A publication of the North American Lake Management Society

LakeLine

Volume 46, No. 2 • Summer 2026

Lake DNA

Swimming Upstream: Tackling Environmental Challenges through Partnership, Innovation, & Science

Photo: Courtesy of tourismkelowna.com – Brett Loeppky

46th NALMS International Symposium

November 3–6, 2026

Kelowna, British Columbia, Canada • Delta Hotels Grand Okanagan Resort

Kelowna appears to have abundant water, but the city is in the most water-scarce region of Canada. Water resources in this semi-arid setting are under increasing pressure, compounded by watershed-scale disturbances and a warming climate. Warmer and drier conditions during the growing season often lead to agricultural, urban, and environmental water demands surpassing the available water resources. To discuss these and other important management issues, NALMS is pleased to return to Canada (after ten years) for NALMS 2026!

Contact Information

Sponsorship, Exhibition, Registration, and General Conference Information: NALMS Office • nalms2026@nalms.org

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Program Co-Chairs: Liz Favot • liz.favot@gmail.com / Andrew Paterson • andrew.paterson@ontario.ca

nalms.org/nalms2026

Tentative Schedule

Tuesday, November 3
- Workshops
- Field Trips
- Exhibitor Set Up
- Welcome Event

Wednesday, November 4
- Opening Plenary Session
- Technical Sessions
- Exhibits Open
- NALMS Membership Meeting
- Exhibitors Reception and Poster Session

Thursday, November 5
- Plenary Session
- Technical Sessions
- Exhibits Open
- Clean Lakes Classic 5K

Friday, November 6
- Technical Sessions
- Exhibits Open

Field Trips

The NALMS 2026 host committee has organized a series of educational field trips on Tuesday, November 3. Visit the conference website for more details on the available field trips. Space is limited.

Clean Lakes Classic

The 2026 edition of our annual 5K run / walk will take participants on a route along the shores of beautiful Okanagan Lake on Thursday, November 5. Visit the conference website to register.

Student Silent Auction

Please consider participating in the annual silent auction either as a bidder or by donating an item to the auction. All proceeds will go to the Eberhardt Memorial Student Fund which supports student travel scholarships and other student programs.

Registration Fees

Add a 2027 NALMS membership to your registration and receive 15% off the membership!

	Early Bird by Sept 11	Regular by Oct 23	On-site after Oct 23
NALMS Member	$590	$650	$740
Non-Member	$720	$790	$880
Student	$340	$430	$510
Single Day	$310	$350	$420
Guest	$325	$355	$405

Technical Program

The NALMS 2026 Program Committee has organized an excellent array of presentations on diverse aspects of lakes, ponds, reservoirs, their watersheds, and their many users and inhabitants. Below is just a sample of session topics, so please check the symposium website for complete program information.

Aquatic Invasive Species • Data Management • HABs • Latin American Lakes & Reservoirs • Mining Impacts • National Lakes Assessment • Nutrient Management • Salmon Nursery Lakes • Wilderness Lakes • and much more!

#NALMS2026 • nalms.org/nalms2026

Workshops

We will be offering a full slate of full- and half-day workshops on Tuesday, November 3. These workshops provide attendees the opportunity for in-depth focus on a topic of interest, and many will provide hands-on experience.

Visit the conference website, www.nalms.org/nalms2026, for full details on workshop offerings. Conference registration is not required to attend a workshop.

Photos: Todd Tietjen

LakeLine

Contents

Volume 46, No. 2 / Summer 2026

4 From the Editor

5 From the President

Lake DNA

6 What is eDNA?

8 Beyond what meets the eye: DNA barcoding and aquatic plant identification

11 Plant identification using DNA "barcodes"

14 Meteorology, climatology, & lakes

20 Student Corner: Voices from the water . . . .

IBC Lakespert

On the cover:
"Seeking clarity in the Rocky Mountains" Photo by Laura Bates, submitted as an entry to the NALMS 2025 photo contest. This was the runner-up photo in the Popular Vote category.

Advertisers Index

Aquarius Systems	19
Easy-Pro	5
In-Situ	IFC
PhycoTech	21

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From Amy P. Smagula the Editor

Happy summer!

This issue of *LakeLine* explores alternative methods of species identification in aquatic systems. Environmental DNA, or eDNA, has proven to be a useful tool in cataloguing which species are present in a waterbody, confirming the identification of a species, and gaining a better understanding of species diversity within a family of plants, and much more.

Alison Watts with the University of New Hampshire discusses the use of eDNA in identifying the presence or absence of various aquatic organisms in aquatic systems. This work has aided managers in determining if a target species is present in a system, and it has served as an early detection tool as well as a bit of peace of mind in some cases.

Ryan A. Thum, **Gregory M. Chorak**, **Del Hannay**, **Zachary J. Kuzniar**, and **Ashley L. Wolfe** at Montana State University contributed an article about the DNA barcoding work they do for aquatic plant identification.

Nic Tippery with University of Wisconsin, Whitewater shares some of his work with eDNA and barcoding. While some of his work has some crossover with that described in the Thum et al. article, Nic describes some of the work with plant identification using DNA barcodes that has opened up new avenues for understanding aquatic plant diversity, as well as some verifying discoveries of hybrid invasives, documenting newly arrived aquatic plants in North America, identifying distinct subspecies of plants, and identification of a previously overlooked species.

In this issue we also see the first of three articles in a new column called "Meteorology, Climatology and Lakes." In this column, **Rick Sherma** with Penn State Extension and Wayne Conservation District in Pennsylvania will be examining the influence of weather on lake water quality.

For our "Lakespert" column, we welcome a guest Lakespert **Ashley Bruhn**, a Water Quality Scientist- Denver, Colorado, and a colleague of our regular Lakespert (Steve Lundt) contributed the enclosed Lakespert article. Ashley shares her experience with the use of eDNA in fisheries studies in Colorado, and the utility of this technique in identifying species expected to be present, as well as some unexpected species.

Also in this issue, we hear from NALMS President Julie Chambers, as well as our NALMS Executive Director, Philip Forsberg, who prepared a conference preview for the NALMS 2026 Annual Symposium, to be held in Kelowna, British Columbia, from November 3-6, 2026. To learn more about the conference, find the layout in this issue, or visit https://www.nalms.org/nalms2026/.

Lastly, while you are out and about visiting lakes this summer, please remember to snap some photos, and submit your best shot to the NALMS 2026 Photo Contest. Details on the contest are also included in this issue.

We hope you enjoy this issue. Have a great summer!

Amy P. Smagula is the Chief Aquatic Biologist and Director of the Jody Connor Limnology Center at the New Hampshire Department of Environmental Services.

From Julie Chambers
the President

The theme of this issue of *Lakeline*, environmental DNA (eDNA) and genetics, is a timely follow-up to our previous edition which focused on the National Lake Assessment. eDNA has been incorporated into the National Aquatic Resource Surveys (NARS) as a research indicator, enabling more comprehensive data on the biodiversity of lakes across the survey. It also supports the development of biological condition estimates for the nation's waterbodies, furthering the goal of assessing the status of, and changes in, water quality nationwide.

Monitoring programs often struggle with the limitations of collecting physical, visual, and other data types to identify the biodiversity and species present in systems, all while working within tight budgetary constraints. Compounding this, identification has traditionally required specialized taxonomic expertise, which is often quite costly. These challenges have driven the search for alternative methods to monitor biodiversity, both qualitatively and quantitatively. Collection of eDNA samples offers one such alternative, with a wide range of applications. By taking advantage of the fact that organisms shed and leave behind DNA in the natural environment, eDNA analysis provides a sensitive, rapid, and cost-effective tool for detecting species presence in a given waterbody – offering valuable insight into a system's condition based on the organisms and biodiversity present.

In this issue, we explore how eDNA is reshaping the way we understand and manage lake ecosystems – from emerging applications to the growing role of genetics tools in long-term monitoring strategies. As eDNA methods continue to mature, they promise to complement, and in some cases transform, how monitoring programs assess the health of our nation's waters.

Julie Chambers leads the Oklahoma Water Resources Board's Beneficial Use Monitoring Program (BUMP) Lake Monitoring section. She has 25 years of experience in statewide water quality management, from program design through data collection, management, reporting, and dissemination of information. Over the last 22 years her program has thrived and is responsible for conducting water quality studies, assessments, and bathymetric surveys on reservoirs across Oklahoma, as well as managing lake and wetland projects funded through federal grants and other contracts. Julie serves on the water quality steering committee for the EPA's National Lake Assessment as well as on several state technical workgroups focused on the assessment of lakes and field protocol development. Julie has been an active member of The North American Lake Management Society (NALMS) for 20 years serving on various committees and representing as past president since 2016.

What is **eDNA?**

Alison Watts

You've probably heard of eDNA, a technique used for detecting fish, invasive plants, or rare species in lakes and streams. But perhaps you've wondered what it is or wanted to know more about science and how we can apply it. Environmental DNA (eDNA) is DNA (deoxyribonucleic acid) that is collected from the environment. Fish, amphibians, plants, and other organisms constantly leave tiny traces of genetic material in the water around them. By collecting water samples, scientists can identify many of the species living in a lake without having to catch or even see them.

