Nadu estuaries and *Trichodesmium* blooms across the Indian Ocean, with *T. erythraeum* and *T. thiebautii* linked to fish kills in Thailand and Indonesia.

CyanoHAB expansion is driven by nutrient loading, toxin-based competition, and hydrological and land-use shifts. *Microcystis aeruginosa* is the most widespread species—reported in >108 countries and responsible for ~40% of global freshwater HABs. Its microcystin production and preference for warm, nutrient-rich, stratified waters make it a prime target for algicidal bacterial-consortium control strategies.

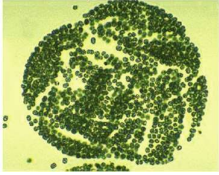
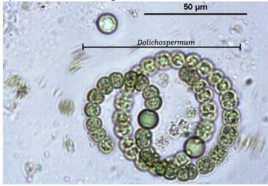
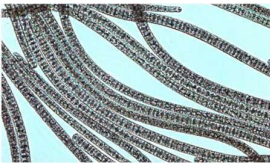
Taxon	Major toxins reported	Mode of Nutrition strategy	References
<i>Microcystis</i> 	Microcystins; some strains are also reported to produce minor peptides like aeruginosins and cyanopeptolins.	Non-diazotrophic (Cannot fix N ₂); relies on DIN Have the ability to develop stringent response in low Nitrogen.	(Harke et al., 2016; Song et al., 2023)
<i>Dolichospermum</i> (formerly <i>Anabaena</i>) 	Anatoxin-a, Saxitoxins, Cylindrospermopsin, Microcystins (strain-dependent)	Diazotrophic (N ₂ -fixing); adapts to N-depleted waters; some species also utilize phosphorus efficiently under limitation	(D'Agostino et al., 2020; Paerl & Otten, 2016; Song et al., 2023)
<i>Raphidiopsis</i> (aka <i>Cylindrospermopsis</i>) 	Cylindrospermopsin (CYN), Saxitoxins (STX)	Diazotrophic; capable of N ₂ -fixation and efficient phosphorus uptake; blooms under warm (>25 °C), stratified, low-N conditions	(Paerl & Otten, 2016; L. Zheng et al., 2023)
<i>Nodularia</i> 	Nodularin (NOD) and some peptides	Diazotrophic (N ₂ -fixing); utilizes methylphosphonic acid under P limitation; blooms in brackish to saline waters	(Konkel et al., 2020; Mazur-Marzec et al., 2016)
<i>Planktothrix</i> 	Microcystins, Aeruginosins, Oscillapeptins has been reported.	Non-diazotrophic; efficient in low-light and P-limited environments; winter persistence under ice conditions	(Mallia et al., 2019; Selmeczy et al., 2025; Suda et al., 2002)

Table 1: Key Taxa, Toxins, and Nutritional Strategies of CyanoHABs

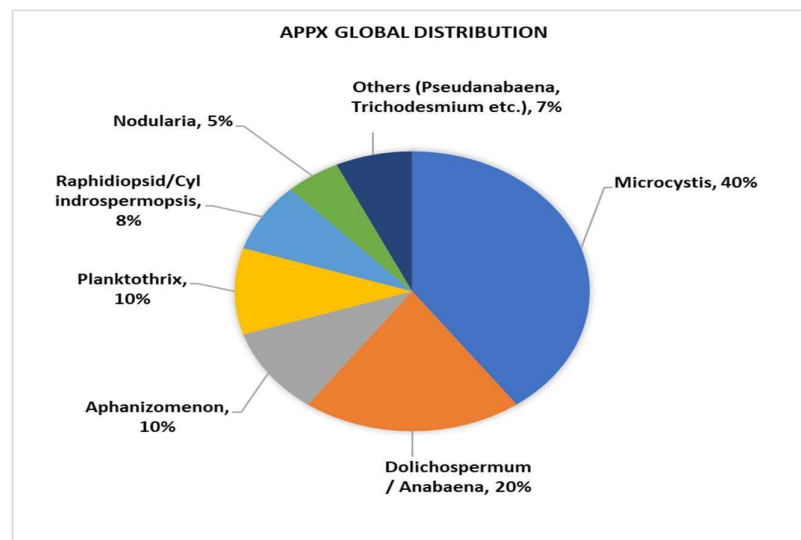


Fig. 3: Global distribution of Cyanobacteria based on the peer-reviewed studies and regional reports

2.11 Dinoflagellates

Dinoflagellates are unicellular eukaryotic plankton dominant in marine and brackish systems, and many species form HABs that cause fish kills, shellfish toxicity, and major ecosystem disturbance. Unlike cyanobacteria—which dominate freshwater—dinoflagellate HABs occur mainly in estuarine and marine waters. Over 200 dinoflagellate species are linked to HABs, with ~80 producing biotoxins. Key toxin-producing groups include *Alexandrium* and *Pyrodinium* (PSP), while *Karenia*, *Karlodinium*, and *Margalefidinium* are frequently associated with large fish-kill events.

Dinoflagellates exhibit strong ecological flexibility, vertically migrating between nutrient-rich deep layers and surface waters, allowing recurrent blooms under favorable temperature–salinity conditions. Multiple case studies highlight their impacts: the heterotrophic *Noctiluca scintillans* forms massive, oxygen-depleting blooms across the Indian Ocean, Bay of Bengal, and Southeast Asia, causing fish kills despite producing no classic toxins. *Karenia mikimotoi* has caused repeated fish-kill events in China, Korea, Japan, and Southeast Asia (San Diego-McGlone et al., 2024b). In the Philippines, *Pyrodinium* blooms (1983–2001) caused numerous PSP outbreaks through saxitoxin-contaminated shellfish (Gacutan et al., 1985).

Among dinoflagellates, *Noctiluca scintillans* is the most frequently reported in regional HAB assessments. Although non-toxic, its enormous biomass drives hypoxia and severe ecological harm, making it a priority target for mitigation via bacterial consortia.

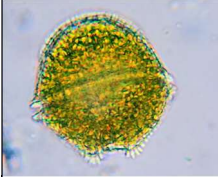
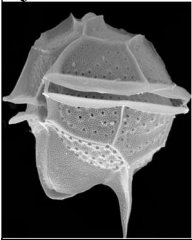
Taxon	Species	Major reported toxins	Mode of Nutrition strategy	References
Alexandrium 	<i>A. catenella</i> / <i>A. tamarense</i> complex, <i>A. minutum</i>	Paralytic shellfish toxins (PSTs / saxitoxins)	under N-limitation; utilizes dissolved nitrate and ammonium.	(Rolton et al., 2022; San Diego-McGlone et al., 2024b)
Pyrodinium 	<i>Pyrodinium bahamense</i>	PSTs (saxitoxins)	Autotrophic: photosynthetic dinoflagellate; relies on nitrate and phosphate uptake; forms benthic cysts.	(San Diego-McGlone et al., 2024b; Usup et al., 2012)
Dinophysis 	<i>D. acuminata</i> , <i>D. fortii</i> , <i>D. caudata</i>	okadaic acid, dinophysistoxins	Depends on organic N & P from prey.	(Reguera et al., 2014; San Diego-McGlone et al., 2024b)

Table.2: Key Taxa, Toxins, and Nutritional Strategies of Dinoflagellates.

2.12 Diatoms

Diatoms are silica-walled, non-flagellated microalgae common in marine and freshwater systems, with growth driven by nutrient availability and mixing that maintains silica and macronutrients. While most are beneficial, several species especially *Pseudo-nitzschia* and some *Nitzschia* produce the neurotoxins domoic acid (DA) and BMAA, causing shellfish poisoning and mass mortality of seabirds and marine mammals. These taxa are the principal global DA producers, with major events documented on the U.S. West Coast and in Southeast Asia (Watson et al., 2015).

Other harmful diatoms include *Chaetoceros* spp., whose sharp setae damage fish gills, and *Skeletonema hantzschii*, which formed severe blooms in the Hanjiang River (China, 2012) and disrupted Wuhan's drinking water supply (Yang et al., 2012).

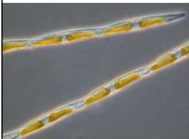
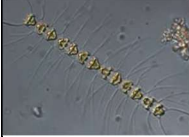
Genus (taxon)	Representative species	Main toxins / impacts	Mode of nutrition / trophic strategy	Key references
Pseudo-nitzschia 	<i>P. australis</i> , <i>P. multiseries</i> , <i>P. seriata</i> , <i>delicatissima</i>	Domoic acid (DA) - amnesic shellfish poisoning (ASP)	Autotrophic (photosynthetic)	(Bates et al., 2018; Cochlan et al., 2023)
Nitzschia 	<i>N. navis-varingica</i> , <i>N. bizertensis</i>	Domoic acid reported in some species (less common than Pseudo-nitzschia)	Autotrophic; toxigenicity strain-specific	(Bates et al., 2018)
Chaetoceros 	<i>C. concavicornis</i> , <i>C. coarctatus</i>	Mechanical gill damage (spiny setae)	Autotrophic (photosynthetic)	(Roberts et al., 2019)

Table.3: Key Taxa, Toxins, and Nutritional Strategies of Diatoms.

2.13 Raphidophytes

Raphidophytes are flagellated microalgae primarily found in marine and brackish waters, with *Gonyostomum* semen as the main freshwater which are the highest in number. Major bloom-forming marine genera include *Chattonella*, *Heterosigma*, *Fibrocapsa*, and *Olisthodiscus*. Unlike many HAB taxa, raphidophytes rely on reactive oxygen species (ROS), mucus production, hypoxia, and hemolytic activity rather than classic biotoxins. *Chattonella* produces extracellular superoxide and other ROS that damage fish gills and erythrocytes, driving repeated aquaculture kills across the western Pacific (Shikata et al., 2021). In freshwater, *Gonyostomum* semen forms dense blooms in humic, low-conductivity lakes, causing ecological disruption even without toxin production (Johansson et al., 2013).

Genus (taxon)	Representative species	Main toxins / impacts	Mode of nutrition / trophic strategy	Key refs (select)
Chattonella 	<i>C. marina</i> <i>C. complex</i> , <i>C. antiqua</i> , <i>C. subsalsa</i>	Ichthyotoxic effects: ROS (superoxide)	Mixotrophic / opportunistic: photosynthetic + phagotrophy	(Lum et al., 2021; Shikata et al., 2021)
Heterosigma 	<i>H. akashiwo</i>	Hemolytic ichthyotoxic activity	Mixotrophic	(Guidi-Rontani et al., 2010; Viana et al., 2019)
Fibrocapsa 	<i>F. japonica</i>	Ichthyotoxicity (hemolytic activity)	Photosynthetic / opportunistic; can benefit from nutrient pulses and stratification	(Guidi-Rontani et al., 2010; Viana et al., 2019)

Table.4: Key Taxa, Toxins, and Nutritional Strategies of Raphidophytes

2.14 Chrysophytes

Chrysophytes (golden algae) are freshwater microalgae found in lakes, ponds, and rivers. Their golden-brown pigmentation, driven by fucoxanthin and β -carotene, allows efficient light capture under low-light, nutrient-poor conditions. Although generally non-toxic, chrysophytes strongly influence food-web dynamics, carbon and silica cycling, and water quality through taste- and odor-producing compounds. Many taxa are mixotrophic, supplementing photosynthesis by ingesting bacteria and dissolved organic matter, enabling success in humic, oligotrophic lakes.

They are most abundant in temperate and subarctic waters during spring–early summer when nutrients are limited. Reports from North America, Scandinavia, and East Asia document dense blooms of *Uroglena* and *Synura*, which cause significant organoleptic problems in drinking-water reservoirs. *Hydrurus* spp. thrive in cold, turbulent streams, forming gelatinous mats that produce strong odors upon decay (Gusev et al., 2024).

