



# LUNGFISH

## 2025 Annual Report



INKFISH



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# INTRODUCTION

When traditional public health surveillance falters, the environment keeps talking. Pathogens leave traces in the water we flush and the air we breathe, signals that can warn communities about disease spread days or weeks before people show up sick at clinics. **Lungfish exists to help communities listen to these signals, expanding environmental monitoring programs that provide timely, unbiased information about circulating pathogens.**

The need for this work has never been more urgent. The COVID-19 pandemic revealed both the promise and fragility of public health infrastructure in the United States. In the years since, that infrastructure has continued to erode, with federal support for surveillance programs declining sharply under the current administration. Environmental monitoring offers something increasingly rare: pathogen data that doesn't depend on whether individuals have access to healthcare, whether they choose to get tested, or whether conventional testing programs exist at all. **It provides a community-level view of disease that complements, and sometimes substitutes for, clinical surveillance.**

Metagenomics, detecting all the pathogen genetic material in a sample, is at the heart of our work. **Rather than testing for one pathogen at a time, metagenomic sequencing captures genetic material from everything in a sample, creating a comprehensive snapshot of what's circulating in a community.** Applying metagenomic tools to wastewater and air samples is a major focus of the Lungfish project.

We have already built a network of **more than twenty wastewater sites** using this technology. Eight of these sites now share their data publicly through a dashboard we created, and we're actively working to bring more partners into this transparent model. By sharing data directly with health departments, our team helps public health professionals identify key data and insights that they can message to their local communities to help the public protect themselves. This builds trust with all of our partners and the communities they serve.

Metagenomic sequencing has already proven its value. This year, we detected measles in wastewater from two different states before any cases had been reported to public health authorities. That early warning gave public health officials precious time to respond and encourage vaccination among hesitant community members. This work is critical as measles makes a troubling comeback amid declining vaccine confidence. **Beyond pathogen detection, wastewater can reveal how communities respond to illness through metabolomics.** We can detect spikes in cough syrup metabolites when influenza-like illnesses surge, adding another dimension to our understanding of disease burden.

Wastewater monitoring works best where wastewater treatment exists and provides community-level data. **To extend pathogen surveillance to specific facilities like schools, hospitals, airports, and homes, we've deployed air samplers to collect material from the air.** In the United States, we partner with facilities to collect air samples whose data can be shared with local public health departments, and in some cases, like Public Health Madison and Dane County, this data appears on public dashboards alongside other respiratory illness indicators. Air sampling can be paired with rapid, on-site testing using point-of-care instruments like the Cepheid GeneXpert or Biofire. These tools deliver results in under two hours, giving facility managers actionable information about circulating pathogens that they've never had access to before. We've published preprints this year describing our air sampling work in schools and airports, demonstrating the feasibility of this approach across different settings.

Air monitoring is equally valuable in low- and middle-income countries where respiratory virus testing is limited or unavailable, and where wastewater infrastructure may not exist. This year, we successfully detected SARS-CoV-2 and influenza A through air sampling at the Macha Hospital in Zambia, demonstrating that **this technology works in resource-limited settings.** We're expanding our air monitoring work to track tuberculosis in Nepal, with programs in multiple locations in Brazil and Taiwanese hospitals expected to launch early next year.