The process is relatively straightforward (Figure 1); water samples are collected from a lake, filtered to capture microscopic fragments of DNA, and sent to a laboratory where the DNA is extracted and analyzed. The lab methods are tailored to meet different needs: single-species analyses focus on one organism of interest, which could be a fish, a plant or a harmful bacteria, while multispecies methods provide a broad inventory of fish, amphibians, and other aquatic organisms present in the ecosystem.

What do we learn from eDNA?

The information gained from eDNA can be used in many ways. Resource managers can monitor changes in fish communities over time, detect invasive species before they become established, confirm the presence of rare or endangered species, and evaluate the effects of habitat restoration or water quality changes. Because collecting water samples is relatively easy and does not disturb wildlife, eDNA also allows lake associations, schools, and citizen scientists to contribute to monitoring efforts. Anyone can collect samples with a little bit of training. Used alongside traditional methods such as netting and electrofishing, eDNA provides a powerful new tool for understanding and protecting lakes and ponds.

In New England, eDNA has been used to detect invasive species such as northern pike and zebra mussels (Figure 2) before they become widespread, to

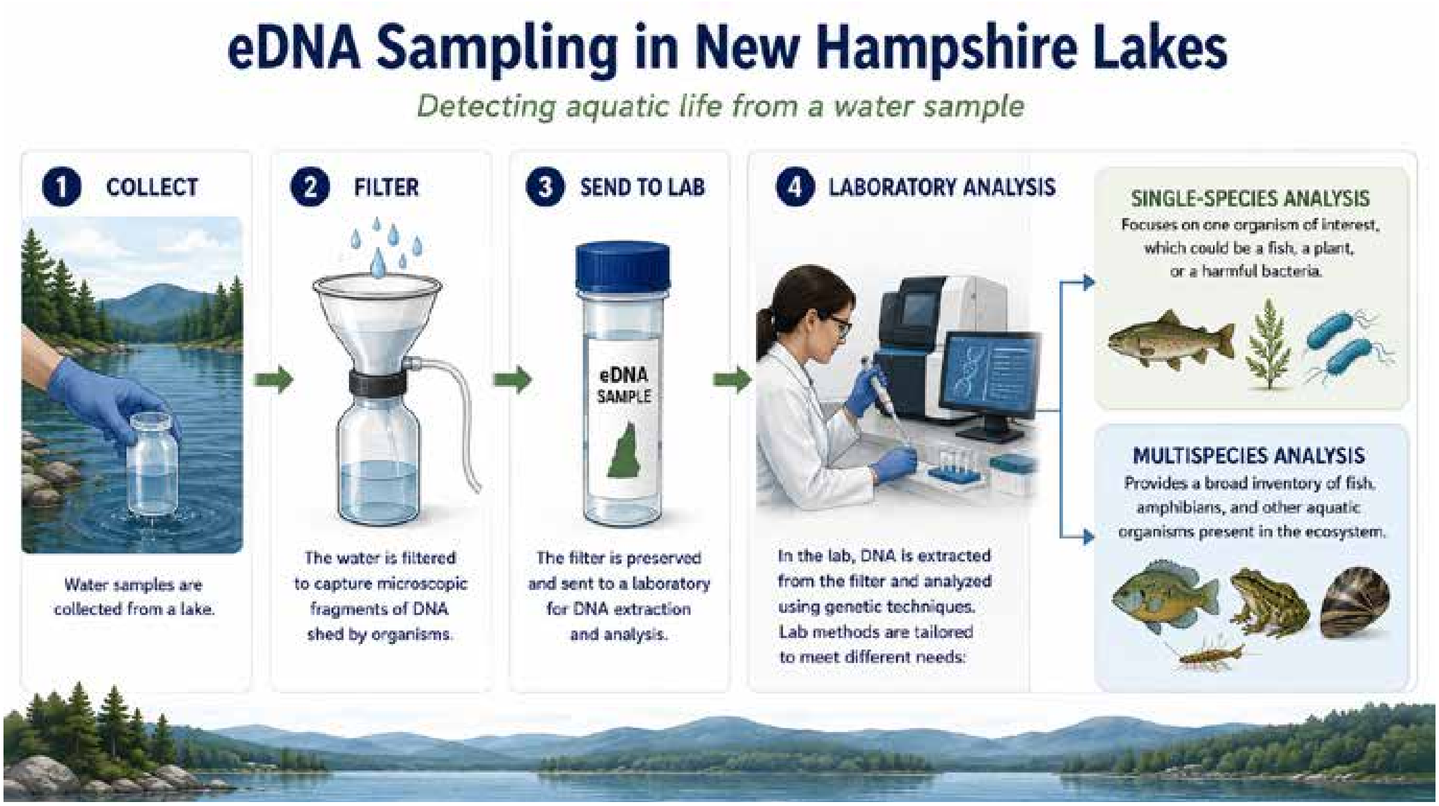


Figure 1. The process and method behind eDNA analysis.

Figure 2. Sampling for Zebra Mussels in Lake Bomoseen, Vermont.

monitor native brook trout populations, and to search for rare species. In large lakes such as Lake Winnipesaukee and Lake Champlain in the East, eDNA can reveal the presence of dozens of species providing a rapid and non-invasive way to understand biodiversity ((Figure 3).

Not a magic wand

It is important to remember that eDNA is not magic! As with any method, eDNA has limitations; a single sample will not provide detailed information for a whole lake, and multiple analyses are needed to detect the full range of species that may be present. A sampling program should be designed to provide enough coverage to capture areas where the target is likely to be present, and multiple samples will increase the chance of detection. Additional samples increase the cost of a program, so managers need to balance the value of more information with the cost (both laboratory and personnel) required to collect and process samples.

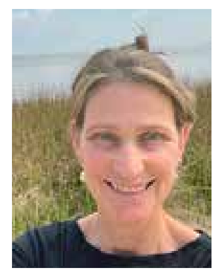
Figure 3. The author sampling for spiny water flea eDNA in Lake Winnipesaukee, New Hampshire.

Projects on the horizon

Here in New Hampshire, the state Department of Environmental Services is working with the University of New Hampshire to test eDNA methods to detect spiny water flea, a tiny invertebrate that is invading our lakes. Currently, three lakes are infested with this species, that we know of, but dozens more could potentially already harbor infestations that are yet undetected.

This summer we will collect eDNA water samples at Lake Winnipesaukee, the state's largest lake, where we know the species is present. This information will be used to compare results to net tows where we capture and enumerate individuals. We will use the results to determine how many samples are needed, and what lab methods are most effective. If we are able to successfully detect the spiny water flea, we will expand the program to do initial surveillance at other lakes with the goal of detecting these invasives before they are too established.

Want to know more about eDNA? Here's [more information.]



Dr. **Alison Watts** is a member of the Department of Civil and Environmental Engineering at the University of New Hampshire. Her research interests include working with regulatory agencies and resource managers to assess and remediate water resource impacts. Her current work is focused on the use of molecular methods, primarily eDNA, and includes early detection of invasive species, water quality indicators, impacts of aquaculture, and baseline assessments in coastal and freshwater systems.

?? link

Beyond what meets the eye: DNA barcoding and aquatic plant identification

Ryan A. Thum, Gregory M. Chorak, Del Hannay, Zachary J. Kuzniar, and Ashley L. Wolfe

Successful aquatic plant management depends on the correct identification of the species slated for management. However, even for experienced botanists, aquatic plants can be difficult to identify based on appearance alone. Aquatic plants are especially prone to identification problems because many unrelated species have evolved similar growth forms. Whorls of finely divided leaves, for example, can be found in watermilfoils, hydrilla, coontails, and bladderworts, making reliable identification difficult. Further, introduced and invasive species can have closely related native species that can be difficult to distinguish based on morphology alone.

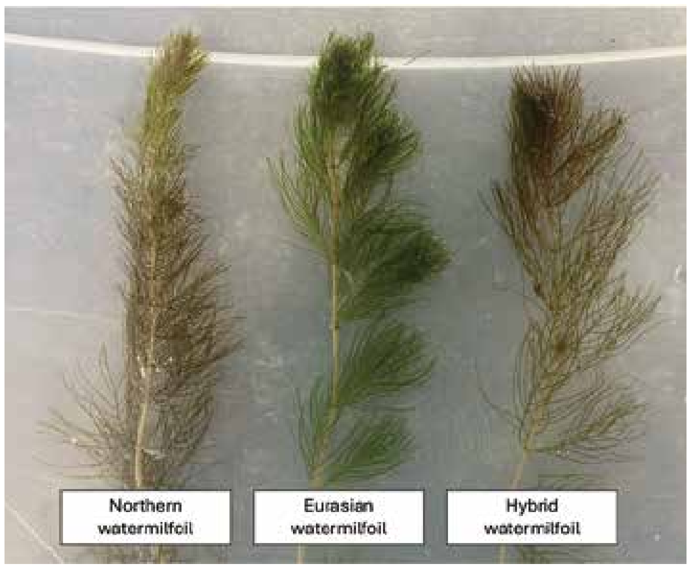


Figure 1. Visual comparison of (left to right) Northern, Eurasian, and hybrid watermilfoil. Photo courtesy of Hannah Hoff.

For example, several recently discovered invasive eelgrass species in the United States that are morphologically similar to ecologically important native species, *Vallisneria americana* and *V. neotropicalis*, highlights the critical need for additional species identification tools. Similarly, invasive Eurasian and hybrid watermilfoil are difficult to distinguish from native northern watermilfoil (Figure 1). Finally, even for morphologically distinct species, diagnostic characters such as flowers or fruits may be missing during life stages or times of the year, making visual identifications challenging.