Among these groups, *Synura* spp. stand out as the most widespread and impactful bloom-formers due to their frequent dense blooms and production of unsaturated fatty acids and aliphatic alcohols that degrade water quality.

Genus (taxon)	Representative species	Main toxins / impacts	Mode of nutrition / trophic strategy	Key references
Uroglena 	<i>Uroglena americana</i> , <i>Uroglena volvocina</i>	Non-toxic but forms taste and odor blooms (earthy/musty smell); can cause drinking-water issues	Mixotrophic	(Pusztai & Škaloud, 2019)
Dinobryon 	<i>D. divergens</i> , <i>D. sertularia</i> , <i>D. sociale</i>	Non-toxic but alters food-web structure; can dominate plankton communities causing reduced biodiversity	Mixotrophic: phagotrophic (feeds on bacteria) + photosynthetic; efficient under low light / low nutrient conditions	(M. Jeong et al., 2023)

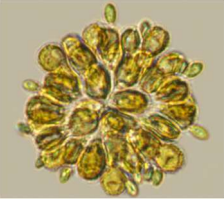
Synura 	<i>S. petersenii</i> , <i>S. uvella</i>	Produces fishy or cucumber-like odors	Mixotrophic: photosynthetic and bacterivorous; prefers low N:P and moderate light	(Knotek et al., 2025)
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Table.5: Key Taxa, Toxins, and Nutritional Strategies of Chrysophytes

2.15 Haptophytes

Haptophytes are single celled flagellated algae present in marine, brackish and freshwater environments. Several species form major and dense blooms which include genera such as *Prymnesium*, *Chrysochromulina*, and *Phaeocystis*. Toxins known as prymnesins (glycolipids, proteolipids) from the species *Prymnesium parvum* have been identified and linked to massive fish kills. One major case reported in Northern Norway 2019, that *Chrysochromulina leadbeateri* have formed a destructive bloom which resulted in ~14,500 tons of farmed salmon killed. Even though there are very less reports for chrysophytes bloom forming species, *Prymnesium parvum* is considered as the globally impactful HAB species because of its ability to produce ichthyotoxins known as prymnesins and have been documented for major fish kills across *Europe, the Middle East, North America, and Asia*.

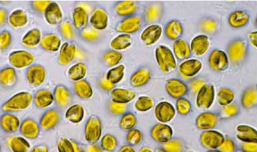
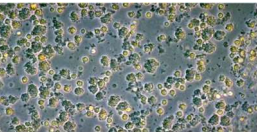
Genus (taxon)	Representative species	Main toxins / impacts	Mode of nutrition / trophic strategy	Key references
Prymnesium 	<i>Prymnesium parvum</i>	Prymnesins & mixed cytotoxins	Mixotrophic / osmotrophic: photosynthetic; thrives on organic N	(Parra-Saldivar et al., 2023)
Chrysochromulina 	<i>Chrysochromulina leadbeateri</i> , <i>C. polylepis</i>	Ichthyotoxic metabolites	Mixotrophic: photosynthetic plus possible prey ingestion	(Fonseca et al., 2024)
Phaeocystis 	<i>Phaeocystis globosa</i> , <i>P. pouchetii</i>	High biomass / foam / mucilage	Mixotrophic	(Koppelle et al., 2022)

Table.6: Key Taxa, Toxins, and Nutritional Strategies of Haptophytes.

The reviewed literature highlights that the global intensification of Harmful Algal Blooms (HABs) is closely linked to climate warming, nutrient enrichment, hydrological changes, and anthropogenic pressures.

2.16 Aquaculture Wastewater as a Linked Driver of Eutrophication and HAB Formation

Aquaculture is a microbial ecosystem that involves interactions between host-related and environment-related microorganisms which is a key point in the growth dynamics. This dynamic microbial ecosystem is strongly influenced by the physicochemical characteristics of the wastewater produced in the system. It typically comprises a mixture of organic and inorganic matters, residual feed, fecal waste, and other chemicals, including antibiotics and heavy metals.²⁴ The high amount of nitrogen and phosphorus present in wastewater mainly comes from the uneaten feed and metabolic excretion, resulting in up to 70-80% being released into the surrounding environment.²⁵

Combining these physicochemical and chemical stresses creates selection pressure that affects the structure, diversity, and functional potential of microbial communities within their hosts and the surrounding ecosystem. Therefore, it is essential to understand how these microbial communities organize themselves and interact with each other to link water quality and fish health.

2.17 Microbial Ecology of Aquaculture Systems and Their Environmental Interface

The gut microbiome of fish is a diverse community, majorly dominated by proteobacteria, firmicutes, bacteroidetes, and actinobacteria. Their species level is influenced by host genetics, diet, water temperature, salinity, and stage of life, etc.²⁸ Metagenomic analysis has revealed that gut microbiota in *Salmo salar*, *Oreochromis niloticus*, and *Litopenaeus vannamei* share some common taxa, including *Lactobacillus*, *Bacillus*, *Aeromonas*, and *Pseudomonas*, however they show a diverse response to dietary and environmental perturbations.²⁸ This flexibility can be either beneficial for microbiome modulation, or it can be a risk for dysbiosis under stress, allowing opportunistic pathogens to sustain.²⁹

In a pond ecosystem, a close link between the fish microbiome and sediment microbiomes has been observed through continuous microbial exchange in water³⁰. Co-existence of nitrogen-fixing heterotrophic bacteria, such as *Nitrosomonas*, *Nitrospira*, and *Paracoccus denitrificans*, has been reported with several pathogenic species, including *Vibrio harveyi*, *Aeromonas hydrophila*, and drug-resistant *Edwardsiella tarda*.^{31,32} Biofilm-producing communities produce a semi-permanent reservoir on the tank surface, sediments, or biofloc particles, which act as a stable reservoir of microbiomes that continuously exchange bacteria with fish, creating an overlap between host-associated and

environmental microbiomes.^{33–35} This synchronized interface between the environment and host could be the most effective target for dual-function microbial strategies.

2.18 Antimicrobial Resistance as an Emerging Risk in Aquaculture Wastewater

In wastewater and aquaculture systems, AMR has emerged as a critical challenge, as diverse microbial communities, residual antibiotics, and selection pressure co-exist. This system is also a hotspot for ARG accumulation and horizontal gene transfer (HGT) due to high microbial density, antibiotic residues, and other co-selective agents, such as heavy metals.^{36–38} Among several ARGs, the tetracycline-resistant genes (*tetA*, *tetB*, *tetM*), integrons (*intI*), sul genes (*sulI*, *sulII*), and β -lactamase-encoding genes (*blaTEM*, *blaCTX-M*) are the most commonly detected in aquaculture and wastewater environments, reflecting the widespread use of tetracyclines, sulfonamides, and β -lactam antibiotics in aquaculture systems.^{39–42} Due to the involvement of several mobile genetic elements (plasmids, transposons, etc.) HGT further facilitates the spread of these ARGs across the microbial population, which are even phylogenetically distant, within a few days under this selection pressure.^{43–46}

The conventional treatment system reduces organic pollutants; however, it is not capable of eliminating ARGs, allowing resistant determinants to persist in treated effluents that eventually enter the natural ecosystem.⁴⁷ The increased occurrence of ARGs in the environment not only disrupts the microbial ecosystem but also poses a serious threat to human and animal health, necessitating urgent combined mitigation strategies. WHO has already classified fluoroquinolones, third-generation cephalosporins, macrolides, and colistin as critically important antimicrobials used for human medicine.⁴⁸ Several jurisdictions, such as the EU, Norway, and Chile, have already restricted the use of prophylactics in aquaculture.⁴⁹ However, the regulatory framework across the Asia-Pacific and Latin American regions collectively produces above 80% of global aquaculture output, which requires a collective reform of policy and biotechnological approaches capable of less dependency on antibiotic usage at the farm level to systematically mitigate AMR.⁵⁰

2.19 Microbiome-Based Intervention for Host Health

PME has emerged as a promising approach for the modulation of host-associated microbiomes in aquaculture to improve fish health, disease resistance, and overall system. PME leverages the application of beneficial microbes such as probiotics, postbiotics, and synbiotics.¹³ These novel strategies function through diverse mechanisms, including competitive exclusion of pathogens, production of bioactive metabolites, and modulation of host immunity (Figure 1). In past years, continued attention has been paid to understanding their combined and individual efficacy under diverse environmental conditions. The mechanisms, advantages, and limitations of these approaches have been discussed thoroughly in this section, providing a comparative evaluation of their effectiveness.

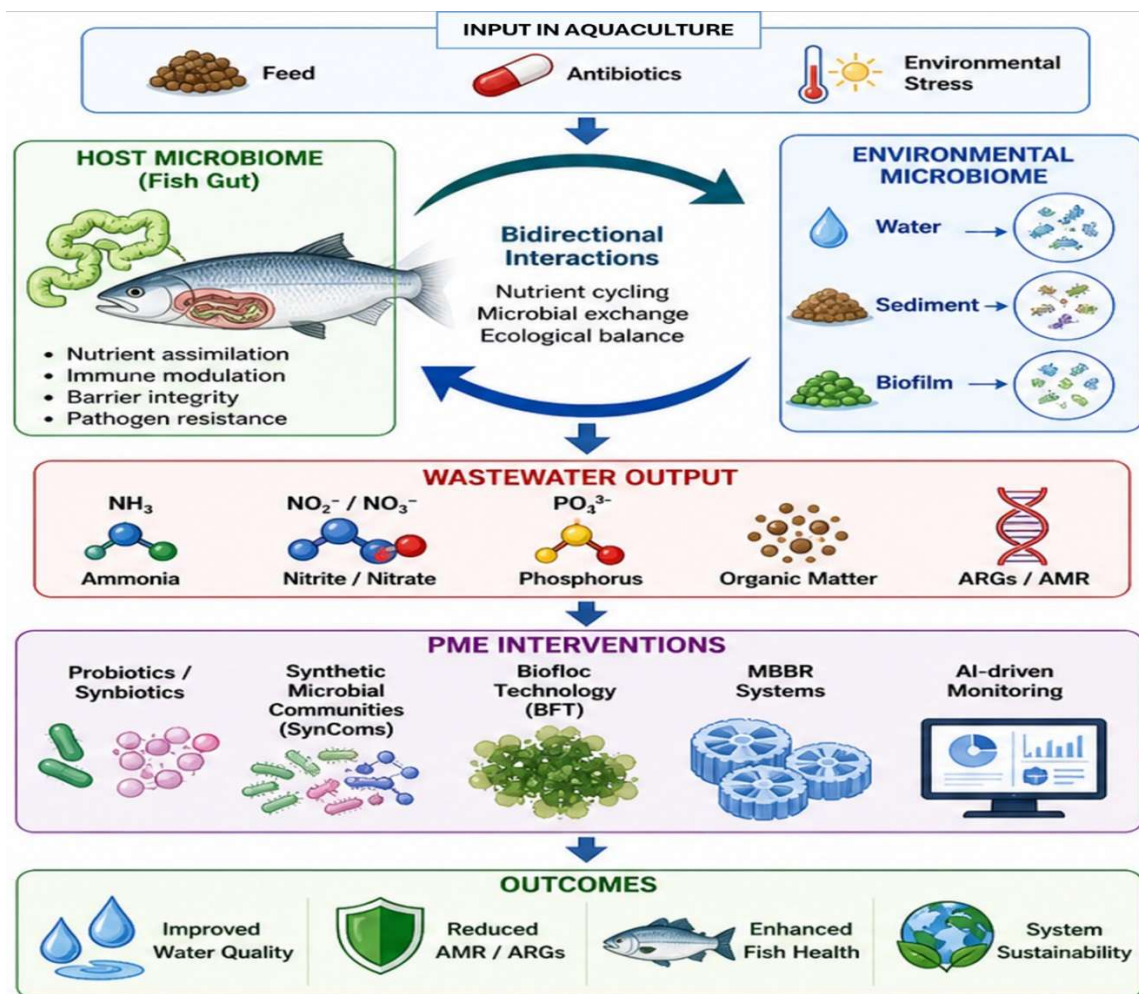


Figure 4: Mechanistic pathways of precision microbiome engineering (PME) in mitigating antimicrobial resistance (AMR) in aquaculture systems.

