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Algal Biodiversity as a Sentinel of Freshwater Ecosystem Health

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Abstract

Freshwater ecosystems are among the most biologically productive yet ecologically vulnerable habitats on Earth, facing escalating pressures from nutrient enrichment, climate change, industrial pollution, and expanding urbanization. Algae encompassing a phylogenetically diverse assemblage ranging from unicellular phytoplankton and benthic diatoms to filamentous green algae and colonial cyanobacteria serve simultaneously as foundational primary producers and sensitive environmental recorders. Their rapid, measurable responses to physicochemical perturbations make them unrivalled bioindicators for the integrated assessment of aquatic ecosystem integrity. This review synthesizes current knowledge on the taxonomy, structural diversity, ecological functions, and environmental sensitivity of freshwater algae, contextualized within a comprehensive framework for water quality monitoring. The principal drivers of algal community change including eutrophication, climate-induced thermal stratification, organic and metal pollution, and hydromorphological modifications was examined and discusses how shifts in assemblage composition, diversity indices, and functional traits reflect these stressors. A systematic evaluation of assessment methodologies is presented, and transformative emerging approaches including environmental DNA (eDNA) metabarcoding, satellite and drone-based remote sensing, and machine-learning-assisted predictive modeling are highlighted for their capacity to overcome the taxonomic, spatial, and temporal limitations of conventional morphology-based assessment. Special focus is directed to harmful algal blooms (HABs), particularly cyanobacterial blooms, and their compounding role as co-stressors alongside climate warming. The review concludes by identifying critical research gaps and advocating for the integration of molecular tools, standardized protocols, expanded genomic reference databases, and artificial intelligence into global algal biomonitoring frameworks.

Introduction

Freshwater ecosystems sustain a disproportionate fraction of global biodiversity relative to their geographic extent, providing irreplaceable services including potable water supply, fisheries productivity, flood regulation, nutrient cycling, and cultural value (Wetzel, 2001; Reid et al., 2019). Yet these systems are under unprecedented anthropogenic stress. Globally, freshwater

biodiversity has declined by an estimated 84% since 1970, a rate of loss that markedly exceeds those observed in terrestrial and marine environments, driven by eutrophication, pollution, hydrological modification, invasive species, and accelerating climate change (Reid et al., 2019; Díaz et al., 2019). Among the biological communities inhabiting these systems, algae occupy a uniquely central position: they are the primary architects of aquatic food webs, contributors to atmospheric oxygen balance, and of particular relevance to this review highly responsive sentinels of environmental change.

Algae constitute an extraordinarily diverse polyphyletic assemblage of photosynthetic organisms, estimated to comprise between 200,000 and 800,000 species globally, of which only approximately 35,000 have been formally described (Dash et al., 2021). Their ecological radiation spans virtually every aquatic and semi-terrestrial habitat from oligotrophic mountain streams and deep lacustrine environments to urban wastewater ponds and hypersaline estuaries and encompasses prokaryotic cyanobacteria, eukaryotic microalgae, and macroscopic seaweeds. This ecological breadth, combined with short generation times, high physiological sensitivity, and well-characterized environmental preferences, positions algae as some of the most powerful and cost-effective biological indicators available to aquatic ecologists and environmental managers (Khalil et al., 2021; Nayak et al., 2024). Biological monitoring using algae has a history spanning over a century, traceable to the foundational saprobic classification system of Kolkwitz and Marsson (1908), subsequently refined into quantitative indices by Zelinka and Marvan (1961). Contemporary algal bioassessment has evolved dramatically, progressing from purely morphology-based community descriptions towards integrative frameworks that combine functional trait analysis, molecular identification, geospatial mapping, and artificial intelligence-driven predictive modeling (Liu et al., 2023; Kim et al., 2026). This transformation reflects both the increasing sophistication of ecological science and the urgent practical need for scalable, high-resolution monitoring tools capable of detecting and predicting water quality degradation across regional and global scales.

The present review integrates to provide a comprehensive, up-to-date synthesis of algal biodiversity as a bioindicator of freshwater ecosystem health. It systematically addresses: the taxonomy and structural diversity of freshwater algae; their ecological roles and the environmental factors governing their distribution; the principal stressors driving algal community change; established and emerging assessment methodologies; representative case studies across diverse geographic and ecological contexts; and research gaps and future directions. By consolidating these themes, this review aims to support researchers, water quality managers, and policymakers in leveraging algal biodiversity as a scientifically robust and practically deployable tool for freshwater monitoring and conservation.

Taxonomy and Structural Diversity of Freshwater Algae

Algae represent a fundamentally polyphyletic assemblage, meaning they do not share a single common ancestor but instead arose through convergent evolution and multiple endosymbiotic events across at least five independent eukaryotic lineages (Hoek et al., 1995; Reynolds, 2006). This evolutionary complexity is reflected in an extraordinary breadth of morphological, biochemical, and ecological diversity, spanning prokaryotic cyanobacteria to advanced eukaryotic macroalgae. Their shared attribute oxygenic photosynthesis is the primary basis for their traditional grouping, although molecular phylogenetics has substantially reorganized their classification in recent decades (Graham et al., 2009). The principal freshwater algal divisions recognized in contemporary phycology are summarized in Table 1, along with their diagnostic pigments, storage products, and cell wall chemistry. Each division exhibits unique functional and ecological characteristics that influence its distribution, environmental responses, and value as a bioindicator.

Diatoms (Bacillariophyta) occupy a position of particular importance in freshwater biomonitoring because of their species-specific responses to nutrient concentrations, pH, conductivity, and organic enrichment. Their silicified cell walls (frustules) are preserved in lake sediments over geological timescales, enabling paleolimnological reconstruction of past environmental conditions (Bellinger & Sigee, 2015; Wu et al., 2025). Cyanobacteria, though prokaryotic, are ecologically dominant in nutrient-enriched systems and are capable of nitrogen fixation, buoyancy regulation, and toxin production traits that render them central to harmful algal bloom (HAB) dynamics (Paerl et al., 2023). Green algae (Chlorophyta) dominate oligotrophic to mesotrophic systems and are sensitive to anthropogenic disturbance, making them valuable indicators of relatively pristine conditions (Roy et al., 2016). Euglenoids (Euglenophyta) thrive in organically enriched waters and are therefore preferentially associated with polluted sites, contributing to Palmer's Pollution Index calculations (Khalil et al., 2021). Figure 1 below showed the major taxonomic divisions of freshwater algae and their principal ecological/functional groupings

Table 1: Major algal divisions, their biochemical characteristics, and primary habitats

Division	Common Name	Key Pigments	Storage Product	Cell Wall	Habitat
Chlorophyta	Green Algae	*Chlorophyll a, b*	Starch	Cellulose	Freshwater, terrestrial
Rhodophyta	Red Algae	Chl. a, phycobilins	Floridean starch	Cellulose, agar	*Mostly* marine
Phaeophyta	Brown Algae	Chl. a, c, fucoxanthin	Laminarin	Alginates	*Cold* marine
Bacillariophyta	Diatoms	Chl. a, c, fucoxanthin	Chrysolaminarin	*Silica frustules*	Freshwater and marine
Cyanophyta	Blue-Green Algae	Chl. a, phycocyanin	Cyanophycin	Peptidoglycan	Freshwater, terrestrial
Dinophyta	Dinoflagellates	Chl. a, c, peridinin	Starch	*Cellulose plates*	Marine & Freshwater
Euglenophyta	Euglenoids	Chl. a, b	Paramylon	No rigid wall	Freshwater

Sources: Hoek et al. (1995); Graham et al. (2009); Bellinger & Sigee (2015); Rosaldo-Benítez et al. (2024).