The consequences of misidentification can be costly. On the one hand, misidentifying an invasive species as a native may fail to control a population that could cause economic or environmental harm locally and spread to other lakes. On the other hand, misidentifying a native species as an invasive species may result in unnecessary economic and environmental costs.

While traditional identification methods based on morphology, ecology, and the phenology of species remain valuable tools, the limitations described above have resulted in increasing interest in using DNA barcoding as an identification tool for aquatic plants. Understanding how DNA barcoding works, as well as its limitations, will allow users to develop and employ this technology to inform management decisions.

What is DNA barcoding?

DNA barcoding gets its name from analogy to how a barcode scanner matches a product at the grocery store to an inventory database. Using a short, standardized region of DNA, researchers can compare the DNA sequence of an unknown specimen to reference sequences from known species. Rather than a pattern of black and white bars, a DNA barcode consists of a short sequence of the four DNA building blocks – adenine (A), thymine (T), cytosine (C), and guanine (G). Barcode regions are selected because they can be compared across many species while still containing enough variation to distinguish among them.

Once a sample has been collected, DNA barcoding typically involves four steps: (1) DNA is extracted from the specimen, (2) a barcode region is amplified, (3) the amplified DNA is sequenced, and (4) the resulting sequence is compared to a reference database of known species (Figure 2). When a strong match is found, the unknown specimen can confidently be identified to species.

DNA barcoding has become a widely used tool for species identification because it can be applied to specimens that are difficult to identify using traditional morphological characteristics, including species that appear very similar to one another, or specimens that lack typical diagnostic characteristics such as flowers or fruits. Because many aquatic plant species look similar, and because they often reproduce primarily through vegetative propagation, DNA barcoding is an attractive method for aquatic plant identification. While DNA barcoding can be a powerful tool for species identification, the approach also has important limitations that users should understand.

Limitations and misconceptions of barcoding

One common misconception is that every species has a unique DNA barcode and that sequencing a barcode gene will automatically identify an unknown organism. While barcodes are often useful for species identification, successful DNA barcoding depends on both the barcode itself and the availability of reference sequences for comparison. Some genes are reliable barcodes for some groups of organisms, but not for others. Researchers build reference databases by sequencing barcode genes from many correctly identified specimens. These databases allow unknown samples to be compared against a catalog of known species. Then, they compare unknown samples to those records. Aquatic plants are underrepresented in many genetic databases compared to other groups of plants and animals. If a species is missing from the reference database, or if the diversity within that species has not been thoroughly documented, identification may be uncertain. This is similar to scanning a product barcode that does not exist in the store inventory system – the barcode is present, but there is no reference available to interpret it.

Another challenge is that species do not always possess unique barcode sequences. Closely related species may share identical DNA barcode sequences because they diverged relatively recently in evolutionary time. In addition, there may be genetic variation at the barcoding gene among individuals of the same species, and so an individual that is not an exact match to a sequence in the reference database may be uncertain as to whether it is a member of a closely related species or a species that has not been cataloged in the reference database. For these reasons, researchers often need to understand how much variation exists both within the target species and among its closest relatives before a barcode can be used confidently for species identification.

Hybridization can further complicate species identification. Many aquatic plants readily hybridize, creating offspring that contain genetic material from multiple species. When researchers examine many genes across the genome, these hybrid relationships can often be detected. However, DNA barcoding typically relies on a single gene. As a result, a hybrid individual may possess a barcode sequence inherited from one parent, while much of the rest of its genome comes from another species. In these cases, DNA barcoding may provide an incomplete picture of an organism's ancestry. This is especially relevant to aquatic plant management when there is hybridization between native and introduced species (e.g., between native northern watermilfoil and invasive Eurasian watermilfoil).

Finally, while correct species identification is essential for determining whether a population should be managed or preserved, that information alone may not be sufficient to determine the specific management strategies or actions. Individuals within a species can differ in traits that are important for management, including growth characteristics and susceptibility to specific control measures. For example, DNA barcodes for species like Eurasian watermilfoil and hydrilla alone would not distinguish known herbicide resistant versus susceptible varieties, which require more extensive genetic research and tools.

Looking ahead

DNA barcoding is helping transform aquatic plant identification from a process that relies on increasingly scarce, specialized taxonomic expertise to one that also incorporates standardized genetic evidence that can be reproduced, shared, and expanded as reference libraries continue to grow. As reference databases grow and additional barcode markers are developed, these tools will become increasingly useful for researchers and lake managers alike. While DNA barcoding is not a replacement for botanical expertise, it is an important

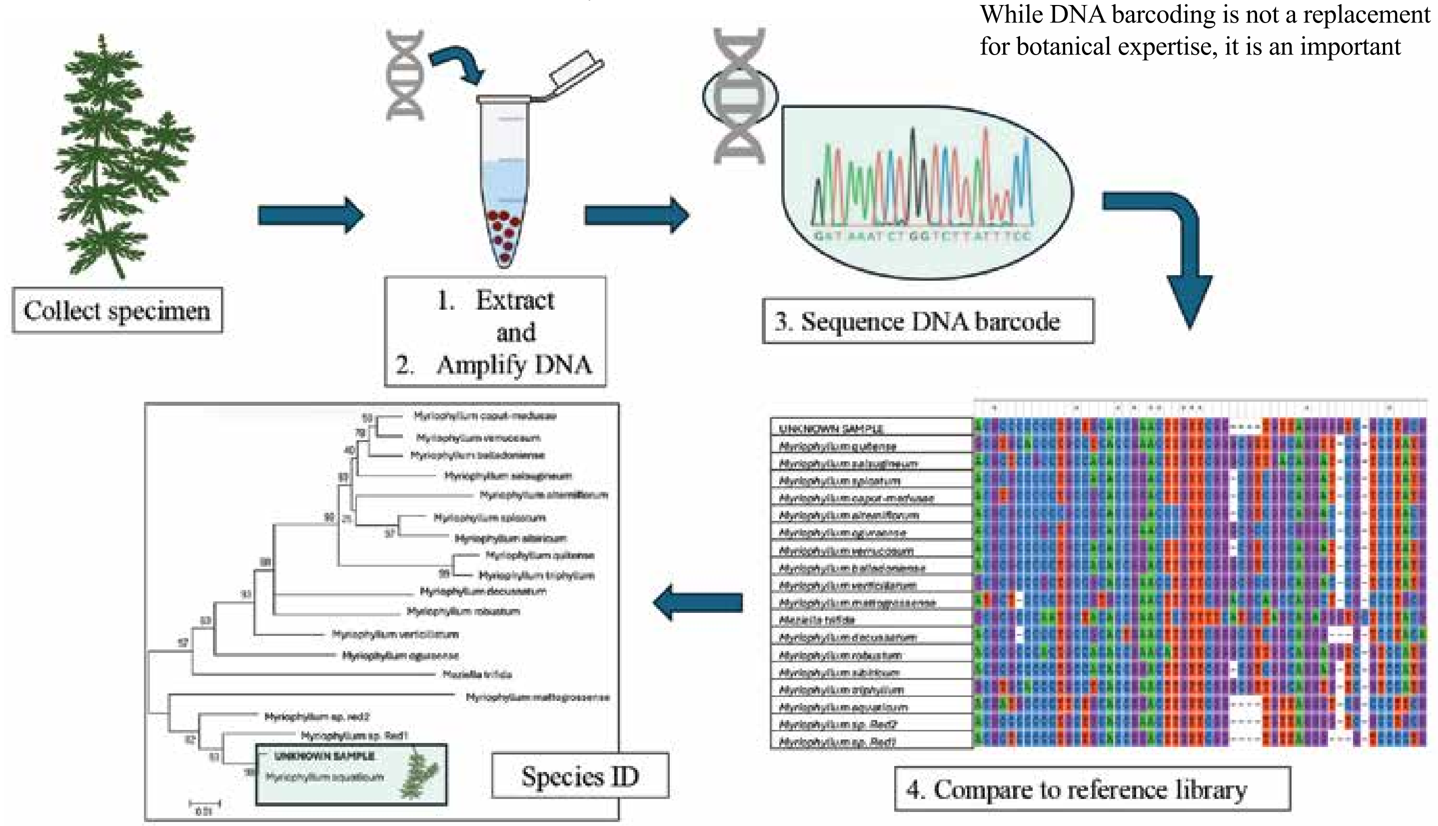


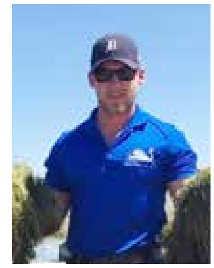
Figure 2. How DNA barcoding works.

addition to the aquatic plant management toolbox. Continued investment in developing and validating barcode resources for aquatic plants will improve species identification, support more informed management decisions, and help protect aquatic ecosystems.

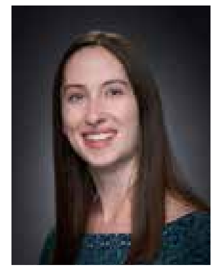
Ryan Thum is a professor of ecological genetics and genomics of aquatic and invasive plants. His general fields of interest encompass evolutionary and molecular ecology, with a specific emphasis on invasive aquatic species. His research is rooted in conceptual evolutionary ecology, but aims to contribute conceptual knowledge and understanding to guide practical decision making and solutions regarding invasive species – one of the world's most pressing environmental problems. Most of his research is organized around the simple idea of how genetic variation influences invasive plant management outcomes.