2.19.1 Classical and Second-Generation Probiotics: Mechanism and Limitations

Living microorganisms that confer health benefits to the host when consumed in adequate amounts are known as probiotics.¹³ Over the last few years, the first-generation probiotics, dominated by *Bacillus* spp. (*B. subtilis*, *B. licheniformis*, *B. pumilus*), *Lactobacillus rhamnosus*, and *Pediococcus acidilactici* have been evaluated across several aquatic animals including Atlantic salmon, Nile tilapia, shrimp, and rainbow trout.^{5,51–53} These microorganisms work in different ways; by competitive exclusion of pathogens, they occupy the host surface and produce antimicrobial compounds like organic acids, hydrogen peroxide, and bacteriocins. As a result, the harmful bacteria cannot attach to the host surface.^{54,55} They also help the host with digestion by releasing proteases and

amylases, and with immunomodulation through Toll-like receptor (TLR) signaling and cytokine induction.^{56,57}

Among second-generation probiotics, *Saccharomyces cerevisiae*, *Enterococcus faecium*, and novel strains identified through metagenomic screening provide additional benefits in mitigation strategies. They can enhance the host's innate immunity, particularly through β -glucans-mediated responses.⁵⁸ They also produce beneficial compounds such as short-chain fatty acid (SCFA) including butyrate, which contribute to gut health.^{55,59} In addition, they can disrupt bacterial communication mechanisms known as quorum sensing. This interference limits the formation of biofilms and reduces the expression of virulence genes in pathogenic bacteria such as *Vibrio harveyi*.⁶⁰ With the help of next-generation sequencing (NGS), the identification of candidate probiotics from gut metagenomes has accelerated significantly. It has enabled the species-specific formulations of probiotics rather than conventional trial-and-error approaches.^{61,62}

2.19.2 Paraprobiotics and Postbiotics

Paraprobiotics are attenuated microorganisms (prepared by heat-inactivation, UV-irradiation, or sonication) that still retain their beneficial immunogenic components. They are devoid of safety concerns linked to live probiotics in aquaculture ecosystems, including HGT and disruption of natural microbial communities.⁶³ Heat-killed *Lactobacillus plantarum* applied to bighead catfish (*Clarias macrocephalus*) with a concentration of approximately 2.0×10^{11} cells g⁻¹ has demonstrated improved growth performance and immune response through reduced FCR and significant enhancement of total white blood cells, or improved digestibility coefficient.⁶⁴

On the other hand, postbiotics are preparations of inanimate microorganisms and/or their components conferring health benefits. It includes bioactive compounds such as SCFAs, bacteriocins, exopolysaccharides, and cell-free supernatants.⁶⁵ In aquaculture systems, SCFAs, including acetate, propionate, and butyrate, play a major role in improving intestinal health by enhancing epithelial barrier function through the regulation of tight junction proteins such as claudin and occluding.⁶⁶

2.19.3 Synbiotics and SynComs: Stability advantage, synergistic effects

Synbiotics are the combination of a probiotic with a cognate prebiotic substrate specially designed for the selective fueling of the probiotic's proliferation inside the gut.⁶⁷ Combination of *Lactobacillus rhamnosus* with fructooligosaccharides or *Bacillus subtilis* with mannan-oligosaccharides.⁶⁸ They have demonstrated greater additive effects on gut microbiome diversity, activation of immune-responsive genes, and pathogen exclusion compared to either component alone.⁶⁹ These bioactive formulations are being delivered rapidly via encapsulated feed pellets or water-dispersible formulations to enable controlled dosing, improved stability, and targeted application in aquaculture.^{56,70,71}

SynComs represent the synthetic microbial communities that are designed consortia of functionally complementary microorganisms to achieve targeted microbiome modulation.

In aquaculture, it has emerged as an alternative strategy to stabilize the fish gut microbiome, enhancing nutrient utilization and improving host immunity. SynComs can engage multiple ecological niches inside the gut, which promotes community resilience and the risk of dysbiosis.^{72,73} Within the aquatic environment, the use of such synthetic communities has been shown to boost microbial diversity, which in turn has resulted in higher disease resistance and improved growth characteristics.^{69,74,75} Such function-based approaches highlight the potential of SynComs as a key tool in PME for sustainable aquaculture.

Current evidence does not treat harmful algal blooms as isolated ecological episodes. They are usually discussed as the result of several pressures acting together, especially nutrient enrichment, warming, hydrological disturbance, and shifts in microbial balance. Bloom-forming taxa differ in how they persist and expand; cyanobacteria, dinoflagellates, diatoms, raphidophytes, chrysophytes, and haptophytes are associated with combinations of toxin release, rapid biomass increase, colony formation, and flexible nutrient use. Aquaculture wastewater adds another layer to that setting by supplying nitrogen- and phosphorus-rich effluents and by linking water-quality decline with antimicrobial-resistance concerns and host-environment microbial interactions. Taken together, these findings favor integrated management built around algicidal bacterial consortia, microbial bioremediation, and smart monitoring rather than single-mechanism HAB control.

CHAPTER 3 METHODOLOGY

This study is a systematic literature-based research design to evaluate the potential of algicidal bacteria for the bioremediation of Harmful Algal Blooms (HABs) and design a smart water-quality monitoring system for early detection and mitigation for the purpose of prevention of spread of algal.

3.1 Research Framework

A structured four-phase approach was adopted:

Identification of the major algal species analysis of global and regional bloom trends, causative taxa, and ecological drivers.

Compilation of algicidal bacterial data from extraction of published reports describing algicidal activity, mechanisms, and environmental performance of the particular taxa.

Comparative mechanistic approach of the algal in evaluation of bacterium and algae interactions, including biochemical and ecological pathways.

Conceptual integration by development of a multi-strain bacterial consortium and a complementary smart monitoring framework to help in controlling the bloom.

3.2 Data Acquisition and Selection Criteria

Peer-reviewed articles and technical reports published were retrieved from Scopus, PubMed, ScienceDirect, SpringerLink, and Google Scholar databases. Search terms included “Harmful Algal Blooms,” “algicidal bacteria,” “bioremediation,” “bacterial consortium,” “eco-engineering,” and “smart water monitoring.”

Data pertaining to dominant HAB taxa (Microcystis, Noctiluca, Pseudo-nitzschia, Heterosigma, Prymnesium) and active bacterial genera (Bacillus, Pseudomonas, Hahella, Phaeobacter, and Pseudoalteromonas) were prioritized.

3.3 Analytical and Comparative Evaluation

Selected publications were analyzed to extract key parameters such as algicidal efficiency, target specificity, metabolic pathways, and ecological safety. Comparative synthesis highlighted primary mechanisms—reactive oxygen species (ROS) induction, extracellular enzymatic degradation, secondary metabolite secretion, and quorum-sensing-regulated algicidal activity.

The results were categorized according to bacterial genus and target algal group to identify synergistic combinations suitable for consortium development.

CHAPTER 4 RESULTS

4.1 Algicidal Bacteria

After the detailed and intensive assessment of all the HABs taxa group and species, it is proved that global HABs produce and spread densely with the help of many factors such as toxin production, and adaptability to nutrient-enriched environments. Some of the major bloom-forming taxa from this research that are known to be more disastrous compared to other groups such as *Microcystis*, *Alexandrium*, *Pseudo-nitzschia*, *Heterosigma*, *Prymnesium*, and *Synura* etc. However, this increasing frequency and spatial extent of HABs which are very harmful for human as well as aquatic ecosystem has proved that there is an urgent need for effective and sustainable mitigation strategies. But there are naturally occurring microorganisms which are known as Algicidal Bacteria which help in inhibiting the growth of HABs, and are considered as an ecofriendly approach for controlling HABs. These bacteria interact with the algal groups in such a way that their growth is inhibited by producing toxins, secretion of reactive oxygen species or enzymatic degradation of these algal cells.

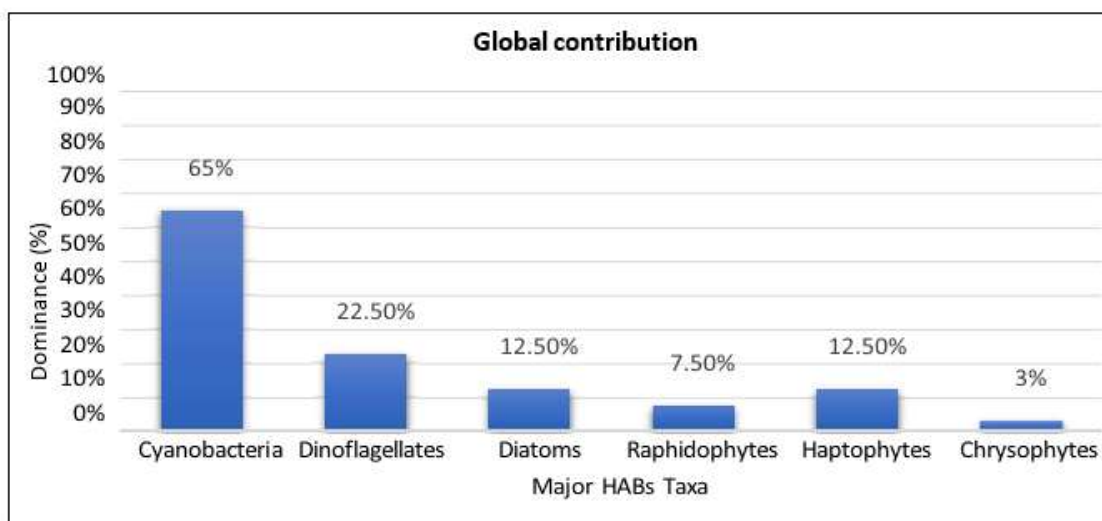


Fig.5: Global Contribution and Dominance of Major HAB Groups

The distribution pattern illustrated here describes that cyanobacteria and dinoflagellates dominate global HAB events, accounting for nearly 80% of HABs. This dominance of this group is mitigated or controlled by algicidal bacterial consortia. Many studies (Jia et al., 2025a; Zhang et al., 2023) have revealed that specific bacterial genera such as *Bacillus*,

Alteromonas, *Roseobacter*, and *Pseudomonas* exhibit strong inhibitory effects against major bloom-forming species, offering the potential methods that can mitigate HABs without causing any harm to aquatic biodiversity.

Target group	HAB	Dominant species	HABs	Algicidal Bacterial Genera	Representative Species
Cyanobacteria		<i>Microcystis aeruginosa</i>		<i>Bacillus</i>	<i>Bacillus subtilis</i>
Dinoflagellates		<i>Noctiluca scintillans</i>		<i>Alteromonas</i> , <i>Roseobacter</i> ,	<i>Roseobacter gallaeciensis</i> (<i>Phaeobacter inhibens</i>)
Diatoms		<i>Pseudo-nitzschia</i> spp.		<i>Pseudomonas</i>	<i>Pseudomonas fluorescens</i>
Raphidophytes		<i>Heterosigma akashiwo</i>		<i>Pseudoalteromonas</i> , <i>Hahella</i>	<i>Pseudoalteromonas</i> sp. LD-B6, <i>Hahella chejuensis</i> (KA22)
Haptophytes		<i>Prymnesium parvum</i>		<i>Bacillus</i>	<i>Bacillus subtilis</i>
Chrysophytes		<i>Synura</i> spp.		<i>Pseudomonas</i>	<i>Pseudomonas fluorescens</i>

Table.7.0: Dominant taxa of blooms-forming species group.