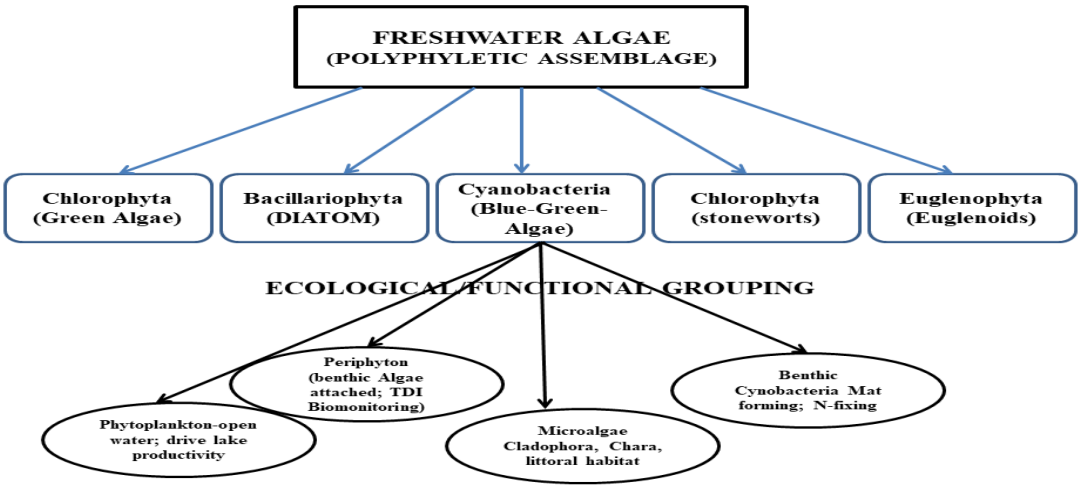

Figure 1: Major taxonomic divisions of freshwater algae and their principal ecological/functional groupings.

Beyond taxonomic classification, freshwater algae are functionally organized into ecological groups based on their habitat and trophic position: Phytoplankton**:** Planktonic microalgae suspended in the water column, dominated by diatoms, cyanobacteria, green algae, and cryptophytes. They are the primary drivers of open-water productivity and are the most widely used group in lake bioassessment (Reynolds, 2006; Amorim & Moura, 2020); Periphyton (benthic algae): Algae attached to submerged substrates rocks (epilithic), sediments (epipsammic), or macrophytes (epiphytic). Diatom-dominated periphytic assemblages are the cornerstone of river and stream biomonitoring using the Trophic Diatom Index (Kulaš et al., 2022; Kim et al., 2026); Macroalgae: Larger, structurally differentiated algae such as Cladophora and Chara that colonize littoral zones, providing habitat structure and influencing nutrient dynamics (Wetzel, 2001); and Benthic cyanobacteria: Mat-forming species on sediment surfaces, contributing to nitrogen fixation and potentially releasing toxins upon senescence (Paerl et al., 2023; Bižić et al., 2020).

Ecological Roles and Importance of Freshwater Algae

Primary Production and Oxygen Generation

Algae particularly phytoplankton are the dominant primary producers in most freshwater ecosystems, converting solar energy into organic biomass through photosynthesis and generating the oxygen that sustains aerobic life in aquatic habitats as showed in Figure 2 below. Phytoplankton are estimated to contribute approximately 50% of global net primary production, underpinning food web energy flows from zooplankton to fish and higher trophic levels (Falkowski et al., 2008). Disruption of algal productivity whether through harmful bloom formation, light limitation due to turbidity, or toxic pollution therefore cascades through entire food webs with far-reaching ecological consequences (Amorim & Moura, 2020; Moustaka-Gouni & Sommer, 2020).

Nutrient Cycling and Biogeochemical Functions

Algae play indispensable roles in freshwater biogeochemical cycles. In the carbon cycle, algal photosynthesis fixes dissolved inorganic carbon into organic matter, while algal respiration and decomposition release it back as CO_2 or export it to sediments as organic carbon. Bižić et al. (2020) demonstrated that both aquatic and terrestrial cyanobacteria produce biogenic methane, a finding with significant implications for understanding greenhouse gas budgets in freshwater systems. In the nitrogen cycle, nitrogen-fixing cyanobacteria (e.g., Anabaena, Nodularia) convert atmospheric N_2 into bioavailable ammonia, enriching nutrient-poor waters and potentially exacerbating eutrophication when nitrogen is limiting (Paerl et al., 2011; Reynolds, 2006). Algal uptake and assimilation of phosphorus further regulate its availability for competing microbial and plant communities (Wetzel, 2001).

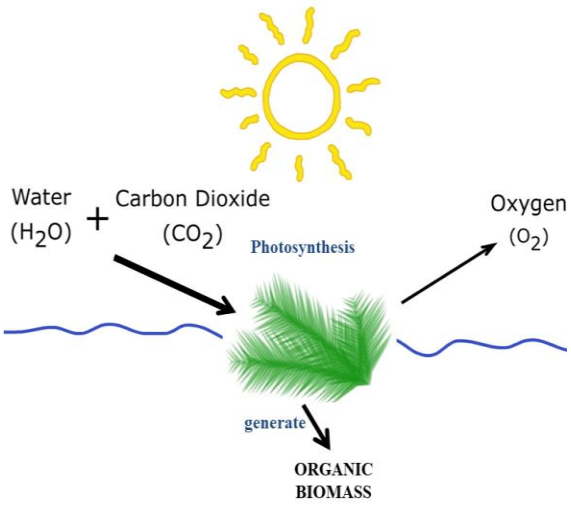

Figure 2: Algae as primary producers in freshwater ecosystems, converting solar energy into organic biomass

Habitat Formation and Support for Biodiversity

Macroalgae and dense periphyton mats provide structural complexity in freshwater habitats, forming microhabitats for invertebrates, fish larvae, and epiphytic organisms. Benthic diatom biofilms stabilize sediment surfaces and influence the microbial ecology of riverbeds. Algae also participate in symbiotic associations for example, *zoochlorellae* in protists and sponges, and cyanobacteria in lichens and cycad root nodules extending their ecological influence beyond purely aquatic realms (Graham et al., 2009). Importantly,

algal primary production supports the base of the trophic pyramid, and changes in algal community composition propagate upward through food webs, affecting zooplankton, macroinvertebrates, and fish populations (Filstrup et al., 2014; Moustaka-Gouni & Sommer, 2020).

Environmental Drivers of Algal Biodiversity

Algal community structure is shaped by an intricate interplay of natural physicochemical factors and accelerating anthropogenic pressures. Understanding these drivers is fundamental to interpreting algal bioindicator signals and predicting ecosystem trajectories under global change scenarios (Khalil et al., 2021; Wu et al., 2025).

Natural Environmental Factors

Light availability governs photosynthetic rate and the vertical stratification of phytoplankton in water bodies. Incident light is attenuated by water depth, dissolved organic matter (brownification), and turbidity from suspended sediments or algal biomass itself. Different algal groups possess distinct pigment compositions optimized for specific light qualities and intensities for example, phycoerythrin-containing cryptophytes and red algae exploit green and yellow wavelengths in deeper or more turbid waters (Graham et al., 2009). Recent experimental work confirms that nutrient availability and light colour interact non-additively in structuring algal communities, with brownification disproportionately favoring cyanobacteria by filtering blue light spectra (Swanson et al., 2025). Water temperature is a primary determinant of metabolic rates, physiological optima, and competitive outcomes among algal taxa. Cyanobacteria generally outcompete diatoms and green algae at temperatures above 25°C, a trait that has profound implications in the context of climate warming (Paerl & Paul, 2012; Paerl et al., 2023). Hydrological factors including water residence time, thermal stratification depth, and flow velocity further modulate nutrient transport, light climate, and the physical mixing that determines whether buoyant cyanobacteria can accumulate at the surface (Reynolds, 2006). Grazing pressure from zooplankton (particularly cladocerans such as Daphnia) selectively removes smaller phytoplankton cells and can suppress bloom development under certain conditions, though cyanotoxins and large filamentous morphologies often render cyanobacteria grazing-resistant (Filstrup et al., 2014).