Dave O'Connor, PhD  
UNIVERSITY OF  
WISCONSIN-  
MADISON



Shelby O'Connor, PhD  
UNIVERSITY OF  
WISCONSIN-  
MADISON



Marc Johnson, PhD  
UNIVERSITY OF  
MISSOURI



# IMPACT

EARLY-WARNING SURVEILLANCE  
TURNS INVISIBLE VIRAL SPREAD INTO  
ACTIONABLE INSIGHT



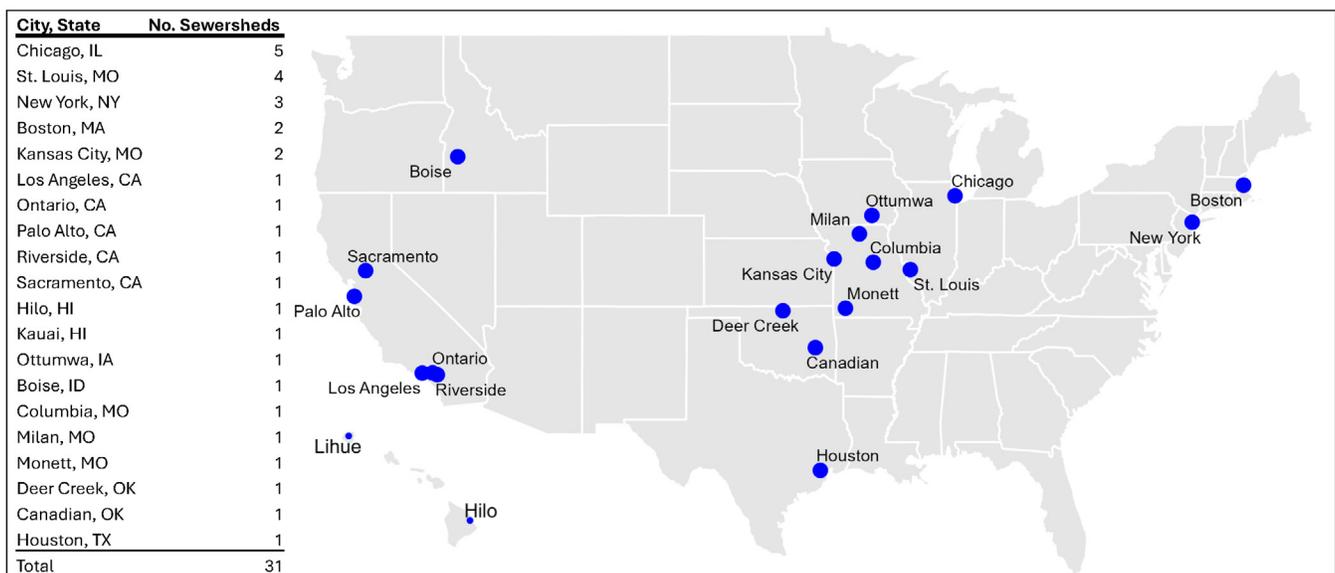
## Water Surveillance Identifying Silent Outbreaks

Wastewater surveillance is a powerful public-health tool that looks for pathogens and other biological signals in sewage and environmental water samples. Because people and animals often shed viruses before they feel sick, wastewater can provide an early warning that an outbreak may be developing. It also offers a practical and cost-effective way to monitor entire communities without relying on large numbers of individual tests.

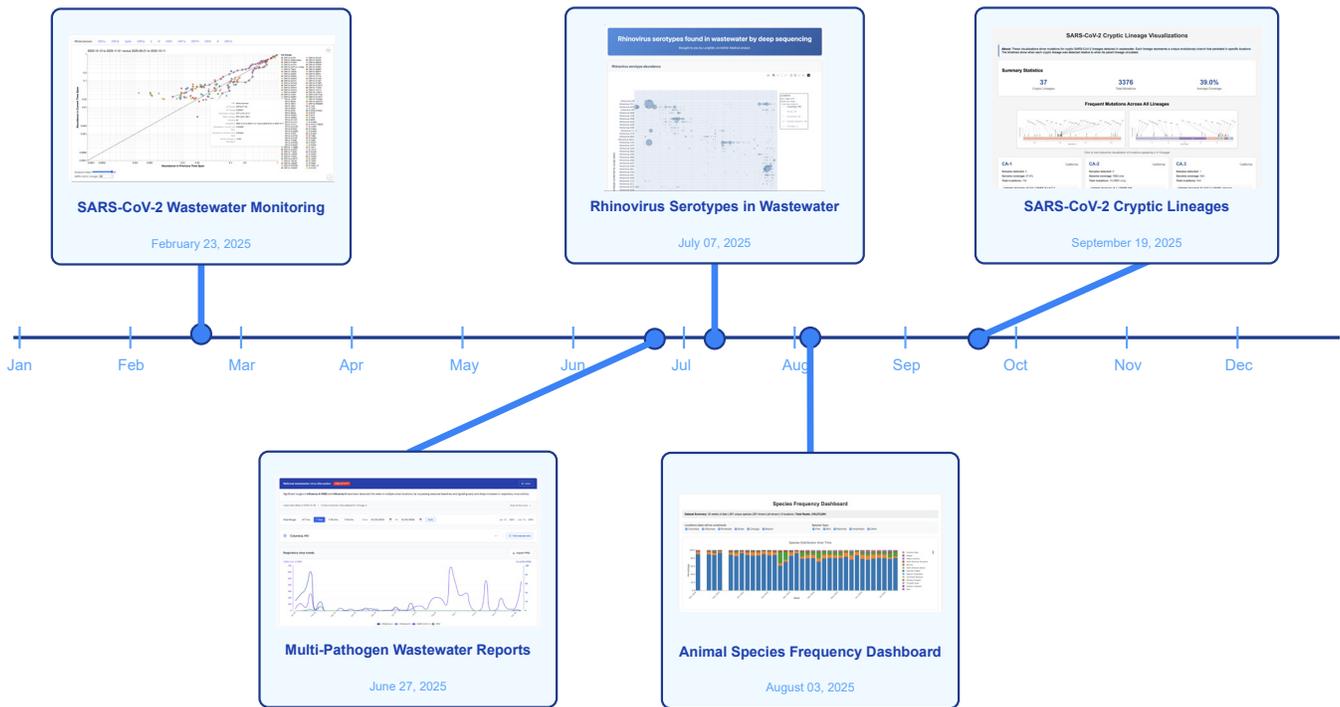
Our team uses a particularly powerful technique for virus detection in wastewater. We use wastewater metagenomics,