Table 7.0 represent the shortlisted dominant taxa of blooms-forming species group. After a detailed assessment, it is established that these HABs taxa are very problematic as they cause high spatial extent, dense blooms and serious problems to marine ecosystems and humans.

4.2 *Bacillus* Spp.

Cyanobacteria account for ~65% of major inland HABs, with *Microcystis aeruginosa* and *Dolichospermum* spp. being the dominant genera.

Bacillus subtilis has emerged as an effective algicidal bacterium against these blooms. Studies show that *B. subtilis* can eliminate ~98% of *M. aeruginosa* cells and degrade ~90% of released microcystins. Its extracellular metabolites rupture cyanobacterial cell walls and break down microcystins, which are otherwise highly stable and resistant to proteases, pH, and heat—highlighting its strong potential for HAB mitigation in aquatic systems (Chen et al., 2024).

The *B. subtilis* S3 strain also demonstrates ~70% algicidal activity against the dinoflagellate *Alexandrium* spp. Other isolates produce lipopeptides (iturin, surfactin,

fengycin) and algicidal compounds such as hexahydropyrrolo[1,2-a]pyrazine-1,4-dione, which disrupt algal cell membranes (Cheng et al., 2022).

Additional mechanisms include the generation of reactive oxygen species (ROS), secretion of extracellular proteases, and quorum-quenching activity. These processes inhibit bloom formation by degrading or destabilizing species like *Karenia mikimotoi*, *Alexandrium tamarense*, *Microcystis*, and *Dolichospermum* (Chen et al., 2024a).

Overall, *Bacillus subtilis* is a robust freshwater bacterium with proven ability to suppress phytoplankton blooms and reduce colony biomass.

4.3 *Phaeobacter inhibens*

Phaeobacter inhibens have the capability to switch between mutualistic and pathogenic interaction with microalgae, and also it is native to marine environments and has direct relevance to marine HABs targeting dinoflagellates, haptophytes and raphidophytes. It has an ability to selectively inhibit the HABs and uses quorum-sensing regulation in aquatic ecosystems.

This bacterium is widely studied for its algicidal activity as it releases secondary metabolites like roseobacticides and also produces tropodithietic acid (TDA) which helps in inhibiting the growth of HABs. When the co-culture of *P.inhibens* was prepared with algae *Emiliana huxleyi*, it initially exhibited symbiotic behaviour, but due to the presence of p-coumaric acid release by algae, the bacterium transitioned to an algicidal mode, releasing roseobacticides leading to algal death (Gram et al., 2015). This species can be considered as a potent algicidal bacteria due to its dual nature and it is also reported that, aside from *E.huxleyi* this bacterium also exhibits its algicidal activity towards some species of dinoflagellates and Rhapsidophytes.

4.4 *Alteromonas* spp

Alteromonas is a marine algicidal bacterium known to target major HAB-forming dinoflagellates and raphidophytes. Its activity relies on the secretion of extracellular proteolytic and oxidative metabolites that degrade algal cell membranes, damage flagella, induce lipid peroxidation, and disrupt chloroplast structure—ultimately inhibiting photosynthesis.

Its algicidal mechanism is indirect: the bacterium releases phenoxazinone derivatives (e.g., quetiomycons), which generate reactive oxygen species (ROS). These compounds destabilize algal cell integrity, inhibit electron transport in photosystem pathways, and lead to rapid cell lysis (Umetsu et al., 2019; Jia et al., 2025a).

Experimental studies show *Alteromonas abrolhosensis* can lyse >90% of *Karenia mikimotoi* cells within 48 hours at a 1:10 bacterium-to-alga ratio (Jia et al., 2025b). A related strain, *Alteromonas* sp. D, caused complete collapse of *Chattonella antiqua* within 24 hours through quetiomycin-like metabolite production (Umetsu et al., 2019).

These results demonstrate that *Alteromonas* spp.—particularly *A. abrolhosensis*—produce highly potent secondary metabolites, making them strong candidates for mitigating marine HABs through ROS-mediated and enzymatic degradation pathways.

4.5 *Pseudoalteromonas* spp

Pseudoalteromonas spp. is considered as the most effective and ecologically versatile algicidal bacteria identified in marine environments. This species targets broad-spectrum inhibition of several harmful algal bloom (HAB) taxa which includes the raphidophytes (*Heterosigma akashiwo*, *Chattonella marina*), and dinoflagellates (*Gymnodinium catenatum*). These species mediate its algicidal activity through secretion of extracellular metabolites and enzymes, such as proteases, lipases, diketopiperazines, and prodigiosin-like compounds, which results in initiating cell membrane rupture, oxidative stress (ROS accumulation), and chloroplast degradation in algal cells. (Lovejoy et al., 1998) revealed the Y strain, closely related to *P. Peptidysin* lysed these three different species of HABs within 1-3 days through complete cell collapse, pigment bleaching, cytoplasmic leakage and rapid pigment loss without direct cell contact between algal and bacterium cells, which proves that bacterial metabolites directly compromise membrane integrity and osmotic balance.

4.6 *Hahella* spp.

Hahella spp., particularly *Hahella chejuensis* strain KA22, exhibit strong algicidal activity against a broad range of HAB taxa, including dinoflagellates, haptophytes, raphidophytes, and cyanobacteria (*Phaeocystis*, *Heterosigma*, *Microcystis*). Their potency is largely due to prodigiosin, a low-molecular-weight tripyrrole pigment that acts as a broad-spectrum algicide.

Prodigiosin induces algal death by rupturing cell membranes, triggering rapid ROS accumulation, organelle collapse, and—specifically in colonial species—breakdown of extracellular polymeric substances leading to colony disaggregation (Zhang et al., 2016). Laboratory studies show prodigiosin is heat- and acid-stable, moderately persistent under alkaline and sunlight conditions, and highly effective against raphidophytes. For *Phaeocystis globosa*, LD₅₀ values fall in the low $\mu\text{g mL}^{-1}$ range ($\sim 2.2 \mu\text{g mL}^{-1}$), producing >75–90% mortality within 24–72 h. Against *Microcystis aeruginosa*, LD₅₀ is $\sim 5.87 \mu\text{g mL}^{-1}$ within 72 h (K. Yang et al., 2017; Zhang et al., 2017).

4.7 *Kordia* spp.

Kordia spp., particularly *Kordia algicida*, are algicidal flavobacteria known for targeting major bloom-forming diatoms such as *Skeletonema costatum*, *Thalassiosira weissflogii*, and *Pseudo-nitzschia*. Their activity is driven by the secretion of high-molecular-weight extracellular proteases that degrade diatom cell walls and membranes. Protease production is induced by algal cues, and in some cases, triggers diatom defenses such as oxylipin release.

Paul & Pohnert (2011) demonstrated that *K. algicida* secretes a >30 kDa protease responsible for algicidal activity; protease inhibitors block this effect, confirming proteolysis as the primary mechanism. Susceptible diatoms like *Skeletonema costatum* undergo near-complete lysis within 2–5 days when exposed to stationary-phase cultures. *K. algicida* is effective against *S. costatum*, *T. weissflogii*, and *P. tricornutum*, whereas some species—such as *Chaetoceros didymus*—are resistant. Additional studies show *K. algicida* can suppress blooms of *Chaetoceros socialis*, a dominant species in the North Sea (Bigalke et al., 2019).

4.8 *Streptomyces* spp.

Streptomyces spp. are filamentous actinomycetes, which is known for antibiotic biosynthesis, also acts against algal blooms present in both freshwater and marine water and shows algicidal activity. These species produce bioactive secondary metabolites that act via multiple biochemical targets such as membranes, redox balance and enzyme systems.

(Luo et al., 2013) reports that *streptomyces* sp. L74 releases the active secondary metabolite which act against *Microcystis aeruginosa*, *Anabaena flos-aquae*, *Oscillatoria animalis*, and *Aphanizomenon flos-aquae*. This compound disrupts

antioxidant defence and triggers ROS accumulation and ruptures membrane. *Streptomyces* sp. L74 directly attacks *A. flos-aquae* by cell-to-cell contact and indirectly attacks *M. aeruginosa*, *O. animalis*, and *Aph. flos-aquae* by using the active substances. This species also exhibits high algicidal activities against harmful types of cyanobacteria. Therefore, this strain can be useful for targeting wide range of CyanoHABs in various environment.

Some other isolates of these species have yielded diketopiperazines and polyketides which act against *phaeocystis* and dinoflagellates, however the efficacy of these compounds can vary by isolated strain (Coyne et al., 2022b).

4.9 Pseudomonas spp. (e.g., Pseudomonas fluorescens)

Pseudomonas species have shown algicidal activity against Freshwater (cyanobacteria) and Marine (raphidophytes, diatoms) groups. They have been widely reported to target *Stephanodiscus hantzschii*, *Heterosigma akashiwo*, *Pseudanabaena* spp. and *Microcystic aeruginosa* through diverse mechanism of action.

One study (Wijesooriya et al., 2023a) reveals that reservoir in Sri Lanka reservoir, *pseudoanabena* species were found which were targeted by *Pseudomonas fluorescens* with the help of secreting extracellular lytic metabolites. Microscopic observations have revealed that cyanobacterial filamentous structures were completely disintegrated after treating with *P. fluorescens*. Other studies also reveals that *P. fluorescens* disrupts algal cell membrane, inhibit photosynthetic pigment synthesis, such as chlorophyll and carotenoid content and also initiate ROS generation against *Heterosigma akashiwo*. Microscopic analysis showed cell lysis, loss of motility, and collapse of cytoplasmic structure, resulting in damage to the plasma membrane and organelles within 48 hrs. The algicidal compounds secreted by *P. fluorescens* were heat-stable and small-molecular-weight substances, proving that they are metabolites or biosurfactants and not enzymes (Kim et al., 2007).

4.10 Key Mechanisms and Interactions

Algicidal bacteria inhibit algal blooms via direct (contact-dependent) and indirect (diffusible metabolite-mediated) mechanisms. Directly, bacteria attach to algal cells or reside in the phycosphere, causing lysis. Indirectly, they release metabolites—peptides, pigments, and proteases—that alter algal physiology. Some bacteria use both modes depending on growth phase, density, and algal cues; for example, *Kordia algicida* secretes proteases targeting diatoms (indirect), while *Streptomyces* lyses cyanobacteria only via close contact (direct) (Coyne et al., 2022b).

Direct interactions involve host-specific lysis via enzymes or adhesion, whereas indirect interactions release algicides into the water column, triggering growth arrest, photophysiological collapse, or lysis through antioxidant depletion, membrane disruption, and DNA damage (Zeng et al., 2021). *Phaeobacter inhibens* senses stress-induced p-coumaric acid from *Emiliana huxleyi*, inducing roseobacticide production, which

penetrates membranes and triggers oxidative stress and apoptosis-like responses (Seyedsayamdost et al., 2011).

Evidences of algicidal activity of bacterial isolates against target algae

4.11 *Phaeobacter inhibens* –

P. inhibens is one of the best-characterized algicidal bacteria, known for its potency, selectivity, and quorum-sensing regulated algicidal activity. It effectively targets dinoflagellates, haptophytes, and raphidophytes, activating the reduction of harmful biomass without the use of chemical algaecides for the purpose of making the environment clean. Its mechanistic pathway is well studied, offering operational clarity and flexibility that make it highly suitable for HAB control. This selectivity minimizes collateral damage, as its algicidal mode is activated only in response to algal-derived cues. Although its target range is not broad across all HAB species, it exhibits high potency against marine microalgae that release strong chemical signals.