Anthropogenic Stressors

Eutrophication, the enrichment of water bodies with nitrogen and phosphorus from agricultural runoff, urban wastewater, and atmospheric deposition is the most pervasive anthropogenic driver of algal community change in freshwater systems globally. Nutrient enrichment typically shifts phytoplankton assemblages from diverse, diatom-rich communities towards cyanobacteria-dominated systems with reduced species richness and diversity index values (Wu et al., 2025; Paerl et al., 2023). The interaction of eutrophication with climate warming is particularly alarming: rising temperatures and extended stratification seasons amplify bloom duration and intensity, creating a positive feedback loop between nutrient loading and climate effects (Feng et al., 2024). Organic pollution from domestic wastewater, food processing effluents, and livestock operations introduces biochemical oxygen demand (BOD) that depletes dissolved oxygen and selectively favours pollution-tolerant algal genera such as *Oscillatoria, Euglena*, and *Nitzschia* the basis of Palmer's Pollution Index (Khalil et al., 2021; Makwana, 2022).

Heavy metal contamination from mining, industrial discharges, and urban runoff inhibits algal photosynthesis, disrupts enzymatic function, and selectively eliminates sensitive taxa. Rosaldo-Benítez et al. (2024) demonstrated that elevated lead concentrations in Mexican karstic lagoons were specifically correlated with the absence of Nannochloropsis and Thraustotheca, underscoring the potential of specific genera as heavy metal bioindicators. Table 2 summarizes the principal environmental stressors affecting algal communities and their bioindicator responses.

Algae as Bioindicators: Principles, Properties, and Index Systems

Theoretical Basis for Bioindicator Use

A bioindicator is an organism or community whose presence, abundance, condition, or compositional attributes provide quantifiable information about the biological and ecological integrity of the environment it inhabits (Bellinger & Sigee, 2015). For a taxon or community to qualify as a robust bioindicator, it must demonstrate: measurable and predictable responses to target stressors; ecological ubiquity sufficient to allow cross-site comparisons; tractability for standardized sampling and identification; and well-characterized ecological preferences (autecology) that enable interpretation of community-level signals (Khalil et al., 2021; Reid et al., 2019). Freshwater algae satisfy all these criteria more comprehensively than most other biological indicators. Their short generation times (hours to days) enable rapid organismal-level responses to acute perturbations, while the persistence of multi-species assemblages over seasons provides an integrated biological record of chronic environmental change a temporal integration that point-in-time chemical measurements cannot achieve (Khalil et al., 2021; Makwana, 2022). Furthermore, algal communities integrate the cumulative effects of multiple co-occurring stressors, whereas chemical parameters measure only individual substances at single time points (Bellinger & Sigee, 2015).

Principal Algal Bioindicator Groups

Diatoms constitute the single most widely utilized algal group in biomonitoring worldwide, underpinning national and European Union Water Framework Directive (WFD) assessment systems across dozens of countries (Kulaš et al., 2022; Kim et al., 2026). Their advantages include: extraordinary species diversity (estimated >100,000 species); highly species-specific responses to pH, conductivity, nutrients, and saprobic conditions; preservation of siliceous frustules in sediments enabling paleolimnological reconstructions; and a continuously growing global reference database of ecological optima and tolerances (Bellinger & Sigee, 2015; Kelly, 1998). Phytoplankton assemblages in lakes and reservoirs are extensively used for trophic state classification, eutrophication assessment, and HAB early warning. Shifts in the ratio of cyanobacteria to total chlorophyll, changes in chlorophyll-a concentration, and the proliferation of bloom-forming species (Microcystis, Cylindrospermopsis) are established indicators of advancing eutrophication and deteriorating water quality (Amorim & Moura, 2020; Paerl et al., 2023). Benthic green algae and filamentous forms are indicators of intermediate disturbance and moderate nutrient conditions, while pollution-tolerant genera (Oscillatoria, Euglena) are reliably associated with organic enrichment across diverse geographic settings (Makwana, 2022; Khalil et al., 2021).

Established Bioindicator Index Systems

A suite of standardized quantitative indices has been developed to translate algal community data into interpretable water quality assessments. Table 3 provides a comparative overview of the most widely applied systems.

Palmer's Algal Pollution Index, developed in 1969, remains in widespread use particularly in tropical and subtropical regions, including Africa and South Asia, because of its simplicity and reliance on genus-level identification. It assigns numerical scores to 20 pollution-tolerant algal genera and to 8 physicochemical parameters, generating a composite pollution index that is readily calculable from basic microscopic surveys (Khalil et al., 2021; Shubha & Sreeja, 2019). The Trophic Diatom Index (TDI), in contrast, exploits the nutrient sensitivity of diatom species through indicator values and sensitivity weightings calibrated from extensive river survey datasets (Kelly, 1998). Its translation into a molecular format (mTDI) using eDNA-based metabarcoding represents one of the most significant recent advances in diatom biomonitoring, enabling rapid, high-throughput assessment without the specialist taxonomic expertise traditionally required for microscopic diatom identification (Kim et al., 2026; Kulaš et al., 2022).

Table 2: Key environmental stressors, their effects on freshwater algal communities, and bioindicator responses

Stressor	Effect on Algal Community	Indicator Response	Reference
Nutrient enrichment (N, P)	Cyanobacteria blooms; species richness decline; diversity loss	TDI increase; Shannon H' decline	Paerl & Paul (2012); Wu et al. (2025)
Climate warming	Extended bloom seasons; shift to cyanobacteria dominance; deepened stratification	Phytoplankton biomass increase	Griffith & Gobler (2020); Earth Interactions (2023)
Organic pollution	Proliferation of tolerant genera (*Oscillatori*a, Euglena)	Palmer's Index elevated	Khalil et al. (2021); Makwana (2022)
Acidification	Diatom community shifts; dissolution of silica frustules	TDI and diatom density change	Passy (2008); Griffith & Gobler (2020)
Heavy metals (Pb, Cd, Hg)	Inhibition of photosynthesis; bioaccumulation	Sensitive taxa disappear	Rosaldo-Benítez et al. (2024)
Hydromorphological alteration	Periphyton community disruption; flow-sensitive taxa loss	Periphytic diatom decline	Reid et al. (2019); Wu et al. (2012)
Land-use change / urbanisation	Reduced alpha diversity; pollution-tolerant taxon proliferation	Diversity index decline	Paul & Meyer (2001); Reid et al. (2019)

Table 3: Principal algal bioindicator indices and assessment tools used in freshwater water quality monitoring

Index / Tool	Description	Algal Group	Reference
Palmer's Algal Pollution Index	Genus-based scoring system detecting organic pollution via tolerant taxa	*Mixed algae*	Palmer (1969); Khalil et al. (2021)
Trophic Diatom Index (TDI)	Nutrient-sensitivity weighted index using diatom assemblages	Diatoms	Kelly (1998); Kulaš et al. (2022)
Shannon-Wiener Index (H')	Quantifies species richness and evenness in a community	All algae	Chon et al. (2013); Amorim & Moura (2020)
Algal Genus Pollution Index (AGPI)	Composite score from pollution-tolerant genus presence	Mixed algae	Shubha & Sreeja (2019); Makwana (2022)
Phytoplankton Index of Biotic Integrity (P-IBI)	Multimetric index integrating biomass, diversity, and functional traits	Phytoplankton	Wu et al. (2012); Nayak et al. (2024)
eDNA Metabarcoding Index (mTDI)	Molecular TDI derived from eDNA amplicon sequencing of planktonic communities	Diatoms	Kulaš et al. (2022); Kim et al. (2026)
Chlorophyll-a Concentration	Proxy for phytoplankton biomass and eutrophication state	Phytoplankton	Amorim & Moura (2020); Bellinger & Sigee (2015)