Gregory M. Chorak, PhD, is research faculty in the Department of Plant Sciences and Plant Pathology at Montana State University. His research focuses on the genetics, genomics, and identification of aquatic plants, with an emphasis on invasive species, hybridization, and the application of molecular tools to support aquatic plant management.

Del Hannay is a graduate research assistant in Dr. Ryan Thum's lab at Montana State University. Their work focuses on the genetic basis of adaptation to herbicide treatment in invasive Eurasian watermilfoil. Broadly, their research interests include answering questions on what patterns of genetic diversity exist within and among species, and how this diversity contributes to adaptation. They can be contacted at del.hannay@student.montana.edu.



Zachary J. Kuzniar was an invasive plant scientist based in Boise, Idaho. He conducts research at Montana State University on the genetic diversity of aquatic plants and how those findings inform management strategies. He also works as a technical sales representative for Cygnet Enterprises, specializing in herbicide-based management of lakes, ponds, and irrigation canals.



Ashley Wolfe received both her BS and MS from Montana State University. She completed her master's degree in Plant Science in Dr. Thum's lab in 2024, during which she developed MilfoilMapper, an interactive database designed to support watermilfoil research and management. Ashley continues her work in Dr. Thum's lab, now serving as a research associate. Her research focuses on exploring the variation in Eurasian watermilfoil strain response to the herbicide florpyrauxifen-benzyl, as well as performing genetic identifications of various invasive aquatic plant species.

Plant identification **using DNA "barcodes"**

Nic Tippery

Overview

Organismal diversity, often measured as the number of biological species present in a habitat, is a primary concern for lake managers. High-quality, pristine habitats often have an abundance of native species, whereas non-native species, particularly invasive species, can be cause for concern. In many cases, closely related native and non-native species can be challenging to tell apart, even for experts. Aquatic plants are particularly notorious for being difficult to identify, because they often have simplified morphology, because specimens may lack reproductive structures like flowers or fruits, and because many species have the potential to hybridize and produce morphologically intermediate plants. Fortunately, there are methods besides morphological features that can be employed to identify plants.

One strategy is to use "molecular" data, typically DNA sequences, to identify plant specimens. DNA consists of nucleotides (A / C / G / T), and the two strands of DNA make complementary "base pairs"(A with T and C with G) (Figure 1). The full set of nucleotide sequences for an organism comprise its genetic code (or "genome"), basically the instructions for how to build and maintain it. In a string of just 20 nucleotides there are over one trillion ways to arrange the nucleotide letters, so it's effectively impossible for two species to have entirely identical DNA sequences. (However, closely related individuals can have very similar DNA, because they inherited the same genetic code from a recent shared ancestor.) Over the past 50 years, there have been myriad efforts to document the diversity of life by sequencing DNA, sometimes one gene at a time, and sometimes an entire genome (i.e., all the DNA that exists in the organism).

"Identifying" an organism by its DNA sequence amounts to matching a sequence from the unknown organism against a database of known sequences (Figure 2). DNA sequences that have been reported in scientific publications reside on a public database called GenBank (https://www.ncbi.nlm.nih.gov/genbank/). If there are enough sequences published online to make an effective comparison, then new DNA sequences can be matched to those. However, if reference sequences are lacking, new sequences must be generated before an effective comparison can be made. Ultimately, DNA sequences are only reliable if the source material was correctly identified and if the molecular lab work was done carefully. Occasionally there are errors in the system, but these occur very rarely; a recent study found only about 50 misidentified sequences out of around 5,000 that were being evaluated (Tippery 2026).

There have been various efforts to decide on a consensus set of DNA regions that can be used across plants as a "universal barcode". When researchers publish data for the same DNA region across many species, then that region can be sequenced in unknown plants, regardless of which group of plants they belong to. Among the most commonly available and frequently used "barcodes" are several chloroplast regions, including the *matK* and *ndhF* genes. DNA from the

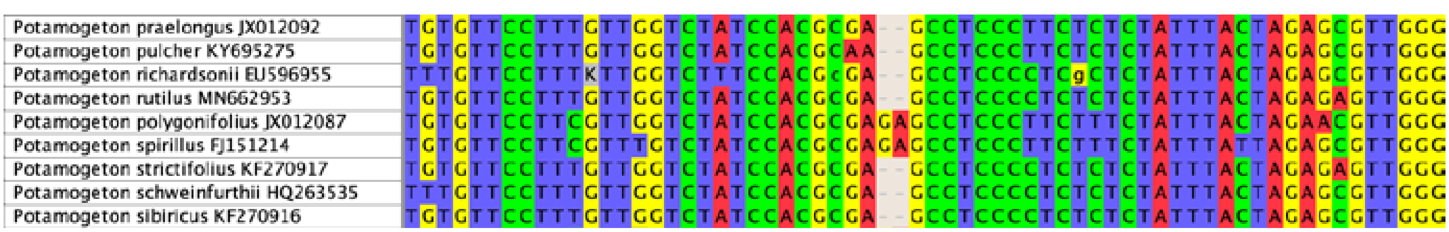


*Figure 1. Portion of an alignment of DNA sequences from the internal transcribed spacer (ITS) region for species of pondweed (*Potamogeton*). One such alignment often consists of 500–2,000 nucleotides (A / C / G / T). (This alignment shows one letter "K,"which means that position could be G or T, indicating some uncertainty or variation.) At most of the positions (i.e., columns), the letters are the same, and this gives a measure of confidence that the same DNA region is being compared across all species. Positions with nucleotide differences are useful for identifying specimens and also for research endeavors like constructing phylogenetic trees. Sometimes DNA sequences have insertions or deletions when compared across species, and these appear as gaps in the alignment (i.e., the positions that have no letters). This alignment was visualized using the program Mesquite (https://www.mesquiteproject.org/).*

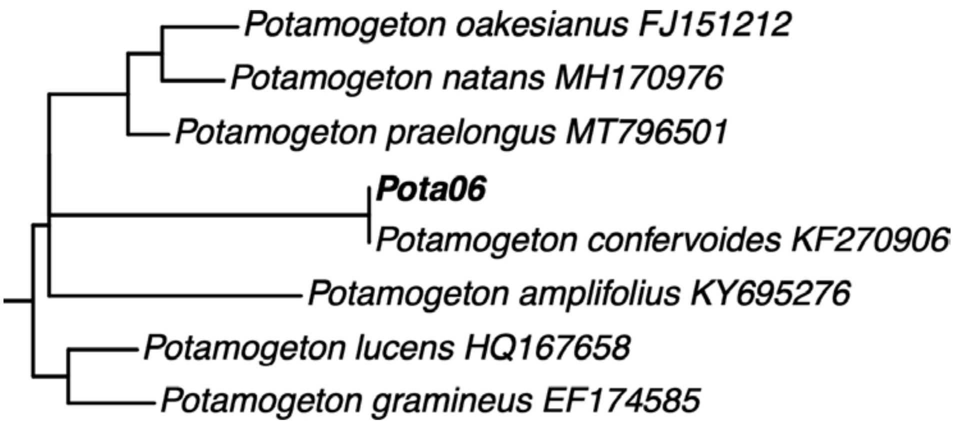


Figure 2. A portion of a phylogenetic tree, showing relationships among species of Potamogeton*. This phylogeny was constructed using DNA sequences from the ITS region. After each species name is an alphanumeric code (e.g., "FJ151212") that represents a sequence in GenBank. The boldface label "Pota06" indicates a plant sample that is being identified, and in this case Pota06 is an identical match to P.* confervoides *KF270906. The phylogenetic tree helps to depict how similar any two species are. Horizontal lines or "branches" have lengths that are proportional to the number of DNA sequence*

chloroplast has two main advantages for barcoding: firstly, there are multiple chloroplasts per cell, thus the DNA can be obtained at a higher frequency from DNA extractions, and secondly, chloroplasts are inherited as one unit, usually from the female parent, thus individual plants usually have only one kind of sequence for a given chloroplast gene. The chloroplast genome is relatively small, at about 150,000 base pairs and 130 genes in most plants (Daniell et al. 2016). DNA from the nucleus, by comparison, is far more expansive and diverse, comprising 125 million base pairs and 25,000 genes in the well-studied model plant *Arabidopsis thaliana* (Arabidopsis Genome Initiative 2000). (Plants also have DNA in their mitochondria, consisting of about 367,000 base pairs and 57 genes, but this DNA has proven to be less useful than chloroplast DNA and is rarely sequenced.)