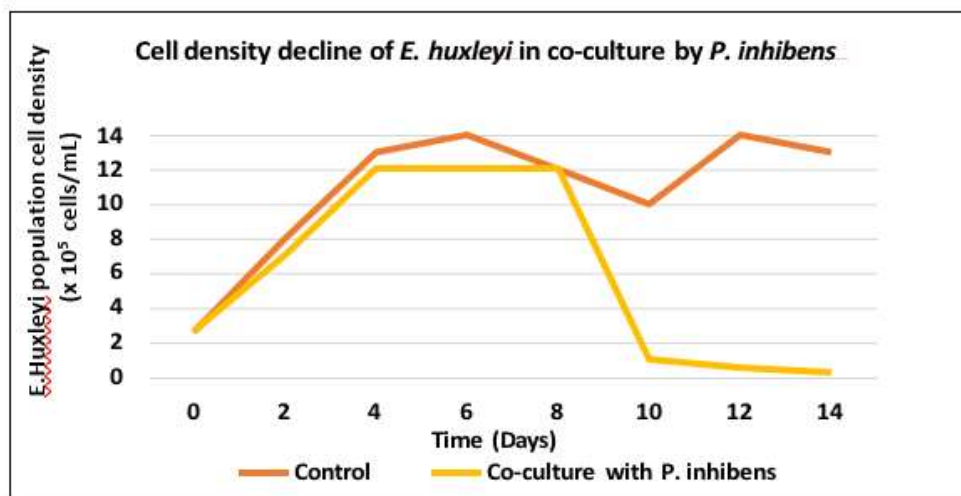


Fig 6: *E. huxleyi* cell density over 14 days in control and *P. inhibens* co-culture. Control algae grow normally, while co-cultures show a sharp collapse after day 8, demonstrating strong algicidal activity. Data points were taken from (Bramucci & Case, 2019)

4.12 *Pseudomonas fluorescens*

P. fluorescens is a versatile algicidal bacterium that targets freshwater HABs, particularly *Microcystis aeruginosa* and other cyanobacteria. Multiple studies report strong reductions in cyanobacterial biomass and diatoms. Its ubiquity in freshwater systems facilitates the isolation of native, site-specific biocontrol strains, supported by the genus's broad metabolic versatility.

This species employs multiple mechanisms including secretion of extracellular proteases and lytic enzymes, ROS production and oxidative stress induction, and, in some strains,

detoxification via microcystin degradation. This mechanistic diversity reduces the likelihood of resistance or rapid adaptation in target populations.

4.13 *Pseudoalteromonas* Spp.

Pseudoalteromonas spp. showed broad and potent algicidal activity, with strengths in wide taxonomic target range, high production potential, and mechanistic versatility. Many strains show strong lytic effects against marine HABs such as raphidophytes, dinoflagellates and certain diatoms. In one study, one isolate (LD-B6) demonstrated algicidal effects against six HAB species within 24 hours, killing nearly 100% of *Noctiluca scintillans* and *H. akashiwo* (J. Wang et al., 2022a).

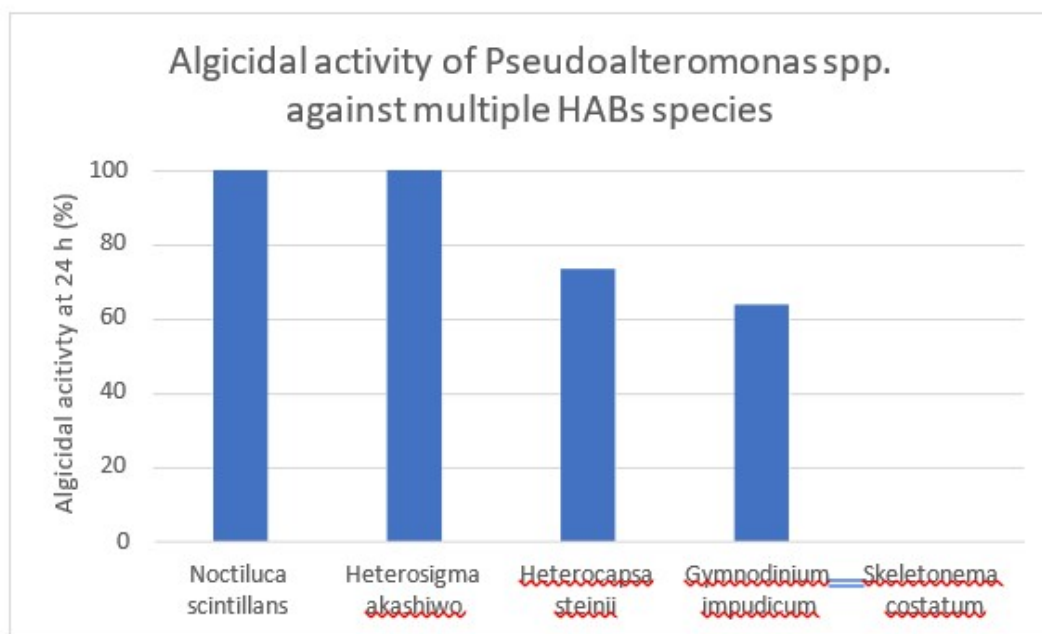


Fig.7: Algicidal activity of *Pseudoalteromonas* sp. LD-B6 against representative harmful algal bloom (HAB) species after 24 h. Bars show percent algicidal activity at a 2% (v/v) inoculum of LD-B6 culture against six algal species. The strain caused complete (100%) lysis of *Noctiluca scintillans* and *Heterosigma akashiwo*, strong activity against *Heterocapsa steinii* ($73.3 \pm 1.3\%$) and *Gymnodinium impudicum* ($63.7 \pm 9.2\%$), moderate suppression of *Prorocentrum micans* ($26.7 \pm 0.68\%$), and negligible algicidal effect on the diatom *Skeletonema costatum*. Data are replotted from (J. Wang et al., 2022b)

4.14 *Hahella* / prodigiosin-producing strains (e.g., *Hahella chejuensis*/KA22)

Hahella species—especially the red-pigmented *Hahella chejuensis*—are among the most potent algicidal bacteria due to their rapid, high-intensity HAB-killing activity and production of the secondary metabolite prodigiosin. This species is a strong marine biocontrol candidate, offering extreme potency, a broad target range, and well-characterized bioactive chemistry. Prodigiosin, a red tripyrrole pigment from *H. chejuensis*, degrades over 90% of *Cochlodinium polykrikoides* and shows strong algicidal effects against dinoflagellates, diatoms, and raphidophytes (H. Jeong et al., 2005). It acts through membrane permeabilization, oxidative stress induction, apoptosis-like responses, and concentration-dependent lysis.

The compound's potency and well-defined biosynthetic pathway make *H. chejuensis* a highly promising agent for marine HAB mitigation.

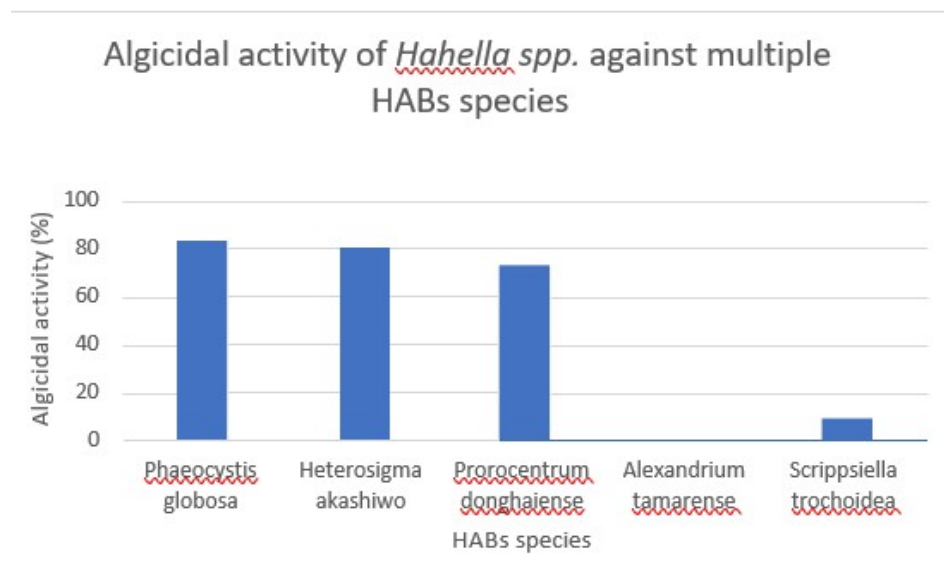


Fig.8: Algicidal activity of prodigiosin from *Hahella sp. KA22* against multiple harmful algal bloom (HAB) species. Bars show the percentage algicidal activity after 72 h exposure to 5 µg/mL purified prodigiosin. The compound caused strong algal lysis of *Phaeocystis globosa* (84.0%), *Heterosigma akashiwo* (82.3%), and *Prorocentrum donghaiense* (73.8%), but showed minimal or no algicidal activity against *Alexandrium tamarense* (5.1%), *Skeletonema costatum* (−3.3%) and *Scrippsiella trochoidea* (9.6%). Data are replotted from (Zhang et al., 2016b).

4.15 *Bacillus subtilis*

Bacillus subtilis is a strong candidate for HAB mitigation due to its high algicidal efficacy against *Microcystis aeruginosa* and its ability to degrade microcystin. The strain *B. subtilis* S4 showed exceptional performance, removing 98% of *M. aeruginosa* and its released toxin across a wide pH and temperature range, demonstrating strong field applicability (Chen et al., 2024b). At the genus level, several *Bacillus* strains (e.g., *Bacillus* sp. Lzh-5, *Bacillus* sp. S51107, *B. licheniformis* Sp34) have been isolated from bloom-affected lakes and shown to kill *Microcystis* via secretion of compounds that induce oxidative stress, membrane damage, and inhibition of microcystin synthesis, underscoring the versatility and reliability of *Bacillus*-based algicidal mechanisms (Li et al., 2015).

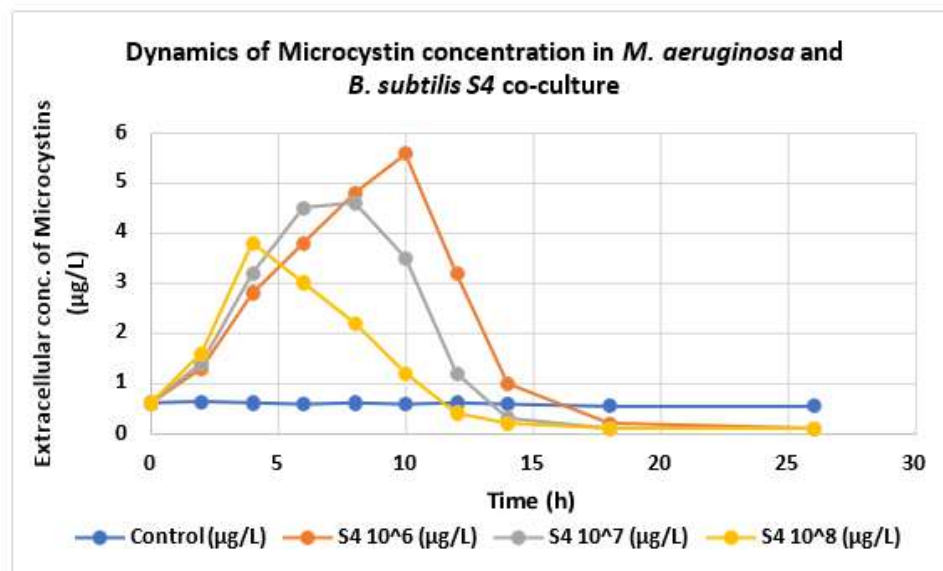


Fig. 9: *Bacillus subtilis* strain with efficient algicide of *Microcystis aeruginosa* and degradation microcystins. Data taken from (Chen et al.,2024b)

The analysis demonstrates that no single algicidal bacterium can help removing all major algal groups, as each species possesses distinct target specificities, mechanisms, and environmental performance profiles. By comparing the potency, mode of action of the bacteria , and safety of **key genera including Bacillus, Pseudomonas, Pseudoalteromonas, Hahella, Kordia, Streptomyces, and Phaeobacter**—the analysis clarifies their synergistic strengths and limitations

5.0 PME for Aquaculture Effluents Bioremediation

For the optimization of microbial communities for simultaneous enhancement of water quality and suppression of AMR in the aquaculture system, PME provides a system-level solution. Use of functionally designed microbial consortia, PME, enables efficient removal capability of excess nutrients, organic matter, and microbial contaminants from aquaculture effluents. The most widely used PME strategies include Biofloc Technology (BFT), Moving Bed Biofilm Reactor (MBBR), Synthetic Microbial Communities (SynCom), and microalgae-bacteria consortium systems. They offer distinct advantages that can be tailored in operation context of rigorous aquaculture. Table 1 provides an overview of bioremediation technologies for aquaculture effluents.