Table 4: Established and emerging methods for freshwater algal assessment and water quality monitoring

Method / Tool	Principle & Application	Advantages / Limitations	Reference
Light Microscopy	Morphological identification of algal taxa using keys	High accuracy; time-intensive; requires taxonomic expertise	Bellinger & Sigee (2015); Rosaldo-Benítez et al. (2024)
Scanning Electron Microscopy (SEM)	Ultrastructural imaging of diatom frustules for species-level ID	Excellent resolution; costly and destructive	Graham et al. (2009)
Chlorophyll-a Analysis	Spectrophotometric quantification of biomass	Simple, rapid proxy; non-specific to taxa	Amorim & Moura (2020); Bellinger & Sigee (2015)
DNA Barcoding / Metabarcoding	Next-generation sequencing of marker genes (18S, rbcL) for community profiling	High throughput; detects cryptic taxa; database gaps in freshwater species	Kulaš et al. (2022); Rosaldo-Benítez et al. (2024)
eDNA Sampling	Environmental DNA extraction from water for community assessment without collection	Non-invasive; integrative; sensitive to degradation	Kim et al. (2026); Kulaš et al. (2022)
Remote Sensing (Satellite)	Spectral detection of chlorophyll-a and phycocyanin from Sentinel-2/3, MODIS, Landsat	Large-scale, cost-effective; spatial resolution limits for small water bodies	Wang et al. (2023)
Machine Learning / AI	Predictive modelling of bloom occurrence and ecological status from multi-variable datasets	High predictive power; needs large training datasets	Liu et al. (2023); Kim et al. (2026)
Flow Cytometry	Automated high-throughput cell counting and pigment sorting	Rapid; expensive equipment	Nayak et al. (2024)

Assessment and Monitoring Methodologies

The methodological toolkit for algal-based water quality assessment has expanded dramatically over the past decade, driven by advances in molecular biology, satellite remote sensing, and computational data analysis. Table 4 presents a comparative evaluation of established and emerging methods.

Classical Methods: Microscopy and Physicochemical Parameters

Light microscopy combined with morphological identification using authoritative taxonomic keys remains the gold standard for diatom and periphyton community assessment in regulatory monitoring programmes (Bellinger & Sigee, 2015; Graham et al., 2009). Scanning Electron Microscopy (SEM) resolves fine ultrastructural features of diatom frustules required for definitive species-level identification, particularly within taxonomically complex genera such as Gomphonema and Nitzschia. Physicochemical parameters including pH, dissolved oxygen, conductivity, temperature, turbidity, and nutrient concentrations (total nitrogen, total phosphorus, nitrate, and orthophosphate) provide the environmental context required to interpret algal indicator signals. The relationship between chlorophyll-a concentration and phytoplankton biomass is non-linear but robust enough to provide a standardised proxy for eutrophication state, widely used in regulatory frameworks (Amorim &

Moura, 2020; Reynolds, 2006). Diversity indices derived from species lists and abundance data particularly the Shannon-Wiener Diversity Index (H'), Simpson's Dominance Index (D), and Pielou's Evenness Index (J') provide integrative metrics of community structure that respond sensitively to pollution gradients and habitat disturbance. Multivariate statistical analyses including Canonical Correspondence Analysis (CCA), Non-metric Multidimensional Scaling (NMDS), and Self-Organising Maps (SOM) are routinely applied to identify species-environment relationships and visualise pollution gradients across multi-site datasets (Chon et al., 2013; Rosaldo-Benítez et al., 2024).

Molecular Tools: DNA Barcoding and eDNA Metabarcoding

The molecular revolution in algal biomonitoring is well underway, with environmental DNA (eDNA) metabarcoding now established as a powerful complement and in many contexts a viable replacement for microscopic community assessment (Bush et al., 2017; Kulaš et al., 2022). eDNA metabarcoding involves the extraction of total DNA from a water or sediment sample, amplification of standardized marker genes (18S V4 for eukaryotic algae, rbcL for diatoms, 16S for cyanobacteria) using universal primers, high-throughput sequencing, and taxonomic assignment of amplicon sequence variants (ASVs) against reference databases (Kulaš et al., 2022; Zimmermann et al., 2015). Key advantages of this approach include the detection of rare, cryptic, and non-culturable taxa invisible to microscopy; the elimination of subjectivity in species identification; the capacity for high-throughput sample processing; and the simultaneous characterization of entire multi-trophic communities (Yang et al., 2023). Rosaldo-Benítez et al. (2024) exemplify these advantages, employing combined microscopy and shotgun metagenomics to reveal an average of 362 microalgal genera per lagoon in Mexican karstic systems, a richness that would be entirely inaccessible through morphological methods alone. Significant limitations remain, however: reference databases for freshwater algae are substantially incomplete compared to those for marine or terrestrial taxa; eDNA results can be confounded by differential DNA degradation rates among species; and sample collection, preservation, and processing require rigorous standardisation to ensure reproducibility (Rosaldo-Benítez et al., 2024; Bush et al., 2017). Recent advances in eRNA-based metabarcoding complement eDNA by targeting transcriptionally active cells, reducing the detection of signals from dead or degraded material (Bush et al., 2017).

Remote Sensing and Satellite-Based Monitoring

Optical remote sensing has emerged as an operationally powerful tool for monitoring algal blooms and phytoplankton dynamics at spatial and temporal scales impossible to achieve through ground-based sampling alone (Wang et al., 2023). Satellite sensors including Sentinel-2 MSI (10–60 m resolution, 5-day revisit), Sentinel-3 OLCI (300 m, daily), Landsat 8/9 OLI (30 m, 8-day), and MODIS (250–500 m, daily) are widely used to estimate chlorophyll-a and phycocyanin concentrations from spectral reflectance data, enabling near-real-time detection and mapping of cyanobacterial blooms across large water bodies (Lopez Barreto et al., 2024).

The integration of Unmanned Aerial Vehicles (UAVs) equipped with hyperspectral sensors has extended these capabilities to small-scale water bodies ponds, irrigation reservoirs, and urban lakes where the spatial resolution of orbital platforms is insufficient (Olivetti et al., 2023). The United States Environmental Protection Agency and the European Environment Agency both now incorporate satellite-derived HAB alerts into public health advisory systems, reflecting the operational maturity of this technology (Lopez Barreto et al., 2024). Machine-learning algorithms including random forests, support vector machines, and deep learning convolutional neural networks are increasingly applied to satellite imagery to improve bloom detection accuracy, discriminate between cyanobacteria species, and generate probabilistic bloom forecasts (Remote Sensing, 2024; Liu et al., 2023).