DNA in the nucleus is far more diverse and expansive than chloroplast DNA. One popular nuclear DNA region used in molecular studies is the internal transcribed spacer (ITS), which is fairly reliable to sequence and provides a rich amount of data across species. Nuclear DNA generally exists as two copies per gene (i.e., "alleles"), and plants can have multiple copies of gene regions if they are "polyploid" (i.e., having 2×, 4×, or more copies of the normal amount of chromosomes). Having multiple gene copies to work with can be helpful for some research endeavors like phylogenetics, but the multiple copies can introduce complications when it comes to simple plant identification. However, nuclear DNA has one major advantage over chloroplast DNA for plant identification, namely that it can be used to identify hybrids. Hybrids are the result of mating between genetically dissimilar individuals, and the term "hybrid" is often used to describe combinations between two biological species. At the level of DNA, hybrids typically retain one version of a nuclear gene from each parental species. Several noteworthy invasive plants are hybrids, such as the hybrid between Eurasian watermilfoil and northern watermilfoil (*Myriophyllum spicatum* × *M. sibiricum*; Moody and Les 2002), and their hybrid origin may allow them to evade detection, adapt in new ways to compete against native species, or escape control efforts like herbicides (Ellstrand and Schierenbeck 2000). Aquatic managers are keen to know when hybrids are present in their lakes, because they might require different control approaches or additional vigilance.

Examples from aquatic plants

Plant identification using DNA barcodes has opened up new avenues for understanding aquatic plant diversity. Several important discoveries have relied upon DNA sequencing, and additional insights are gained every year. Hybrid invasives have been identified in watermilfoil (*Myriophyllum*; Moody and Les 2002), floating heart (*Nymphoides*; Harms et al. 2021), *Phragmites* (Meyerson et al. 2010), and other terrestrial and aquatic plant genera. Some newly arrived aquatic plants in North America have been confirmed using DNA evidence, including *Potamogeton wrightii* (Tippery and Warman 2024), *Utricularia tenuicaulis* and *U.* × *neglecta* (Tippery et al. 2024b), and a distinct subspecies of hydrilla (*Hydrilla verticillata* subsp. *lithuanica*; Tippery et al. 2020; Tippery 2023). A study of DNA sequences in naiads (*Najas*) led to the identification of a previously overlooked species, *N. canadensis*, that is minimally different from the related *N. flexilis* (Les et al. 2015).

Ongoing efforts to catalog and produce reference DNA sequences for plants in North America have enabled a more thorough understanding of some groups. Studies of bladderworts (*Utricularia*; Tippery et al. 2024b), waterhyssop (*Bacopa*; Tippery et al. 2024a), marsh-pennywort (*Hydrocotyle*; Tippery et al. 2026), and others have filled gaps in the available sequence data and enabled all North American species in the respective groups to be identified with barcodes. In addition to targeting specific taxonomic groups, an alternative approach is to barcode all species in a particular geographic region, and such efforts have been fruitful in Canada (Kuzmina et al. 2017) and Wisconsin (Spalink et al. 2018). It is increasingly feasible to build a global database of DNA sequences for all plant species (Zeng et al. 2018; Brewer et al. 2019), and such efforts may be complete in the next decade.

New technologies that enable DNA-based plant identification are enticing and show great promise, but it remains important to stay grounded in traditional taxonomy and morphological plant identification techniques. Plant identifications are only meaningful if we understand them in the context of the biology and ecology of the species involved.

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Nic Tippery is a professor in the Department of Biology at the University of Wisconsin-Whitewater. He conducts DNA sequencing to identify plants, predominantly aquatic plants, and he has published the results of several focused efforts to document the molecular side of plant diversity.

Meteorology, climatology, & lakes

Why weather context belongs in lake assessments

Rick Shema, CCM

Weather Matters: A Three-Part Series

Article 1: Why meteorological context is necessary for interpreting lake and watershed data. (Summer 2026)

Article 2: Case studies showing how weather information has been overlooked, misapplied, or drawn from nonrepresentative stations. (Fall 2026)

Article 3: Practical ways to improve meteorological observations, station selection, analysis, and reporting.(Winter 2026)

The missing story In a water sample

Lake professionals devote considerable effort to measuring what is in the water: phosphorus, nitrogen, chlorophyll-*a*, dissolved oxygen, suspended sediment, temperature, plankton, and other indicators. Those measurements are essential, but they do not tell the entire story. To interpret them properly, we must also ask what the atmosphere was doing over the lake and watershed before, during, and after sampling.

Rainfall moves water and materials across the landscape. Wind mixes the water column, resuspends sediment, drives currents and seiches, and redistributes floating algae. Solar radiation and air-water heat exchange regulate warming, cooling, evaporation, and stratification. Drought reduces inflow and flushing, while fronts and thunderstorms can alter lake conditions within hours.

Weather is not background scenery. It establishes the physical setting in which lake and watershed observations occur. When the weather story is not told, short-term variability may be mistaken for a long-term trend, a watershed response may be confused with an in-lake process, or a sampling-location effect may be interpreted as a lakewide condition.

A lake sample is a snapshot. Meteorology provides the setting needed to understand that snapshot.

Weather, climate, and mesoscale conditions

These terms are related but not interchangeable. Weather describes atmospheric conditions associated with a particular time or event. Climate describes the statistical distribution of conditions over longer periods. Mesoscale weather includes thunderstorms, frontal rainbands, lake breezes, terrain-driven winds, and other features that can vary substantially across a lake or watershed.

Climatological averages are useful for describing what is typical, but lakes respond to actual events, sequences, and energy exchanges. A monthly rainfall total does not reveal whether the rain arrived gently over several days or in a single intense storm. A monthly mean air temperature does not reveal whether the period included calm, clear days that strengthened stratification or windy nights that cooled and mixed the surface layer. The thermal response to changing weather and climate varies among lakes because depth, surface area, volume, and fetch influence heat storage, stratification, and the effectiveness of wind-driven mixing (Figure 1) (Magee and Wu 2017).

Water and material transport

Rainfall: How Much, How Fast, and Where?

Rainfall is often summarized as a daily, monthly, or seasonal total. For lake management, that is rarely enough. Intensity, duration, location, timing, and antecedent soil conditions often matter more than the accumulated amount alone (Figure 2).

One inch of rain falling gently over 24 hours may infiltrate into relatively dry soil with limited runoff. The same amount falling in 45 minutes during a thunderstorm can produce rapid runoff, erosion, channel scour, and a concentrated inflow plume. After several dry weeks, the first runoff pulse may carry pollutants that accumulated across roads, lawns, agricultural areas, and other surfaces. On already saturated soils, even moderate rainfall may generate extensive runoff.

Spatial representativeness is equally important. A storm that strikes an airport but misses the watershed may appear in the official record while having little relevance to the lake. Conversely, a localized thunderstorm over the watershed may be poorly represented by a distant gauge. Radar estimates, nearby gauges, and watershed-based observations should be considered together when convective rainfall is important.

Rainfall can affect lake and stream conditions through several pathways:

- Nutrient loading. Runoff can transport phosphorus and nitrogen from soils, lawns, agriculture, septic-influenced areas, roads, and eroding banks.

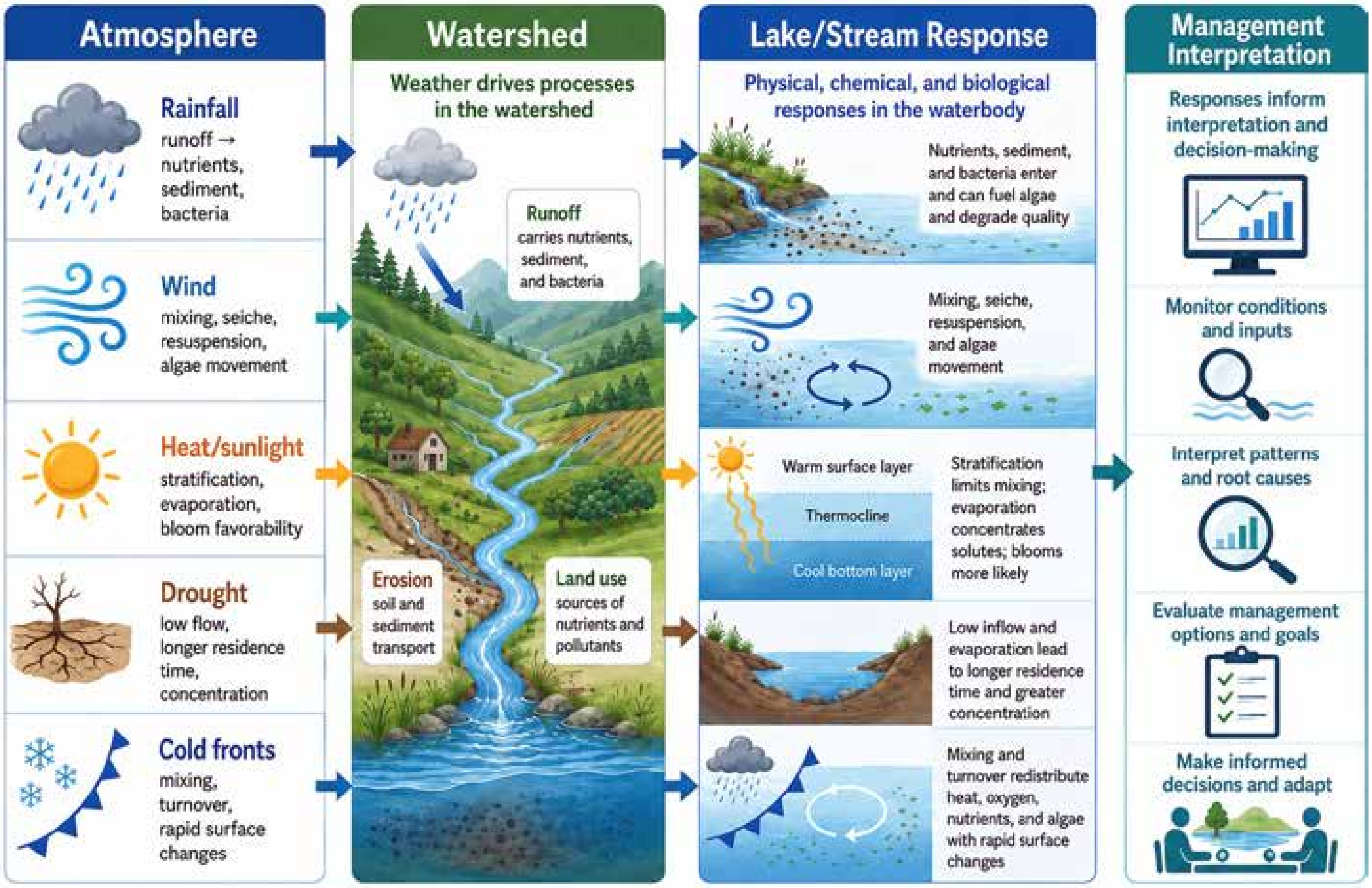

Figure 1. Weather affects lakes through water, energy, and motion. Rainfall moves materials from the watershed, wind redistributes water and algae, and heat controls stratification, evaporation and biological response.