5.1 Biofloc Technology (BFT): Microbial Conversion of Nitrogenous Waste and Water Quality Enhancement

It is a largely adopted microbial-based system converting dissolved nitrogenous waste into microbial biomass using heterotrophic bacterial communities through carbon supplementation. It also reduces the feed conversion ratio and overall production costs. BFT can promote the assimilation of ammonia and nitrate into biofloc aggregates to reduce the nitrogen toxicity level and improve the water quality.^{34,75,76} Bioflocs are composed of bacteria, algae, protozoa, and organic particles that cannot recycle nutrients but serve as a supplemental food source. It has been shown to improve microbial diversity and suppress opportunistic pathogens, including several species of *Vibrio* spp, through competitive exclusion and inhibiting quorum sensing.^{75,77} However, this technology also has some limitations, including complex regulation of the carbon-to-nitrogen ratio, accumulation of suspended substances, and acidification of bottom sludges that directs toward the use of a hybrid configuration of BFT coupled with MBBR and associated multi-trophic aquaculture systems.^{77–79}

5.2 Moving Bed Biofilm Reactor (MBBR) for Enhanced Nitrogen Removal in Aquaculture Systems

Moving bed biofilm reactor (MBBR) is an advanced biofilm-based wastewater treatment technology, utilising suspended plastic carrier media to support the growth of microbial biofilms capable of nitrogen fixing and organic matter degradation. These are efficient to

facilitate the nitrification and denitrification processes by providing a large surface for the colonisation of autotrophic and heterotrophic microorganisms.^{80,81} In the aquaculture system, MBBR has shown high efficiency in removing ammonia, nitrite, and organic carbon, which makes it suitable for recirculating aquaculture systems (RAS).⁸¹ At the microbial level, biofilms in MBBR contain a large amount of *Nitrospira*, promoting nitrification. These biofilm-associated communities demonstrate higher functional abilities for the removal of nitrogen compounds as compared to other sediment communities.^{82,83} MBBR offers a platform for targeted enhancement of microbial communities, including nitrifiers and denitrifiers, that can be used for omics-guided strategies to improve nutrient removal efficiency. One major challenge of MBBR is the requirement of a prolonged colonisation period before the efficient nitrification process. This has been recently addressed by integrating MBBR with BFT- the advanced biofloc system, resulted in improved water quality and fish health with genes linked to denitrification.^{75,80,81}

5.3 SynComs in aquatic bioremediation

Strategies with SynCom aim to integrate nutrient removal, pathogen suppression, and AMR mitigation using a single engineered microorganism strain. Direct applications of SynCom are still limited in aquaculture, however, these consortia can be designed to include nitrifiers, denitrifiers, organic matter degrading microbes, and probiotic strains to enable simultaneous removal of nitrogen, phosphorus and pathogenic microbes through metabolic.^{34,75,84} SynComs have the potential to reduce the abundance of ARGs by promoting competitive microbial environments that limit the growth of resistant species.^{85,86} Despite their promises, employing SynComs in open aquaculture systems remains in a nascent stage, but it is maturing rapidly, with concerns about ecological stability and regulatory frameworks that require resolution.

Table 8: Technologies for bioremediation of aquaculture effluents

Technology	Operational Principle	Key Microbial Players	Target Pollutants	Removal Efficiency	Advantages	Limitations
Biofloc Technology (BFT)	Heterotrophic assimilation via C:N balance	Heterotrophic bacteria, algae	Ammonia, nitrate, organic	High (N removal)	Cost-effective, improve	Requires C:N control, sludge

			carbon		s FCR	buildup
MBBR	Biofilm-based nitrification/denitrification	<i>Nitrospira</i> , <i>Nitrosomonas</i>	NH ₃ , NO ₂ ⁻ , organic matter	Very high	Stable, scalable	Slow startup (biofilm formation)
Microalgae-Bacteria Consortia	Photosynthetic nutrient uptake	Algae + heterotrophs	N, P, CO ₂	Moderate to High	Carbon capture + nutrient removal	Light dependency
SynCom-based Systems	Engineered microbial interactions	Functional consortia	N, P, pathogens, ARGs	Emerging	Multi-functional, targeted	Early-stage, regulatory issues
Hybrid Systems (BFT + MBBR)	Combined suspended + attached growth	Mixed communities	Broad-spectrum removal	Very high	Synergistic efficiency	Complex management

PME as a Convergent Dual Strategy: Integrating Host and Environmental Microbiomes for Sustainable Aquaculture

Aquaculture systems operate as tightly coupled ecological networks in which host-associated microbiomes and surrounding microbial communities interact continuously. Fish, water, sediment, and biofilm-associated microbiota are connected through a constant microbial exchange that forms a dynamic ecosystem influencing nutrient cycle, disease dynamics, and overall system productivity.^{75,87} In this interconnected network, disturbances in one section can rapidly affect the ecosystem, increasing susceptibility to

disease outbreaks and the proliferation of opportunistic pathogens. PME offers an opportunity to address these challenges through coordinated microbial interventions that target host health and improve environmental quality as well (Figure 2). A comparative overview of microbiome engineering strategies has been given in Table 2.

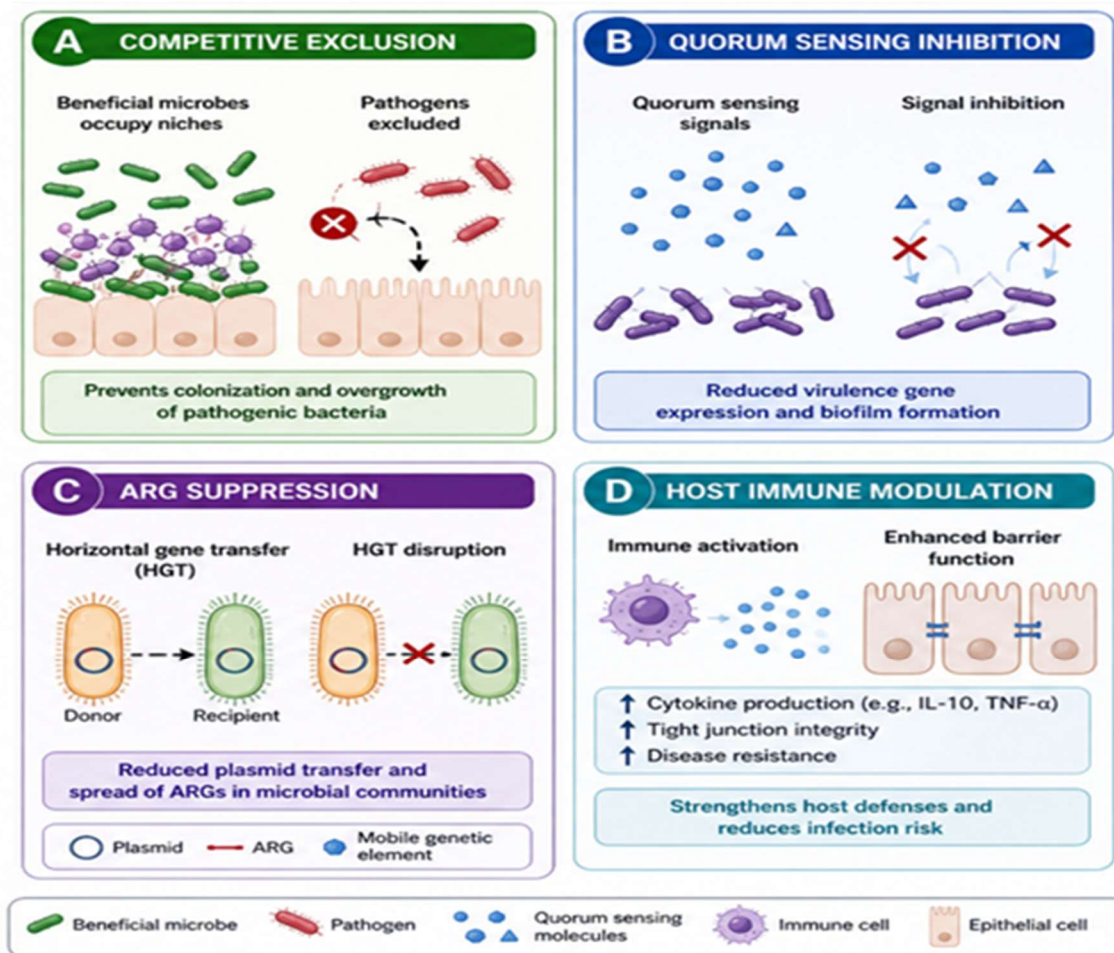


Figure 10: Integrated framework of precision microbiome engineering (PME) for host aquaculture bioremediation and antimicrobial resistance (AMR) mitigation.

5.4 Linking Host and Environmental Microbiomes

The fish gut microbiome is essential in the metabolism of nutrients, immune response, and disease resistance, whereas the water and environmental microbiomes control biogeochemical activities such as nitrogen and carbon cycles. The processes do not occur independently but interact by exchanging microorganisms via ingestion, excretion, and direct contact with the aquatic environment, thereby forming a cycle of interaction between the host and environmental microbiomes.^{62,87} For example, beneficial bacteria

introduced as probiotics in fish feed can be released into the surrounding water via faeces, where they can contribute to nutrient cycling and pathogen suppression. On the contrary, environmental microbes can colonise the fish gut, influencing microbial composition and the host's pathology. This bidirectional exchange between host and environment highlights the importance of considering the aquaculture system as an integrated microbiome rather than a single unit. Species from different taxa, such as *Bacillus* and *Lactiplantibacillus* have demonstrated their ability to function across both domains, enhancing the host's gut immunity while also improving water quality through organic matter degradation and competitive exclusion of pathogenic strains.^{55,88} PME utilises these multifunctional microbes to develop a coherent strategy that bridges the gap between host and environmental development, thereby enhancing system resilience.