Machine Learning and Artificial Intelligence in Algal Biomonitoring

Machine learning (ML) approaches have rapidly penetrated algal biomonitoring as analytical tools capable of handling the high-dimensional, non-linear ecological datasets generated by molecular and remote sensing methods. Kim et al. (2026) applied ML algorithms to planktonic eDNA data to compute a molecular TDI (mTDI) and demonstrated its feasibility as a rapid regulatory assessment tool equivalent to microscopy-derived TDI values. Yang et al. (2023) used unsupervised ML to integrate multi-trophic eDNA data spanning algae, invertebrates, fish, and bacteria into a biological integrity index, demonstrating the potential of AI-assisted multi-taxon bioassessment. Liu et al. (2023) employed ensemble ML models to predict algal community structure from environmental variables, achieving high predictive accuracy for dominant taxa and functional groups across geographically diverse Lake Datasets. Key challenges for ML applications in algal ecology include the need for large, geographically balanced training datasets; the ecological interpretability of black-box models; and the management of class imbalance when rare taxa are present (Liu et al., 2023; Yang et al., 2023). Nevertheless, the trajectory of this field suggests that integrated AI frameworks combining eDNA community profiles, remote sensing data, physicochemical parameters, and meteorological inputs will constitute the next generation of operational algal water quality monitoring systems.

Harmful Algal Blooms: Mechanisms, Drivers, and Ecosystem Consequences

Nature and Causes of Harmful Algal Blooms

Harmful algal blooms (HABs) are episodes of anomalous algal proliferation typically exceeding thresholds of 10^6 cells per litre for cyanobacteria that generate ecologically, economically, or public-health-relevant impacts through toxin production, oxygen depletion, light attenuation, or physical fouling of water treatment infrastructure (Paerl et al., 2023; Griffith & Gobler, 2020). Cyanobacterial HABs (CyanoHABs) are the dominant concern in freshwater systems, with *Microcystis aeruginosa*, *Cylindrospermopsis raciborskii*, *Anabaena flos-aquae*, and *Planktothrix agardhii* among the most globally prevalent bloom-forming species. Their competitive success in eutrophic systems stems from multiple physiological advantages: gas vesicle-mediated buoyancy control enabling surface accumulation, nitrogen fixation capacity, tolerance of high temperatures and low light, and production of allelopathic and bioactive compounds that suppress competing taxa (Paerl et al., 2023).

Eutrophication and climate warming act synergistically to promote CyanoHAB proliferation. Nutrient loading particularly the co-enrichment with nitrogen and phosphorus fuels algal biomass accumulation, while rising water temperatures, extended stratification seasons, and intensified drought periods create thermal and hydrodynamic conditions that preferentially advantage buoyant cyanobacteria over sinking diatoms and green algae (Griffith & Gobler, 2020; Earth Interactions, 2023; Wu et al., 2025). Model projections consistently indicate that CyanoHAB concentrations are likely to increase in frequency, spatial extent, and duration across major temperate and tropical water bodies under climate change trajectories (Earth Interactions, 2023; Paerl et al., 2023).

Ecological and Toxicological Consequences

The ecological impacts of CyanoHABs cascade across the entire aquatic food web; Amorim and Moura (2020), in a study of ten tropical Brazilian reservoirs, documented that cyanobacteria-dominated blooms elevate pH, increase chlorophyll-a concentrations, intensify eutrophication, reduce water transparency, and markedly decrease zooplankton species richness and resource use efficiency. The suppression of zooplankton grazing mediated by cyanotoxin production, poor nutritional quality, and the formation of large indigestible filaments and colonies disrupts carbon transfer from primary producers to higher trophic levels, creating a community limited by food quality rather than quantity (Filstrup et al., 2014; Moustaka-Gouni & Sommer, 2020). Bloom senescence exacerbates

these effects: microbial decomposition of algal biomass consumes dissolved oxygen, generating hypoxic and anoxic conditions that can trigger mass fish mortality and release additional nutrients from sediments in a positive feedback loop (Bižić et al., 2020; Rabalais et al., 2010; Yan et al., 2017). HABs also function as co-stressors alongside other climate change-driven perturbations. Griffith and Gobler (2020) reviewed the interactive effects of HABs with ocean and freshwater warming, acidification, and hypoxia, demonstrating that these stressors often produce synergistic rather than additive impacts on aquatic biota. The toxicological risks to drinking water consumers, livestock, and recreational users from microcystin, cylindrospermopsin, anatoxin, and saxitoxin four major classes of cyanotoxins represent a critical public health concern driving the prioritisation of HAB monitoring in water management frameworks globally (Paerl et al., 2023; Griffith & Gobler, 2020).

Beyond cyanobacteria, the invasive freshwater dinoflagellate Ceratium spp. has emerged as a secondary bloom-forming concern in reservoirs and lakes across temperate regions, generating taste and odour compounds, causing oxygen depletion after bloom collapse, and reducing water treatment efficiency. The species-specific nature of these HAB impacts underscores the importance of taxonomic resolution rather than generic 'total algal biomass' measurements in biomonitoring programmes (Amorim & Moura, 2020). Figure 3 below highlight the Ecological and Toxicological Consequences of CyanoHABs cascade across the entire aquatic food web.

Regional Case Studies: Algal Biodiversity and Water Quality Assessment

The ecological principles reviewed above are grounded in a growing body of empirical case studies documenting algal community dynamics and bioindicator performance across diverse geographic and climatic contexts. Table 5 presents a synthesis of key studies; selected cases are elaborated in Table 5..

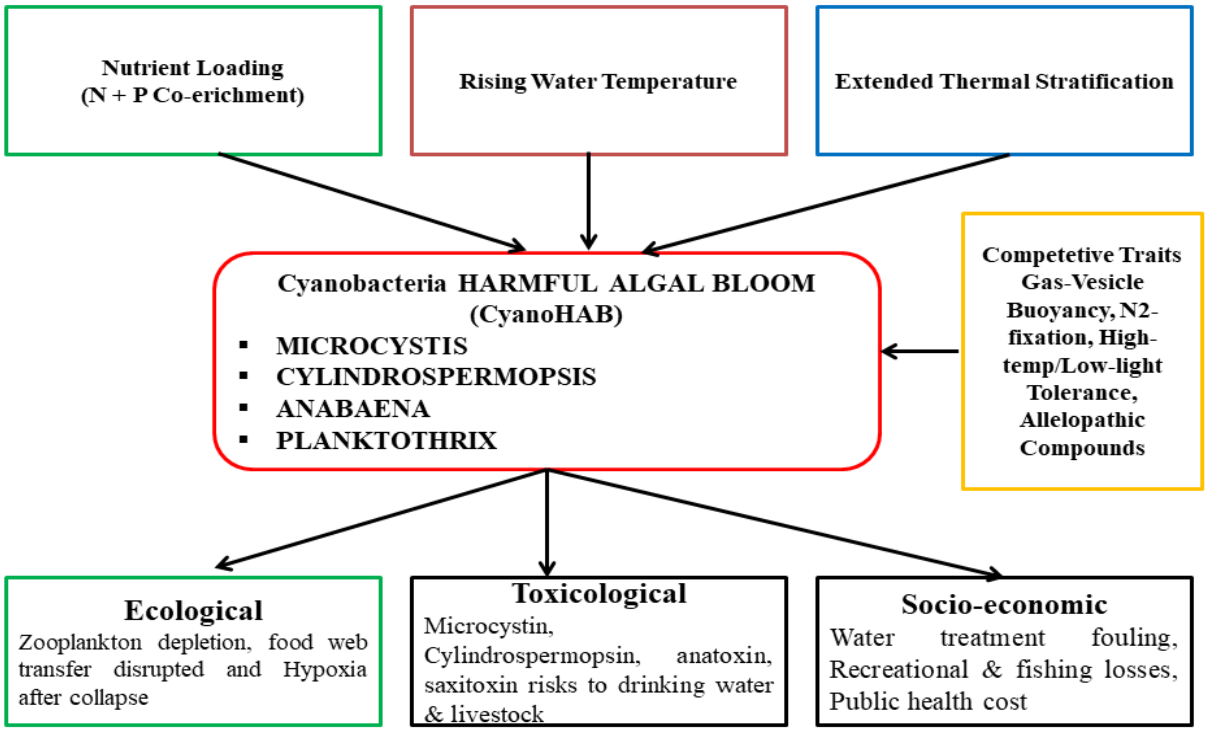

Figure 3: Drivers, competitive traits, and ecological, toxicological, and socio-economic consequences of cyanobacterial harmful algal blooms (CyanoHABs)