How Rainfall Totals Can Mislead

Three historical events at the same location produced the same rainfall total (1.00 inch) but very different runoff and water-quality responses.

	Event 1: Gentle rain May 15, 2012	Event 2: Steady rain June 28, 2014	Event 3: Thunderstorm August 21, 2018

Event	Gentle rain	Steady rain	Thunderstorm
Rainfall total	1.00 inch	1.00 inch	1.00 inch
Duration	24 hours	6 hours	45 minutes
Peak intensity	0.06 in/hr	0.18 in/hr	0.50 in/hr
Watershed response	Slow, diffuse runoff	Moderate runoff	Rapid runoff
Measured streamflow (Esopus Creek at Allaben, NY)	+35 cubic feet per second (cfs) above baseflow	+310 cfs above baseflow	+2,450 cfs above baseflow
Measured turbidity (Esopus Creek at Allaben, NY)	+12 NTU above baseflow	+85 NTU above baseflow	+310 NTU above baseflow

Figure 2. Equal rainfall totals can produce very different runoff and water-quality responses. Rainfall intensity, duration, soil moisture, land cover, and storm location all influence how much water and material reaches the lake.

- Sediment and turbidity. High-intensity rainfall can detach and transport fine sediment, reducing water clarity and carrying particle-bound nutrients.
- Bacteria. Storm runoff, failing septic infrastructure, wildlife sources, and sediment resuspension may increase bacterial concentrations.
- Channel response. Rapid runoff can scour stream channels, damage habitat, and transport sediment and organic matter downstream.
- Inflow plumes. Tributary water may enter a lake at a different temperature, density, or turbidity and travel over, under, or through the receiving water column.

As an example, a phosphorus concentration measured after a storm may be influenced by watershed runoff and sediment transport. The same concentration after a prolonged dry period may increase the plausibility of an internal source, but timing alone cannot establish causation. Depth profiles, inflow data, sediment conditions, and other evidence remain necessary.

Drought: Low Flow, Long Residence Time, and the Next Storm

Drought is more than the absence of rain. Reduced tributary inflow can decrease flushing, increase residence time, lower lake and groundwater levels, concentrate some dissolved constituents, and expose or alter littoral habitat. Warm, slow-moving water may also favor conditions associated with cyanobacterial blooms.

The sequence matters. A long dry period followed by intense rain can mobilize accumulated material and produce a response disproportionate to the storm total alone. Monitoring and interpretation should therefore account for both the immediate event and the weeks that preceded it.

Motion and redistribution

Wind: Mixing, Waves, Seiches, and Surface Accumulation

Wind is one of the most important and overlooked drivers in lake studies. Wind stress transfers momentum to the water surface, generating waves and currents, producing seiches, tilting the thermocline, mixing the upper water column, and transporting floating material (Figure 3).

In shallow areas, wind-generated waves can resuspend bottom sediment, release nutrients, and increase turbidity. In stratified lakes, strong or persistent wind can deepen the mixed layer, erode thermal stability, and generate internal waves or localized upwelling. Whether substantial mixing occurs depends on wind speed, direction, duration, fetch, lake depth, and the strength of stratification.

Wind also influences what people see. Buoyant cyanobacteria can accumulate near the surface under favorable conditions. Light to moderate winds may

Figure 3. Wind can concentrate floating material along downwind shorelines. A shoreline scum may reflect both biological growth and physical accumulation.

then transport surface material toward a shoreline, cove, marina, or swimming area. A visible shoreline scum can therefore reflect both biological growth and physical redistribution. One part of a lake may appear worse than another even though the spatial difference is partly wind driven.

For lake monitoring, several wind questions should be routine:

- What was the wind speed and direction during the hours and days before the observation?
- Was the wind aligned with the lake's longest fetch?
- Were there several calm days before a bloom report?
- Did a frontal passage deepen the mixed layer or alter the temperature profile?
- Could wind have moved floating algae toward or away from the sampling site?
- Could waves have resuspended sediment in shallow water?

Warmer water, altered rainfall, drought, and stronger stratification may increase the frequency, duration, or severity of freshwater harmful algal blooms, particularly in nutrient-enriched waters (U.S. EPA 2026).

Energy exchange and thermal structure

Solar Radiation and the Lake-Surface Heat Budget

Solar radiation is a primary driver of a lake's heat balance. Some incoming radiation is reflected according to sun angle and surface conditions, while the remainder is absorbed by the water. During sunny, calm periods, surface water warms and becomes less dense, allowing a stable layer to form above cooler, denser water. This reduces vertical mixing and promotes thermal stratification.

Water clarity controls the depth at which solar energy is absorbed. Clear water allows shortwave radiation to penetrate more deeply, distributing heat through a greater depth. Turbid or algae-rich water tends to absorb more energy near the surface, potentially strengthening shallow temperature gradients.

The lake also emits longwave infrared radiation upward, while clouds, humidity, and air temperature influence the longwave radiation returned downward. Additional heat exchange occurs through sensible heat transfer and evaporation. Wind enhances these exchanges and determines whether heat remains near the surface or is mixed downward.

Simplified Lake-Surface Heat Balance

$$Q_{net} = (1 - \alpha)Q_{SW\downarrow} + Q_{LW\downarrow} - Q_{LW\uparrow} - Q_H - Q_E$$

Q_{net}: net heat flux into the lake.

$(1 - \alpha)Q_{SW\downarrow}$: absorbed incoming solar radiation after reflection by the water surface.

$Q_{LW\downarrow}$: atmospheric longwave radiation received by the lake.

$Q_{LW\uparrow}$: longwave radiation emitted by the water surface.

Q_H: sensible heat exchange associated with the air-water temperature difference.

Q_E: latent heat loss associated by evaporation.

With this sign convention, a positive net flux warms the lake and a negative net flux cools it.

Air temperature alone does not explain lake response. Similar air temperatures can produce different outcomes depending on solar radiation, wind, humidity, cloud cover, water clarity, and nighttime cooling. Hot, humid, cloudy nights can limit heat loss. Dry, windy conditions can cool a lake through evaporation even when the air remains warm. These differences affect stratification, dissolved oxygen, habitat, evaporation, and biological activity.

Describing a month simply as "warm" can conceal the processes that control the lake's thermal response.

Rapid Weather Transitions

Cold Fronts, Partial Mixing, and Turnover

Lakes can change quickly during weather transitions. A cold front may bring stronger winds, cooler and drier air, changing cloud cover, and rapid surface heat loss. Together, these changes can weaken stratification, deepen the mixed layer, or produce partial mixing (Figure 4). During spring and fall, frontal passages may accelerate seasonal turnover when density differences within the water column have already weakened. A single event does not necessarily mix every lake from top to bottom. The response depends on lake depth and morphometry, thermal stability, fetch, wind duration, and prior cooling. A calm autumn may delay mixing, while a strong wind event following surface cooling may accelerate it. A subsequent warm period may temporarily restore shallow stability. These transitions can redistribute dissolved oxygen, nutrients, suspended sediment, and organisms. A lake that appeared clear and stable one week may be mixed or turbid the next. Without meteorological context, the change may seem puzzling or may be attributed to the wrong cause.

A Meteorological Record for Lake Interpretation

A full observing network is not always feasible, but every monitoring program should document enough meteorological information to establish the physical setting of each sample or observation. The following should be recorded, evaluated, and incorporated into studies.

- Rainfall amount, duration, peak intensity, and location within the watershed.
- Antecedent rainfall, soil wetness, drought status, and recent inflow conditions.
- Wind speed, direction, duration, gustiness, and alignment with lake fetch.
- Air temperature, surface-water temperature, humidity or dew point, and cloud cover.
- Solar radiation when available, especially for thermal and bloom studies.