5.5 AMR Mitigation through PME

The occurrence and spread of AMR in the aquaculture system is driven by a combined events of antibiotic usage, high microbial population, and environmental selection pressure that promote horizontal gene transfer (HGT).^{10,85} The effluents discharged from aquaculture farms act as reservoirs and routes for the transmission of ARGs, thus posing a threat to the environment and public health. Traditional sewage treatment methods are not sufficient for removing ARGs, allowing them to spread in the natural environment. PME serves as an alternative approach to AMR mitigation by minimising antibiotic use and promoting microbial ecosystems, which inhibit the growth of resistant microbial populations. Probiotics, synbiotics and postbiotics play a crucial role in enhancing host immune response and reducing disease incidence, minimising the need for chemotherapeutic interventions.⁵⁷ Engineered microbial consortia can compete with pathogenic bacteria and ARG-carrying microorganisms through niche occupation, resource competition and production of antimicrobial substances under water.^{34,75} Antibiotics used in aquaculture, including fluoroquinolones, third-generation cephalosporins, and colistin, are classified by the World Health Organization (WHO) as the highest priority antimicrobials for humans, highlighting the One Health dimensions of aquaculture-derived AMR.^{48,89}

Unlike conventional approaches that treat host health and environmental remediation separately, PME aims to improve both simultaneously. Many of the same microbial taxa that improve gut immunity in fish (e.g., *Bacillus subtilis*, *Lactiplantibacillus plantarum*) also contribute significantly to the improvement of water quality through competitive exclusion of potentially resistant microorganisms, ammonia oxidation, and organic matter decomposition^{88,90–92}.

Table 9: Comparative overview of strategies for microbiome engineering in aquaculture systems

Strategy Type	Key Components	Mechanism of Action	Target Domain	Key Benefits	Limitations	Representative Examples
Probiotics	Live beneficial microbes	Competitive exclusion, antimicrobial production, immune modulation	Gut + Water	Improved immunity, pathogen suppression	Risk of HGT, stability issues	<i>Bacillus subtilis</i> , <i>Lactobacillus rhamnosus</i>
Paraprobiotics	Inactivated microbial cells	Immunogenic stimulation without colonization	Gut	Safer alternative, no gene transfer risk	Reduced persistence	Heat-killed <i>Lactobacillus plantarum</i>

Strategy Type	Key Components	Mechanism of Action	Target Domain	Key Benefits	Limitations	Representative Examples
Postbiotics	Microbial metabolites (SCFAs, bacteriocins)	Barrier enhancement, metabolic modulation	Gut	High safety, stable formulations	Limited multifunctionality	Butyrate, bacteriocins
Synbiotics	Probiotic + prebiotic	Selective microbial enrichment	Gut	Enhanced microbiome stability	Requires precise formulation	<i>Bacillus</i> + MOS
SynComs	Engineered microbial consortia	Functional complementarity (nutrient removal + pathogen suppression)	Gut + Environment	Dual-functionality, system-level impact	Regulatory and ecological concerns	Multi-strain consortia

5.6 Novel bacterial consortium development for controlling harmful algal bloom

Based on this extensive review, five key algicidal bacteria were chosen as bacterium consortium based on their mode of action, broad spectrum activity and ecological compatibility and safety assessments. This consortium integrates *Bacillus subtilis*, *Pseudomonas fluorescens*, *Hahella chejuensis*, *Phaeobacter inhibens*, and *Pseudoalteromonas spp*, each selected for its demonstrated algicidal efficacy against major bloom forming species.

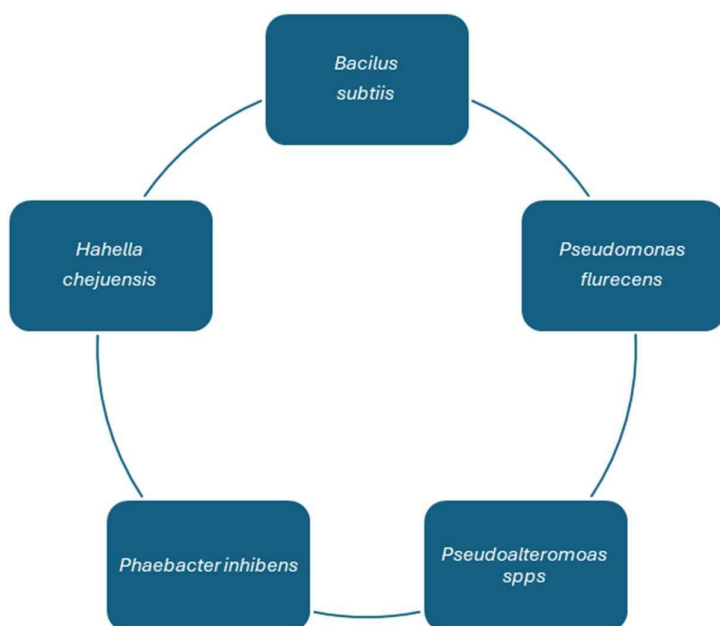


Fig. 11 - Proposed bacterial consortium for controlling harmful algal blooms (HABs)

They have diverse and complementary strategy or mechanistic pathway by which they target the HABs such as extracellular lytic enzymes, production of secondary metabolites, targeted oxidative stress and QS regulation.

This proposed consortium needs to be first tested under controlled laboratory test to confirm the efficacy and safety assessment and their impact on ecological system, so that they can be field-ready and can be used for real-time HAB mitigation.

5.7 Smart water-quality monitoring system

The proposed smart water-quality monitoring and analytics platform is provide continuous, high-resolution environmental surveillance across diverse freshwater ecosystems for the purpose of preventing algal bloom before they start. The device integrates hydrodynamic stability, multi-parameter sensing, intelligent data processing, and autonomous navigation into a single, compact platform capable of long-duration deployment with minimal human intervention. Its design philosophy emphasizes robustness, reliability, and scientific accuracy, aligning with the operational requirements of environmental research institutes, municipal water authorities, aquaculture managers, and ecological risk-assessment programs

5.7.1 Structural Architecture and Buoyancy Design

The primary structural assembly has been engineered to ensure stable floatation while maintaining optimal sensor immersion. Central to this architecture is a sealed flotation tube, internally filled with air at a controlled pressure. This tube provides static and dynamic buoyancy, enabling the device to withstand fluctuations in water level, moderate wave action, and prolonged exposure to environmental stressors. The buoyant module has been evaluated for long-term material fatigue, UV degradation, and corrosion resistance, ensuring durability in real-world deployment scenarios.

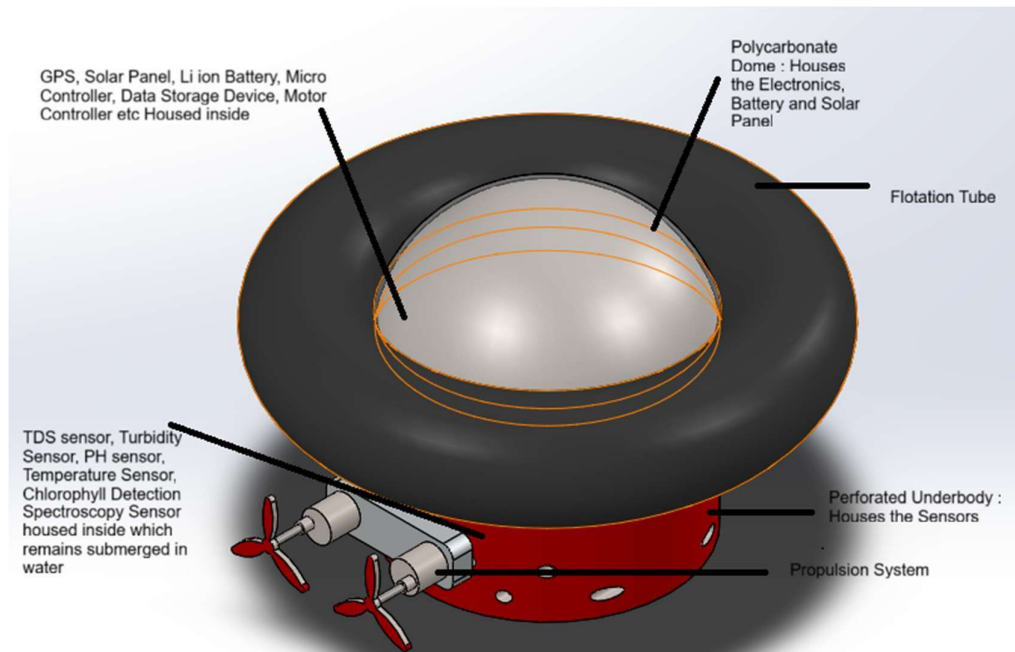


Fig. 12 – Smart water monitoring system for early detection of algal blooms (HABs)

5.7.2 Protective Electronics Housing and Power Subsystem

Above the water level, the device incorporates a transparent, impact-resistant polycarbonate dome, designed to shield the electronic subsystems while enabling uninterrupted solar irradiation. This dome is fabricated from UV-stabilized polycarbonate, a material chosen for its high optical clarity, structural resilience, and resistance to thermal deformation. The enclosure houses the complete electronics stack, including:

- a central microcontroller-based processing unit,
- an integrated solar panel,
- a battery management system (BMS) for regulated energy storage, sensor interface electronics with noise-minimizing circuitry,
- SD-card module for local data logging,
- GPS receiver for geospatial referencing and navigation, and
- motor-driver assembly for propulsion and steering control

The transparent cover additionally ensures efficient thermal dissipation and prevents moisture ingress, thereby protecting sensitive circuitry from condensation and particulate contamination. This integrated power-electronics configuration enables the

device to operate autonomously for extended periods, powered exclusively by solar energy, thus eliminating the need for frequent manual intervention.

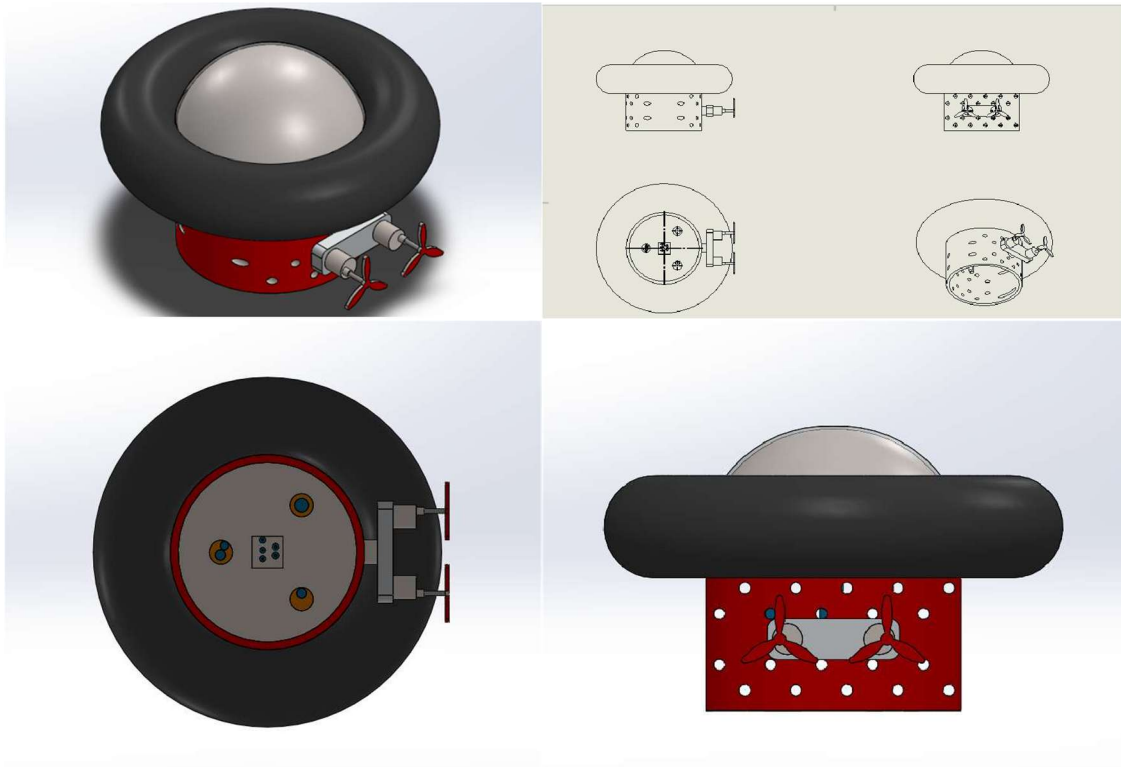


Fig. 13. Profile views of Smart water monitoring system

5.7.3 Autonomous Navigation and Field Coverage Strategy

To achieve comprehensive spatial sampling, the system is equipped with an onboard guidance and propulsion mechanism operating under real-time GPS-assisted navigation. Upon deployment in a lake, pond, reservoir, or canal, the device dynamically references a user-defined geo-fenced boundary stored within its navigation module. Using this geospatial dataset, it performs systematic patrolling of the designated area at a controlled, pre-configured velocity.