Table 5: Summary of regional case studies on algal biodiversity and water quality assessment

Location	Ecosystem Type	Dominant Algal Groups	Key Finding	Reference
Brazil (10 tropical reservoirs)	Eutrophic reservoirs	Cyanobacteria, Chlorophyta, Dinophyta	HABs elevated pH, reduced zooplankton richness, impaired food web transfer	Amorim & Moura (2020)
Campeche, Mexico	Karstic freshwater lagoons	*Diverse eukaryotic microalgae*	362 genera/lagoon; Nannochloropsis correlated negatively with Pb; metagenomic diversity highest in pristine lagoon	Rosaldo-Benítez et al. (2024)
Kerala, India	Temple ponds	*Chlorophyceae dominant*	Palmer's Index revealed moderate organic pollution; anthropogenic activities key drivers	Shubha & Sreeja (2019)
Bhubaneswar, India	Urban freshwater bodies	Botryococcus, Spirulina, Spirogyra	9 genera identified; B. braunii dominant due to hydrocarbon exudates; biotechnological potential highlighted	Roy et al. (2016)
South Korea (streams)	Polluted & reference streams	Macroinvertebrates, algae, microorganisms	SOM + NMDS revealed algae effective across pollution gradient; multi-taxa approach most informative	Chon et al. (2013)
Lake Victoria, East Africa	Large tropical lake	Cyanobacteria	*Shift from diatom to cyanobacteria dominance following eutrophication; oxygen depletion recorded*	Hecky (1993); Reid et al. (2019)
Dehradun District, India	Rivers and lakes (lotic & lentic)	Myxophyta, Chlorophyta, diatoms	ArcGIS + PAST software used; AGPI and Shannon indices calculated; physico-chemical-algal correlations mapped	Graham et al. (2009)

Tropical Reservoirs (Brazil)

Amorim and Moura (2020) conducted one of the most comprehensive multi-reservoir assessments of bloom impacts available in the recent literature, investigating plankton dynamics and ecosystem functioning across ten tropical Brazilian reservoirs experiencing varying degrees of eutrophication. Their results demonstrated that cyanobacteria blooms generated the most severe water quality deterioration including the highest turbidity, elevated pH, and greatest reductions in water transparency compared with blooms dominated by Dinophyta or Chlorophyta. Zooplankton species richness and resource use efficiency declined precipitously during cyanobacteria-dominated periods, while phytoplankton resource use efficiency increased, indicating suppressed food web energy transfer. These findings confirmed all three key hypotheses advanced in the study and provided quantitative evidence for the cascading ecosystem impacts of CyanoHABs in tropical systems.

Karstic Lagoons (Mexico)

Rosaldo-Benítez et al. (2024) combined traditional microscopy with shotgun metagenomics to characterize eukaryotic microalgal communities in

three tropical karstic lagoons in Campeche, Mexico, subjected to varying anthropogenic disturbance intensities. The integrated approach revealed an average of 362 microalgal genera per lagoon a richness estimate that exceeded previously published values by an order of magnitude, reflecting the detection power of metagenomics relative to microscopy alone. The pristine Mocú lagoon exhibited the highest functional gene diversity, while specific genera (Nannochloropsis, Thraustotheca) showed statistically significant negative correlations with lead contamination. A high proportion of unclassified taxa highlighted a critical limitation of current biomonitoring approaches: insufficient coverage of freshwater algal diversity in global genomic reference databases.

Temple Ponds (Kerala, India)

Shubha and Sreeja (2019) applied Palmer's Algal Genus Pollution Index to three temple ponds in Kannur, Kerala, identifying 20 algal genera predominantly from *Chlorophyceae*. Site-level variation in pollution index scores correlated with anthropogenic activity intensity bathing, washing, and organic waste disposal demonstrating the utility of Palmer's Index in rapidly diagnosing organic pollution in small, accessible water bodies. A Comprehensive Pollution Index integrating physical parameters reinforced the algal indicator findings, classifying two sites as slightly polluted and one as acceptable, with strong correlations between turbidity, DO, BOD, and algal community composition.

Multi-Taxa Assessment (South Korea)

Chon et al. (2013) applied Self-Organizing Maps (SOM) and Nonmetric Multidimensional Scaling (NMDS) to simultaneous community data for macro invertebrates, algae, and microorganisms across Korean streams covering a broad pollution gradient. Their analysis demonstrated that while macro invertebrates provided the clearest discrimination of pollution levels, algae and microorganisms exhibited broader distributional responses across the gradient, providing complementary ecological information. The combination of multi-taxa data with computational ordination tools substantially enhanced the diagnostic resolution of stream health assessment a finding that has direct implications for the design of integrated monitoring programmes.

Urban Freshwater Bodies (Bhubaneswar, India)

Roy et al. (2016) surveyed eleven freshwater bodies in the urban landscape of Bhubaneswar, Odisha, identifying nine algal genera through microscopic analysis. The dominance of *Botryococcus braunii* in several temple ponds attributed to its hydrocarbon-rich exudate chemistry that competitively inhibits other species illustrated the ecological specificity of algal community composition to microhabitat conditions. Beyond its bioindication value, the study highlighted the biotechnological potential of several identified taxa: *Botryococcus* for biofuel production, and Spirulina for nutraceutical applications, underscoring the multi-dimensional value of algal biodiversity surveys.

Research Gaps, Challenges, and Future Directions

Despite decades of taxonomic effort, the vast majority of freshwater algal species particularly microalgae in tropical and subtropical regions remain undescribed or insufficiently characterized with respect to their environmental preferences (Rosaldo-Benítez et al., 2024; Crossetti & Bicudo, 2008). Reference databases for eDNA metabarcoding are heavily biased towards temperate Northern Hemisphere taxa, rendering molecular bioassessment less reliable in Africa, South Asia, and tropical South America precisely the regions where freshwater quality pressures are most acute and monitoring capacity is most limited. Concerted investment in taxonomic training, freshwater phycological collections, and DNA barcoding campaigns targeting understudied regions is urgently required to close these gaps (Rosaldo-Benítez et al., 2024; Yang et al., 2023).

A persistent barrier to the cross-regional and cross-institutional comparability of algal bioassessment data is the absence of universally adopted standardized protocols for sampling design, sample preservation, DNA extraction, bioinformatics pipelines, and index calculation. Different national monitoring programmes apply

different primer sets for metabarcoding, different sequence similarity thresholds for taxonomic assignment, and different index calibration datasets, rendering meta-analyses and international comparisons methodologically challenging (Kulaš et al., 2022; Kim et al., 2026). The European Union Water Framework Directive has made significant progress towards harmonization within Europe, but global frameworks equivalent in rigour and geographic scope do not yet exist for developing regions (Reid et al., 2019).

There is a critical paucity of long-term, multi-decadal algal monitoring datasets particularly outside Europe and North America that would enable the detection of biodiversity trends, the attribution of change to specific drivers, and the validation of predictive models (Bush et al., 2017; Crossetti & Bicudo, 2008). Wu et al. (2025) demonstrated the power of combining multidecadal monitoring records with palaeogenetic reconstruction to reveal century-scale algal community responses to nutrient loading and climate warming an approach that underscores both the value of historical data and the need for continuity in ongoing monitoring programmes. The integration of climate model projections with algal community models represents a priority research frontier for anticipating future water quality trajectories and informing adaptive management strategies (Earth Interactions, 2023; Griffith & Gobler, 2020).