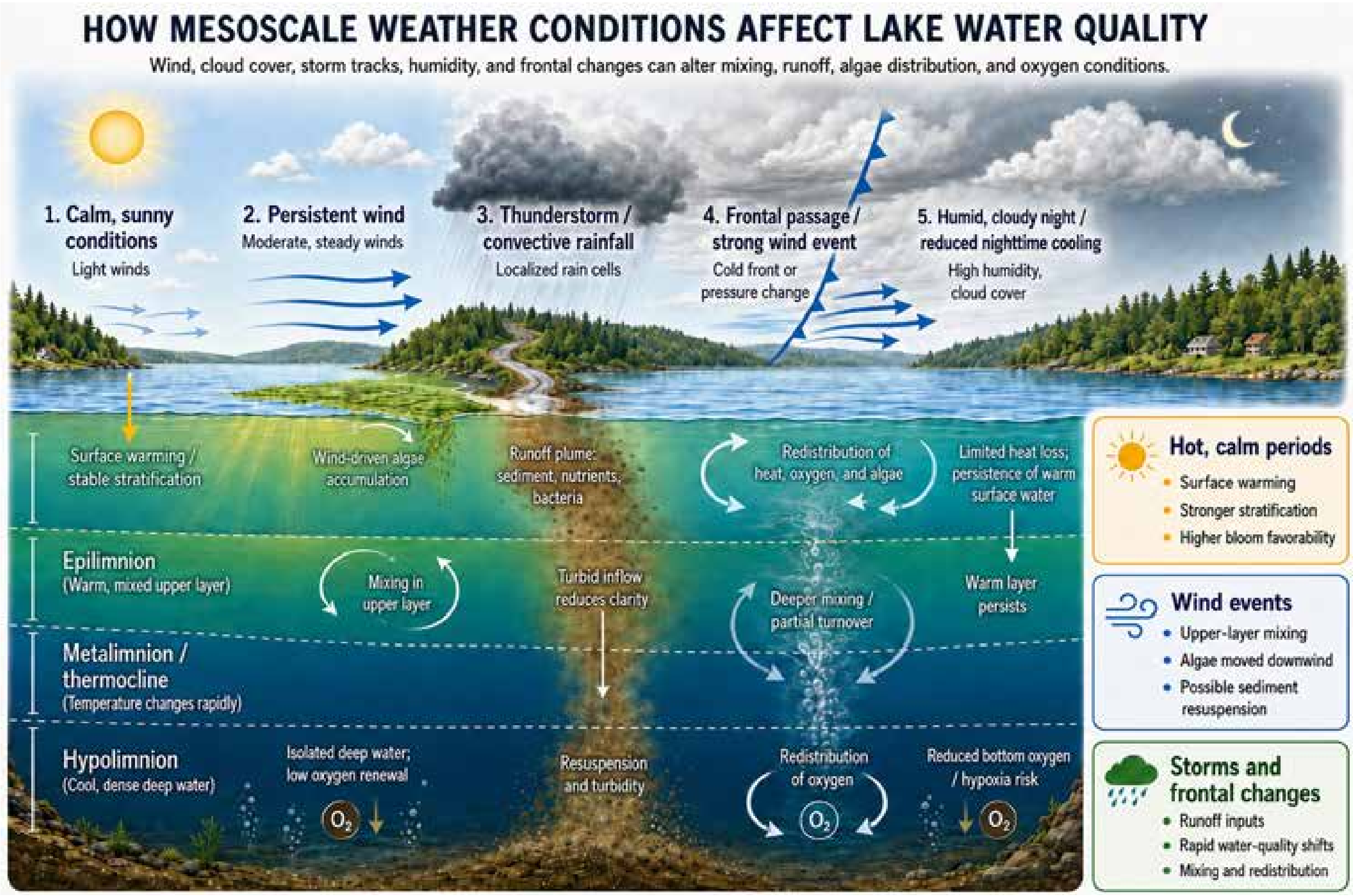

Figure 4. Water quality responds not just to air temperature, but to changing mesoscale weather patterns. Wind, storm timing, cloud cover, and rainfall location determine whether lakes stratify, mix, or receive runoff.

- Passage of fronts, thunderstorms, heat waves, or other rapidly changing conditions.
- The location, elevation, exposure, and representativeness of each weather station or data source.

The third article in this series will discuss appropriate and some practical ways to record weather data in lake assessments.

Station representativenessis essential to data quality

An official station is not automatically representative of a particular lake or watershed. Suitability depends on distance, elevation, terrain, exposure, watershed position, and the meteorological variable being considered. Airport observations may describe regional air temperature reasonably well while missing localized rainfall, lake-breeze winds, cold-air drainage, or terrain-enhanced precipitation.

The appropriate question is not whether a station is official, but whether it measures the conditions that affected the water body. Investigators should document why a station was selected, identify known limitations, and supplement it with radar, gridded data, local gauges, lake buoys, or portable observations when necessary.

Lake sampling already recognizes spatial and temporal variability by using multiple sites and repeated visits. Meteorological observations deserve the same attention.

From Weather Data to Better Decisions

Lake and watershed management is increasingly challenged by intense storms, drought-to-deluge cycles, harmful algal bloom concerns, and public demand for timely answers. Integrating meteorological observations into lake assessments helps managers reach more complete and defensible conclusions by defining the physical setting in which water-quality observations occurred.

Proper meteorological analysis can help answer practical questions such as:

- Was a phosphorus increase associated with a recent runoff event?
- Did drought reduce inflow and increase residence time?
- Did wind move a surface accumulation toward the beach?
- Did a heat wave strengthen stratification and increase oxygen demand below the mixed layer?
- Was a sample representative of the lake, or strongly influenced by timing and location?
- Did the monitoring schedule miss an important storm or frontal passage?
- Was the selected weather station appropriate for the variable and watershed?
- Should future sampling include event-triggered or storm-response measurements?

These are not abstract scientific questions. They affect public communication, management priorities, regulatory interpretation, restoration planning, and funding decisions.

Summary

A lake sample is a snapshot. Weather explains the conditions surrounding that snapshot. Rainfall helps explain runoff pulses and inflow plumes. Wind helps explain mixing, resuspension, and surface accumulation. Surface heat exchange helps explain stratification, evaporation, and thermal habitat. Drought helps explain reduced flushing and the significance of the next storm. Fronts help explain rapid transitions. Simplification of these data can conceal the processes affecting lake water-quality.

Interpreting water-quality data without adequate meteorological context increases the risk of attributing short-term, weather-driven variability to the wrong cause or to a long-term trend. Lakes do not respond to averages. They respond to events, energy, water, motion, and the sequence in which those forces occur. A better understanding of atmospheric drivers leads to better monitoring, more defensible interpretation, and better management decisions.

The next article in this series will examine case studies in which meteorological information was overlooked, misapplied, or obtained from sources that did not adequately represent the lake or watershed.

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Rick Shema is a certified consulting meteorologist (CCM) by the American Meteorological Society. He is also a Penn State Extension Master Watershed Steward and an Associate Director of Wayne Conservation District in Pennsylvania. He received a Master of Science degree in Meteorology and Physical Oceanography.

Student Corner

Edwin O. Wagah

Voices from the Water: Fishers' Ecological Knowledge and Governance Gaps on Lake Victoria, Kenya

Lake Victoria, Africa's largest freshwater lake, is home to one of the continent's most vital and most threatened fisheries. Shared by Kenya, Uganda, and Tanzania, the lake supports the livelihoods of millions of people – yet its fish stocks are declining, invasive species are spreading, and governance remains fragmented. Amid these pressures, one resource is consistently overlooked: the deep ecological knowledge held by the fishers who have lived and worked on the lake for generations.

My research, conducted at two contrasting sites on the Kenyan shore of Lake Victoria – Muhuru Bay and Migingo Island – set out to document that knowledge, understand how fishers adapt to environmental change, and identify the governance gaps that prevent their voices from shaping the policies that affect them. The findings were recently published in *Ecology and Society* (Wagah et al., 2026).

Two very different communities, one shared lake

Muhuru Bay is a mainland fishing community with deep roots in the lake's traditional fishing culture. Life here revolves around Nile perch, tilapia, and dagaa (silver cyprinid), and the community has developed nuanced practices shaped by decades of watching the lake change. Migingo Island, by contrast, is a tiny, rock-strewn outcrop barely 2,000 square metres in size, yet home to hundreds of fishers from both Kenya and Uganda. It sits at the centre of an unresolved territorial dispute between the two countries, creating a uniquely complex governance environment where even basic questions – who makes the rules, and who enforces them? – lack clear answers.

Studying these two sites together allowed us to compare how fishers in very different social and political contexts generate, maintain, and act on local ecological knowledge.

What fishers know – and how they know it

Fishers at both sites demonstrated rich, place-based ecological knowledge accumulated over lifetimes of observation. They could describe seasonal fish movement patterns, identify changes in water colour and temperature as indicators of fish presence, and recount long-term shifts in catch composition that mirror what scientific monitoring has documented – often without access to that monitoring data.

This knowledge is not static. Fishers actively adapt their practices in response to environmental cues: adjusting fishing grounds seasonally, switching gear types as target species shift, and altering hours of operation in response to changes they observe in the lake. Many of these adaptive strategies represent sophisticated responses to ecological variability that formal fisheries science is only beginning to capture.

The governance gap

Despite this wealth of knowledge, fishers at both sites described a persistent sense of exclusion from the decisions that most affect them. Regulations – on gear types, closed seasons, and licensing – are typically designed at the national or regional level, with little meaningful input from fishing communities. Fishers described rules that are difficult to comply with, poorly communicated, and unevenly enforced, particularly on Migingo Island where overlapping Kenyan and Ugandan jurisdictions create confusion and opportunity for exploitation.