5.7.4 Multi-Parameter Water-Quality Sensing Suite

At the heart of the system lies a comprehensive suite of aquatic sensors designed to capture critical physicochemical indicators of water health. The sensing module includes instruments for real-time measurement of:

- pH, indicating acidity or alkalinity,

- Temperature, affecting solubility, biological activity, and ecosystem metabolism,
- Turbidity, quantifying particulate matter and suspended solids,
- Total Dissolved Solids (TDS), assessing dissolved ionic concentration, and
- Chlorophyll-a concentration, estimated using a spectroscopy-based optical sensor. The inclusion of a spectroscopy-driven chlorophyll sensing unit represents a significant advancement over conventional fluorescence-based techniques. This sensor captures spectral signatures associated with algal pigments, thereby enabling early detection of harmful algal bloom (HAB) precursors, even at sub-visual concentrations. Such early-stage detection is essential for preventive management in water-treatment facilities, aquaculture operations, and ecological monitoring programs.

5.7.5 Embedded Data Processing and Machine Learning Analytics

All sensor outputs are continuously acquired and processed by the onboard microcontroller, which performs signal conditioning, noise filtering, and parameter calibration. The processed data is then input to an embedded machine learning (ML) engine, implemented using the K-Nearest Neighbour (KNN) classification algorithm. This ML model will be trained on an extensive dataset comprising historical water-quality records, expert-labeled algal bloom events, and synthetic field scenarios.

5.7.6 Dual-Mode Data Storage and Remote Connectivity

To enhance data reliability and ensure redundancy, the device employs a dual-mode data management framework to provide better analysis.

Cloud Transmission:

All processed sensor readings, geolocation data, and ML-derived diagnostic outputs are transmitted in real time to a cloud-based server. This enables remote monitoring through dashboards, mobile apps, or third-party environmental information systems, ensuring accessibility for researchers and decision-makers regardless of location.

Local SD-Card Logging:

A complete, timestamped record of all measurements is simultaneously stored on a protected local SD card. This helps in make a offline repository for future works.

5.7.8 Environmental Impact

Algicidal bacteria are considered as a nature-based low-chemical alternative which can control Harmful Algal blooms, but it is also important that their impact on environment must be thorough evaluated to ensure they protect the ecological sustainability. There are various positive benefits that helps the environment such as reduced chemical pollution. Algicidal metabolites produced by this bacterium such as TDA, proteases have the ability to biodegrade rapidly, exhibit lower chronic toxicity and act against selective harmful phytoplankton. This helps in reducing environmental load and avoids long-term accumulation of toxic compounds. Some algicidal bacteria are selective, which supresses only HAB species, not harming another algae species. This helps in maintaining ecosystem and effective mitigations reduces toxin release from HABs such as microcystins, domoic acid etc. But there are some other aspects that should also be taken in considerations such as metabolite like prodigiosin can be cytotoxic at high concentrations and some metabolites can influence microbial community structure. The overall environmental impact of algicidal bacteria is more ecologically aligned and can be properly executed with proper controls, monitoring and strategies to restore aquatic ecosystem health.

CHAPTER 5

CONCLUSION

Harmful algal blooms (HABs) have evolved globally over the past few decades, driven by nutrient enrichment, climate warming, altered hydrology, and man-made disturbances. Across countries, aquatic systems have various bloom events caused by cyanobacteria, dinoflagellates, diatoms, raphidophytes, chrysophytes, and haptophytes, producing toxins that compromise fisheries, aquaculture production, drinking water, and animal harm. Constant blooms cause ecological and economic problems scaling from hypoxia and fisheries collapse to toxin bioaccumulation and drinking water issues for human and animals. As the environmental drivers behind HAB intensification continue to strengthen, this highlights the need for sustainable mitigation strategies that go beyond traditional methods.

This study focuses on the mechanistic modes of algicidal bacteria, which involves both direct and indirect pathways such as reactive oxygen species, photosystem II inhibition, enzymatic degradation of extracellular polymeric substances, nutrient competition, membrane disruption, colony matrix dissolution, programmed cell death, and quorum/chemical-cue-triggered activation of algicidal gene clusters. These processes act on vulnerable algal structures like thylakoid membranes, PSII complexes, and extracellular mucilage, leading to apoptosis or metabolic failure.

Given the high correlation of species and strain-specificity in algal susceptibility and the capacity of some algae to activate counter-defensive metabolites, it is sure that no single bacterium provides universal control across the full spectrum of algal blooms. Instead, the most resilient and promising mitigation strategy lies in creating a strong and reliable **bacterial consortia**. Among many species, *Pseudoalteromonas*, *Pseudomonas fluorescens*, *Hahella chejuensis*, *Bacillus subtilis*, and *Phaeobacter inhibens* have as validated algicidal genera, as they exhibit broad-spectrum efficacy against cyanobacteria, dinoflagellates, diatoms, and raphidophytes which make them the perfect candidate for bioremediation.

Quantitative evidence demonstrates extremely rapid algal mortality under laboratory and mesocosm conditions. *Pseudoalteromonas* strains often achieve 90–100% lysis within 24–48 hours; *Pseudomonas fluorescens* suppresses freshwater diatom blooms by >90% in situ; *Hahella* produces prodigiosin and related pigments with potent dose-dependent algicidal activity; and *Shewanella* strains exhibit species-selective killing of dinoflagellates and cyanobacteria. Meanwhile, *Phaeobacter inhibens* illustrates a uniquely sophisticated and context-dependent chemical ecology, producing roseobacticides in response to algal degradation cues and triggering programmed-cell-death-like responses in sensitive microalgal strains. Algal susceptibility varies widely between species, strains, and life-cycle stages, and many HAB taxa possess biochemical defenses which include mucilage formation, antioxidant systems, and oxylipin-mediated chemical deterrence that can hinder the efficacy of algicidal bacteria. Therefore, future HAB management strategies will benefit from mechanistically complementary consortia of algicidal bacteria that collectively target multiple cellular processes such as photosynthesis, membrane integrity, extracellular matrices, ROS balance, and genetic regulation, thereby providing a more resilient and broad-spectrum biocontrol effect.

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LETTER OF ACCEPTANCE

Date: 09-05-2026

Dear Author's,
1MS. AISHWARYA DWIVEDI, *2DR. JAI GOPAL SHARMA

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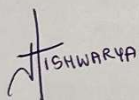
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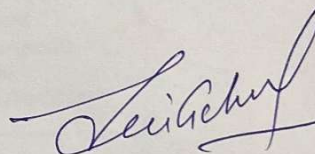
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EDUCATION

2024 - 2026: Masters of technology (2 year program), M.Tech
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1. Result awaited for 1st sem

2020- 2024: Bachelors of Technology (4 years program), B.Tech
(Biotechnology), Amity University, Uttar Pradesh, Lucknow Campus,
India

- 1. Final CGPA: 9.67
- 2. Key focus in laboratory work
- 3. Involved in research and review paper writing

2009-2019: 12th standard and 10th standard
Loreto Convent Intermediate College (IBVM - Institute of blessed
virgin Mary), Lucknow, India

- Major in Biology, Chemistry and Physics
- Also studied Basics of Psychology

OTHER KNOWLEDGE

- Animal biotechnology
- Microbiology
- Database Management System
- Bioinformatics
- Immunology
- Basics of cancer
- Molecular biology
- Genetics

LANGUAGES

- 1. English
- 2. Hindi
- 3. German (Beginner)

TECHNICAL SKILLS AND EXPERIENCE:

- 1. Light microscopy
- 2. Biochemical characterization of cells
- 3. DNA and RNA extraction
- 4. ELISA and Sandwich ELISA
- 5. Blood DLC and TLC
- 6. Spectroscopy
- 7. Polymerase Chain reaction
- 8. Cloning
- 9. Localization studies of protein in cell
- 10. SDS PAGE
- 11. Differential Gene Analysis (Computational Biology)
- 12. Protein Purification
- 13. Affinity Chromatography
- 14. Discovery studio (for computational biology)
- 15. Proficiency in MS Word, MS Excel, MS PowerPoint

Aishwarya Dwivedi

I have cultivated a deep fascination for the living world and a commitment to scientific inquiry. My coursework has provided me with a solid understanding of fundamental biological concepts, including genetics, immunology, physiology, and molecular biology. I have actively engaged in laboratory work, field research, and collaborative projects, honing my analytical, problem-solving, and teamwork skills.

Seeking job/research opportunity in field of biotechnology to apply academic knowledge, gain practical experience, and contribute to groundbreaking research.

WORK EXPERIENCE

1. Research Analyst

eGenome.ai Fundamental Research Private Limited, Gurgaon
Current position

- Primary research to support product innovation, exploring unique ingredient combinations and their mechanisms of action for science-backed formulations. Contribution in Development of AI tools in health-tech and diagnostics as well as creation of SEO optimized content.

2. Intern

Indian Institute of Technology ,Delhi

18th Dec,2023 - 20th July,2024

- Intern Researching on topic: Cloning and characterization of Par B protein in *Rhodospirillum rubrum* PR4

3. Summer Research Fellow

Indian Institute of Technology ,Delhi

29th May - 17th July,2023

- Intern Researching on topic: Theoretical understanding of Bacterial growth.

4. Research Fellow

Krishika, sacred River Agri Technology Pvt. Ltd. (Indian agricultural start-up company), Lucknow, UP - 7th November, 2022 till 7th January, 2023.

- Research Fellow: Analysis of microorganism present in soil and their effect on food crops and finding possible sustainable solutions for Indian farmers.

NOTABLE ACHIEVEMENT:

- 1. Gold Medalist in B.Tech Biotechnology
- 2. Selected as Summer Undergraduate Fellow at IIT Delhi and IIT Hyderabad
- 3. Written book chapter in TINT: Unlock vibgyor (2022/KDP Publisher, 978-93-5619-905-7)
- 4. Won best poster award in National Symposium TBS2023 in undergraduate category (Title of poster - Potential role of Flavonoids and isoflavonoids from *Urtica picta* against *Mycobacterium tuberculosis*)

CONFERENCES ATTENDED:

- 1. National Symposium - TBS2023 on "Emerging techniques for the characterization and therapeutic evaluation of traditional ayurvedic / herbal medicines" Lucknow, India.
- 2. International congress on contemporary scientific research ISPEC, Adana, Turkey. (Online)
- 3. National conference on medicinal plants, natural products and Indian system of medicine, Jhansi, India

OTHER SKILLS:

- 1. Creative problem solving
- 2. Data entry
- 3. Strong written and verbal communication skills
- 4. Detail-oriented with excellent problem-solving abilities
- 5. Ability to work effectively in a team and independently

EXTRA CURRICULAR

- 1. Vice president of AMIBEATS: Cultural club of Amity University Lucknow campus.
- 2. Yoga enthusiast and Active volunteer for animal care and help