Several technological frontiers hold transformative potential for algal-based freshwater monitoring. eDNA and eRNA metabarcoding, combined with machine learning, are progressively replacing labour-intensive morphological identification in both regulatory monitoring and research contexts (Kim et al., 2026; Yang et al., 2023). The development of real-time in situ biosensors capable of detecting algal pigments, specific toxin concentrations, and molecular biomarkers directly in water bodies without the need for laboratory analysis would represent a paradigm shift in monitoring timeliness and cost-effectiveness. Satellite constellations with improved spatial resolution and daily revisit frequencies (such as the commercial Planet Labs SuperDoves) are extending bloom detection to smaller water bodies previously inaccessible to orbital remote sensing (Frontiers in Remote Sensing, 2025). Artificial intelligence platforms that integrate these multi-source data streams into near-real-time dashboards for water quality managers are beginning to move from proof-of-concept to operational deployment (Remote Sensing, 2024; Liu et al., 2023).

Conclusion

Algal biodiversity constitutes one of the most sensitive, scientifically robust, and practically deployable indicators of freshwater ecosystem health available to the scientific and management community. As primary producers, nutrient cyclers, and ecological recorders, algae translate complex multi-stressor environmental conditions into measurable community-level signals interpretable through established index systems and emergent molecular and geospatial tools. This review has demonstrated that algal responses to eutrophication, organic pollution, heavy metal contamination, climate warming, and hydromorphological disturbance are consistent, quantifiable, and ecologically meaningful across diverse geographic and climatic contexts from karstic tropical lagoons in Mexico to experimental boreal lakes in Canada and urban temple ponds in India.

The convergence of eDNA metabarcoding, satellite remote sensing, and machine learning represents a genuinely transformative opportunity for algal biomonitoring enabling high-throughput, spatially comprehensive, and temporally continuous assessment at scales and costs previously unattainable. However, realizing this potential requires concurrent investment in taxonomic infrastructure, standardized protocols, expanded reference databases, and long-term monitoring programmes particularly in tropical and subtropical regions where biodiversity is greatest and data are most sparse. HABs driven by the synergistic combination of nutrient enrichment and climate warming represent the most immediate and globally escalating algal-related threat to freshwater ecosystem services and public health. Their effective management demands not only

robust early-warning monitoring systems but also transformative reductions in nutrient loading from agriculture, urban wastewater, and atmospheric sources. Algal bioindicators provide the ecological data foundation upon which evidence-based water resource management can be built; translating that foundation into policy action remains the defining challenge for the scientific and governance communities. This review advocates for the systematic integration of algal diversity monitoring into national and international water quality frameworks, supported by transdisciplinary collaboration among phycologists, ecologists, molecular biologists, remote sensing specialists, data scientists, and water managers. The ecological intelligence embedded in freshwater algal communities represents a resource of extraordinary value one that, properly harnessed, can guide humanity towards more sustainable stewardship of the planet's most essential freshwater resources.

Conflict of Interest

The authors declares no conflict of interest.

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Author Contribution

ABH conceptualized the review and drafted the original manuscript. SBB contributed to literature synthesis, critical revision, and editing of the manuscript. AH contributed to data organization and review of the final draft. All authors read and approved the final manuscript.

References

Amorim, C. A., & Moura, A. N. (2020). Ecological impacts of freshwater algal blooms on water quality, plankton biodiversity, structure, and ecosystem functioning. *Science of the Total Environment*, 743, 143605. https://doi.org/10.1016/j.scitotenv.2020.143605

Bellinger, E. G., & Sigee, D. C. (2015). Freshwater algae: Identification and use as bioindicators (2nd ed.). *John Wiley & Sons*.

Bižić, M., Klintzsch, T., Ionescu, D., Hindiyeh, M. Y., Günthel, M., Muro-Pastor, A. M., Eckert, W., Urich, T., Keppler, F., & Grossart, H.-P. (2020). Aquatic and terrestrial cyanobacteria produce methane. *Science Advances, 6(3), eaax5343*. https://doi.org/10.1126/sciadv.aax5343

Bush, A., Compson, Z. G., Monk, W. A., Porter, T. M., Steeves, R., Emilson, C. E., & Baird, D. J. (2017). Studying ecosystems with DNA metabarcoding: Lessons from aquatic biomonitoring. *Metabarcoding and Metagenomics*, 1, e14025.

Chon, T.-S., Qu, X., Cho, W.-S., Hwang, H.-J., Tang, H., Liu, Y., Choi, J.-H., Jung, M., Chung, B. S., Lee, H. Y., Chung, Y. R., & Koh, S.-C. (2013). Evaluation of stream ecosystem health and species association based on multi-taxa (benthic macroinvertebrates, algae, and microorganisms) patterning with different levels of pollution. *Ecological Informatics*, 18, 73–83. https://doi.org/10.1016/j.ecoinf.2013.06.004

Crossetti, L. O., & Bicudo, C. E. M. (2008). Phytoplankton as a tool for water quality assessment in a shallow tropical urban reservoir, Garças Pond, São Paulo, Brazil. *Hydrobiologia*, 610(1), 161–173.

Dash, M. C., Panda, S., & Misra, B. N. (2021). Seasonal variation in algal diversity in freshwater ecosystems of Odisha. *Aquatic Ecology Studies*, 14(2), 101–109.

Díaz, S., Settele, J., Brondízio, E. S., Ngo, H. T., Agard, J., Arneth, A., & Zayas, C. N. (2019). Pervasive human-driven decline of life on Earth points to the need for transformative change. *Science*, 366(6471), eaax3100. https://doi.org/10.1126/science.aax3100

Falkowski, P. G., Fenchel, T., & Delong, E. F. (2008). The microbial engines that drive Earth's biogeochemical cycles. *Science*, 320(5879), 1034–1039. https://doi.org/10.1126/science.1153213

Feng, L., Wang, Y., Hou, X., Qin, B., Krumholz, L. R., & Jeppesen, E. (2024). Harmful algal blooms in inland waters. Nature Reviews Earth &

Environment, 5(11), 631–644. https://doi.org/10.1038/s43017-024-00578-2

Filstrup, C. T., Heathcote, A. J., Kendall, D., & Downing, J. A. (2014). Phytoplankton taxonomic compositional shifts across nutrient and light gradients in temperate lakes. *Inland Waters*, 4(2), 234–242.

Graham, L. E., Graham, J. M., & Wilcox, L. W. (2009). Algae (2nd ed.). *Pearson Benjamin Cummings.*

Griffith, A. W., & Gobler, C. J. (2020). Harmful algal blooms: A climate change co-stressor in marine and freshwater ecosystems. *Harmful Algae*, 91, 101590. https://doi.org/10.1016/j.hal.2019.03.008

Hecky, R. E. (1993). The eutrophication of Lake Victoria. Verhandlungen der Internationale Vereinigung für Theoretische und Angewandte Limnologie, 25, 39–48.

Hoek, C. van den, Mann, D. G., & Jahns, H. M. (1995). Algae: An introduction to phycology. *Cambridge University Press*.