The result is a growing disconnect between formal governance and the lived realities of lake-dependent communities. Rules that might work in theory fail in practice because they are designed without the contextual knowledge that fishers hold.

Why this matters beyond East Africa

The challenge of integrating local ecological knowledge into formal governance is not unique to Lake Victoria. Across North America and beyond, lake managers are grappling with similar questions: how do we move from top-down regulatory frameworks to more inclusive, adaptive co-governance models? How do we formally recognize the knowledge of people who have spent decades watching a lake from the water rather than from a laboratory?

NALMS members working on volunteer monitoring, community engagement, and adaptive management will recognize these tensions immediately. The East African context offers both a cautionary tale and a source of inspiration. Fishers on Lake Victoria are not passive observers of decline – they are active problem-solvers whose knowledge and adaptive capacity represent an under-utilized asset for sustainable lake management.

A call for co-governance

Our paper argues for a fundamental shift in how fisheries governance on Lake Victoria – and in freshwater systems more broadly – is approached. Specifically, we call for the formal recognition of fishers' ecological knowledge as valid evidence in policy processes, the meaningful inclusion of fishing communities in governance structures, and the development of co-management frameworks that bridge local adaptive strategies and formal regulation.

Sustainable freshwater stewardship in the African Great Lakes, as elsewhere, will require that we listen to the people who know these waters best. Their knowledge is not merely anecdotal – it is a resource we cannot afford to ignore.

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Wagah, E. O., E. A. Nyboer, Z. M. Gichana, E. O. Ogello, J. Bonzo Osodo, O. Ogeda, T. Kalapos, and Z. Molnár. 2026. Negotiating change in the African Great Lakes: Fishers' knowledge, adaptive strategies, and governance gaps in Lake Victoria's Muhuru Bay and Migingo Island, Kenya. *Ecology and Society* 31(2):12. https://www.ecologyandsociety.org/vol31/iss2/art12

Edwin O. Wagah is a PhD Candidate at Eötvös Loránd University, Budapest, in the Traditional Ecological Knowledge Research Group. His research focuses on local ecological knowledge, fisheries governance, and community-based conservation in the African Great Lakes region. He can be reached at edwinwagah@gmail.com.

UPCOMING IN *LAKELINE*

Below is a list of the proposed topics for upcoming issues of LakeLine. Please take a look and consider submitting an article for a topic of interest. Articles are generally 2000 words or less in length, and should include photos, graphs and/or tables. Co-authors are welcome.

FALL 2026: TOPICS IN LAKE MANAGEMENT – *Draft articles are due by September 30, for publication in October.*

The fall issue will include a range of topics on lake management, without a specific theme. Please consider sharing one of your projects or some aspect of your work related to lakes and lake management for this issue.

WINTER 2026: AGRICULTURE IN WATERSHEDS – Draft articles are due by December 30, for publication in January.

A range of topics related to agriculture in watersheds is welcome, including farm pond management, nutrient runoff, erosion, agriculture BMPs for lake protection, and more.

SPRING 2027: FISHERIES – Draft articles are due by March 30 for publication in April.

Topics related to fisheries ecology, biology, food webs, and management, along with toxins in fish tissue, fish habitat, and other fisheries related topics are welcome

Please contact Amy Smagula, *LakeLine* Editor, with any questions, or to propose an article for one of the above-listed themes. Do you have a topic that doesn't match a theme? That's ok, we can include the article in any of these issues or use it to build a themed issue. Amy can be reached at Lakeline@nalms.org.

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"Lakespert" –

Using eDNA as a Field Work Companion

Guest Author: Ashley Bruhn

The use of Environmental DNA data continues to grow in popularity as an efficient way to conduct biomonitoring within aquatic systems, but can it be a companion to or even a replacement for physical surveys? In 2025 our team out of Denver, Colorado, conducted eDNA sampling in concurrence with our electrofishing surveys. The goal was not only exploring the accuracy and feasibility of this method but also to see if it could be used as a tool to help improve our physical survey method as well as allow for more monitoring when physical surveys were not possible.

We set out to collect from eight different sites throughout our survey area. We wanted as few variables between the eDNA and electrofishing results as possible, so samples were collected just after the completion of an electrofishing session. This way we could match the water quality parameters as well as the real time data collected from the field.

We quickly learned that there was one factor that would challenge both the physical survey and the eDNA collection and that was turbidity. We try to avoid electrofishing after any major storm events but clarity can be an issue even in the best conditions. For eDNA samples, the more water volume you can filter the better, but in most of the samples we were limited to about 300mls, and it took some arm strength to complete filtration.

When the results came in, so came time to interpret them. A large Excel file full of ESV numbers and species names to sort through, names both familiar as well as unexpected (I'm looking at you, Atlantic salmon). Immediately we recognized that common sense would need to be used when interpreting the results. For example, we could safely assume that the *Notropis sp.* detected was not the Topeka Shiner native to the Mississippi basin as reported but rather the Sand Shiner that we had collected over 2,500 of electrofishing. The results also gave us a glimpse of what we could be missing during the physical surveys. Our eDNA samples showed the elusive Channel Catfish, which we know is present in our waterway, but which are rarely collected during surveys due to their nocturnal habits.

Overall, the outcome of this study was very promising. We saw a remarkably close match between the eDNA and what we had captured in the field as well as learned additional information about our waterway. While I am not ready to say that eDNA should replace physical surveys all together, I can say that it has been a useful companion and one we will continue to use in the future.

The team conducting an electrofishing survey.

Ashley Bruhn is a Water Quality Scientist at Metro Water Recovery in Denver, Colorado. She began her career in aquaculture and toxicity testing before joining Metro in 2018. Since then, she has worked in both laboratory and research settings, focusing on nutrient and metals analysis, treatment process optimization, and pilot-scale studies. Today, her work centers on macroinvertebrate, fish, and algae monitoring throughout the South Platte River Basin. Outside of work, Ashley enjoys exploring Colorado's trails with her Golden Retriever, Griffin, and spending time kayaking and paddleboarding.

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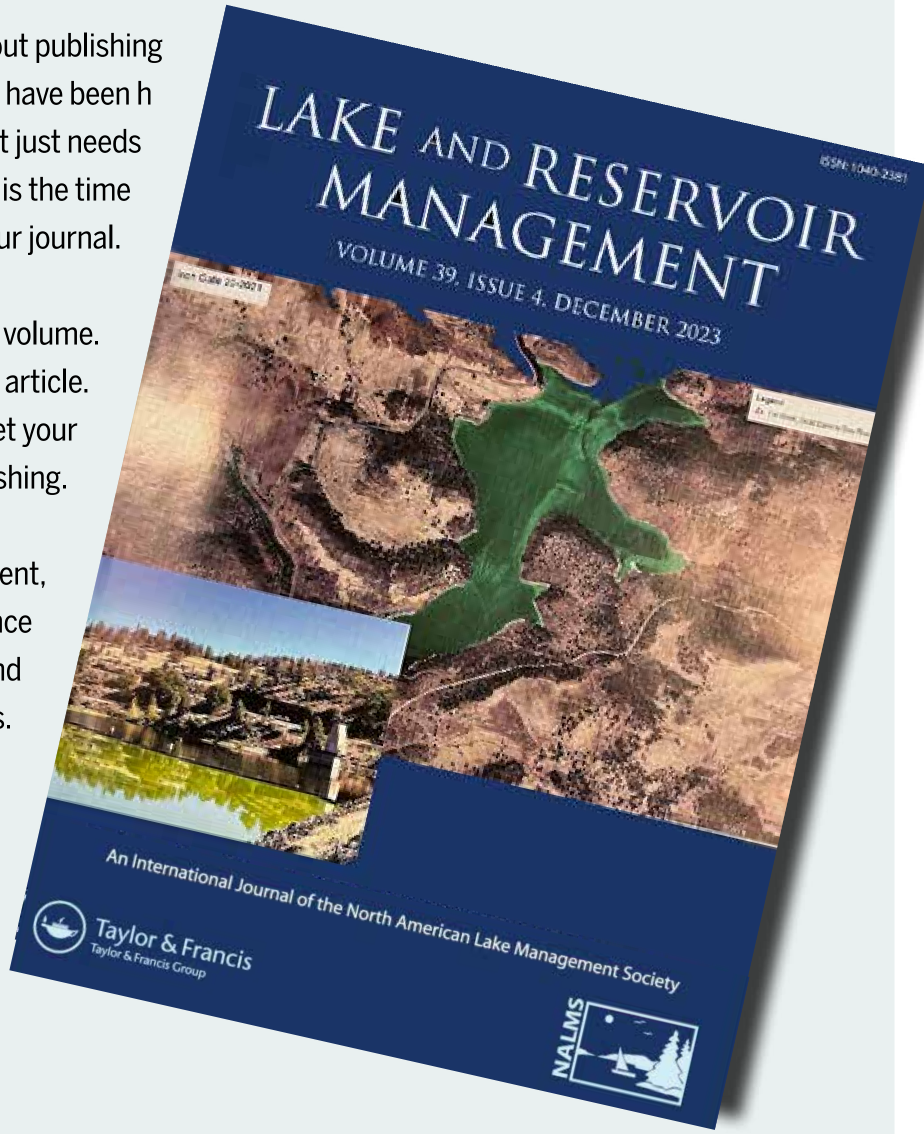

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