Kelly, M. G. (1998). Use of the trophic diatom index to monitor eutrophication in rivers. *Water Research,* 32(1), 236–242. https://doi.org/10.1016/S0043-1354(97)00019-5

Khalil, S., Mahnashi, M. H., Hussain, M., Zafar, N., Khan, F. S., Afzal, U., Shah, G. M., Niazi, U. M., Awais, M., & Irfan, M. (2021). Exploration and determination of algal role as bioindicator to evaluate water quality: Probing fresh water algae. *Saudi Journal of Biological Sciences,* 28(10), 5728–5737. https://doi.org/10.1016/j.sjbs.2021.06.004

Kim, J., Hwang, S., Park, J., Kim, H., & Cho, Y. (2026). Machine learning assessment of molecular trophic diatom index (mTDI) using planktonic eDNA for water quality in freshwater ecosystems. *Journal of Phycology*. https://doi.org/10.1080/02705060.2026.2633108

Kulaš, A., Gligora Udovič, M., Tapolczai, K., Žutinić, P., Orlić, S., & Levkov, Z. (2022). Diatom eDNA metabarcoding and morphological methods for bioassessment of karstic river. *Science of the Total Environment*, 829, 154536. https://doi.org/10.1016/j.scitotenv.2022.154536

Liu, M., Huang, Y., Hu, J., He, J., & Xiao, X. (2023). Algal community structure prediction by machine learning. *Environmental Science and Ecotechnology*, 14, 100233. https://doi.org/10.1016/j.ese.2022.100233

Lopez Barreto, B. N., Hestir, E. L., Lee, C. M., & Beutel, M. W. (2024). Satellite remote sensing: A tool to support harmful algal bloom monitoring and recreational health advisories in a California reservoir. *GeoHealth*, 8, e2023GH000941. https://doi.org/10.1029/2023GH000941

Makwana, K. (2022). Algae the bioindicator for sustainable environment: A review. *Journal of Plant Science and Research,* 9(2), 234.

Moustaka-Gouni, M., & Sommer, U. (2020). Phytoplankton bloom dynamics and species composition in relation to nutrient availability and grazing pressure. *Hydrobiologia*, 848, 1–15.

Nayak, S., Patnaik, A., & Mohanty, D. (2024). Algal population dynamics and nutrient correlations in tropical freshwater lakes. *International Journal of Aquatic Biology*, 12(1), 33–42.

Olivetti, D., Cicerelli, R., Martinez, J.-M., Almeida, T., Casari, R., Borges, H., & Roig, H. (2023). Comparing unmanned aerial multispectral and hyperspectral imagery for harmful algal bloom monitoring in artificial ponds used for fish farming. Drones, 7(7), 410. https://doi.org/10.3390/drones7070410

Paerl, H. W., & Paul, V. J. (2012). Climate change: Links to global expansion of harmful cyanobacteria. *Water Research*, 46(5), 1349–1363. https://doi.org/10.1016/j.watres.2011.08.002

Paerl, H. W., Xu, H., McCarthy, M. J., Zhu, G., Qin, B., Li, Y., & Gardner, W. S. (2011). Controlling harmful cyanobacterial blooms in a hyper-eutrophic lake (Lake Taihu, China): The need for a dual nutrient (N & P) management strategy. *Water Research*, 45(5), 1973–1983. https://doi.org/10.1016/j.watres.2010.09.018

Paerl, H. W., Havens, K. E., Peng, F., & Xu, H. (2023). Harmful cyanobacterial blooms:

Biological traits, mechanisms, risks, and control strategies. *Annual Review of Environment and Resources*, 48, 123–147. https://doi.org/10.1146/annurev-environ-112320-081653

Passy, S. I. (2008). Continental diatom biodiversity in stream benthos declines as more nutrients become limiting. *Proceedings of the National Academy of Sciences*, 105(27), 9663–9667. https://doi.org/10.1073/pnas.0802542105

Paul, M. J., & Meyer, J. L. (2001). Streams in the urban landscape. *Annual Review of Ecology and Systematics,* 32, 333–365. https://doi.org/10.1146/annurev.ecolsys.32.081501.114040

Rabalais, N. N., Turner, R. E., Díaz, R. J., & Justić, D. (2010). Global change and eutrophication of coastal waters. *Biogeosciences*, 7(2), 585–619. https://doi.org/10.5194/bg-7-585-2010

Reid, A. J., Carlson, A. K., Creed, I. F., Eliason, E. J., Gell, P. A., Johnson, P. T. J., & Cooke, S. J. (2019). Emerging threats and persistent conservation challenges for freshwater biodiversity. *Biological Reviews*, 94(3), 849–873. https://doi.org/10.1111/brv.12480

Reynolds, C. S. (2006). *The ecology of phytoplankton. Cambridge University Press*. https://doi.org/10.1017/CBO9780511542145

Rosaldo-Benítez, V., Ayil-Chan, G. A., Labrin-Sotomayor, N., Valdez-Ojeda, R., & Peña-Ramírez, Y. J. (2024). Eukaryotic microalgae communities from tropical karstic freshwater lagoons in an anthropic disturbance gradient: Microscopic and metagenomic analysis. *Microorganisms*, 12(11), 2368. https://doi.org/10.3390/microorganisms12112368

Roy, S. S., Paul, W., Patra, D., Ojha, S. K., & Mishra, S. (2016). Algal biodiversity in selected freshwater aquatic bodies in Bhubaneswar, India. *Journal of Advanced Microscopy Research*, 2(2), 113–119.

Shubha, A., & Sreeja, P. (2019). Algal diversity and water pollution status of temple ponds in Kannur, Kerala. *International Journal of Research and Analytical Reviews*, 6(1), 889–896.

Swanson, J., Abdulrahman, D., & Dudycha, J. L. (2025). Light color and nutrients interact to determine freshwater algal community diversity and composition [Preprint]. bioRxiv. https://doi.org/10.1101/2025.02.27.640658

Wang, X., Zhang, J., & Zhang, W. (2023). Remote sensing for mapping algal blooms in freshwater lakes: A review. Environmental Science and Pollution Research, 30, 9583–9614. https://doi.org/10.1007/s11356-023-25230-2

Wetzel, R. G. (2001). Limnology: Lake and river ecosystems (3rd ed.). Academic Press.

Wu, N., Schmalz, B., & Fohrer, N. (2012). Development and testing of a phytoplankton index of biotic integrity (P-IBI) for a German lowland river. *Ecological Indicators,* 13, 158–167. https://doi.org/10.1016/j.ecolind.2011.06.001

Wu, N., Dong, X., Liu, Y., Wang, C., & Baattrup-Pedersen, A. (2017). Using river microalgae as indicators for freshwater biomonitoring: *Review of published research and future directions. Ecological Indicators*, 81, 124–131. https://doi.org/10.1016/j.ecolind.2017.05.066

Wu, Z., Gu, L., Xu, J., & Zhao, C. (2025). Eutrophication and warming drive algal community shifts: A palaeogenetic and multi-decadal monitoring study of experimental lakes. *Environmental Microbiology*, 27, e70226. https://doi.org/10.1111/1462-2920.70226

Yan, H., Yang, G., Zhou, Y., & Wang, Y. (2017). Algal bloom decomposition increases greenhouse gas emissions from eutrophic lakes. *Environmental Science & Technology*, 51(20), 11237–11246. https://doi.org/10.1021/acs.est.7b02237

Yang, J., Zhang, L., Mu, Y., Wang, J., Yu, H., & Zhang, X. (2023). Unsupervised biological integrity assessment by eDNA biomonitoring of multi-trophic aquatic taxa. *Environment International,* 175, 107950. https://doi.org/10.1016/j.envint.2023.107950

Zimmermann, J., Glöckner, G., Jahn, R., Enke, N., & Gemeinholzer, B. (2015). Metabarcoding vs.

morphological identification to assess diatom diversity in environmental studies. *Molecular Ecology Resources*, 15(3), 526–542. https://doi.org/10.1111/1755-0998.12336