which is a method used to sequence all the genetic material in a sample. Think of it as casting the widest possible net: rather than looking for one specific pathogen in water, we can detect thousands of viruses and microbes simultaneously.

In 2024, we were conducting weekly wastewater testing in Columbia, Missouri using metagenomics. We consistently detected the pathogens we expected such as SARS-CoV-2 and influenza A, and we also identified several surprises, including influenza C, H5N1 avian influenza, and Hepatitis A. These unexpected findings show that comprehensive



Lungfish Wastewater Testing Sites



## 2025 Lungfish Public Dashboard Releases

surveillance can reveal both familiar threats and emerging dangers that might otherwise go unnoticed. We submitted a paper summarizing 18 continuous months of sampling and sequencing from this location. Building on this early success, we have now expanded weekly wastewater sampling and sequencing to 30 sites in 11 states.

To best support public health, we process samples rapidly and provide feedback to public health departments as quickly as possible. Data comes from wastewater that we sequence and wastewater sequenced by other groups whose data is publicly available. Results from these analyses are shared with public health so they can message key points to their communities. For data that can be shared publicly, we have created a compilation of public dashboards that anyone can explore. We currently have five dashboards that we regularly update:

- **SARS-CoV-2 Wastewater Monitoring:** This dashboard compiles publicly available data to track individual SARS-CoV-2 variants circulating globally. It is designed for technical users to track individual viral mutations over recent history and assess whether they are increasing or decreasing in the overall population. This can be valuable for understanding which SARS-CoV-2 variants are spreading and help predict vaccine efficacy.

- **Multi-Pathogen Wastewater Report Cards:** The metagenomic sequence data we generate and have been approved to share publicly are present on this site. Users can select individual pathogens to view trends across the cities over time. Users can also look at an entire panel of respiratory, enteric, or animal viruses detected from a single sewershed over time. Patterns can vary widely across sites; for example, some pathogens that primarily infect pigs are found in Ottumwa, IA which houses a large pig processing facility, rather than at O’Hare airport in Chicago. Other viruses, such as seasonal coronaviruses 229E and NL63, may be found in every city but at different times of the year.
- **Rhinovirus Serotypes in Wastewater:** Rhinovirus is the frequent aetiological agent of the common cold, but there are more than 100 different rhinovirus types. This dashboard shows exactly which types are circulating, where, and when. These patterns provide a detailed insight into one of humanity’s most widespread infections.
- **Species Frequency Dashboard:** For each wastewater sample, we also examine sequences of 12S rRNA. This sequence can be used to identify individual eukaryotic species. What can we do with this data? If there is a

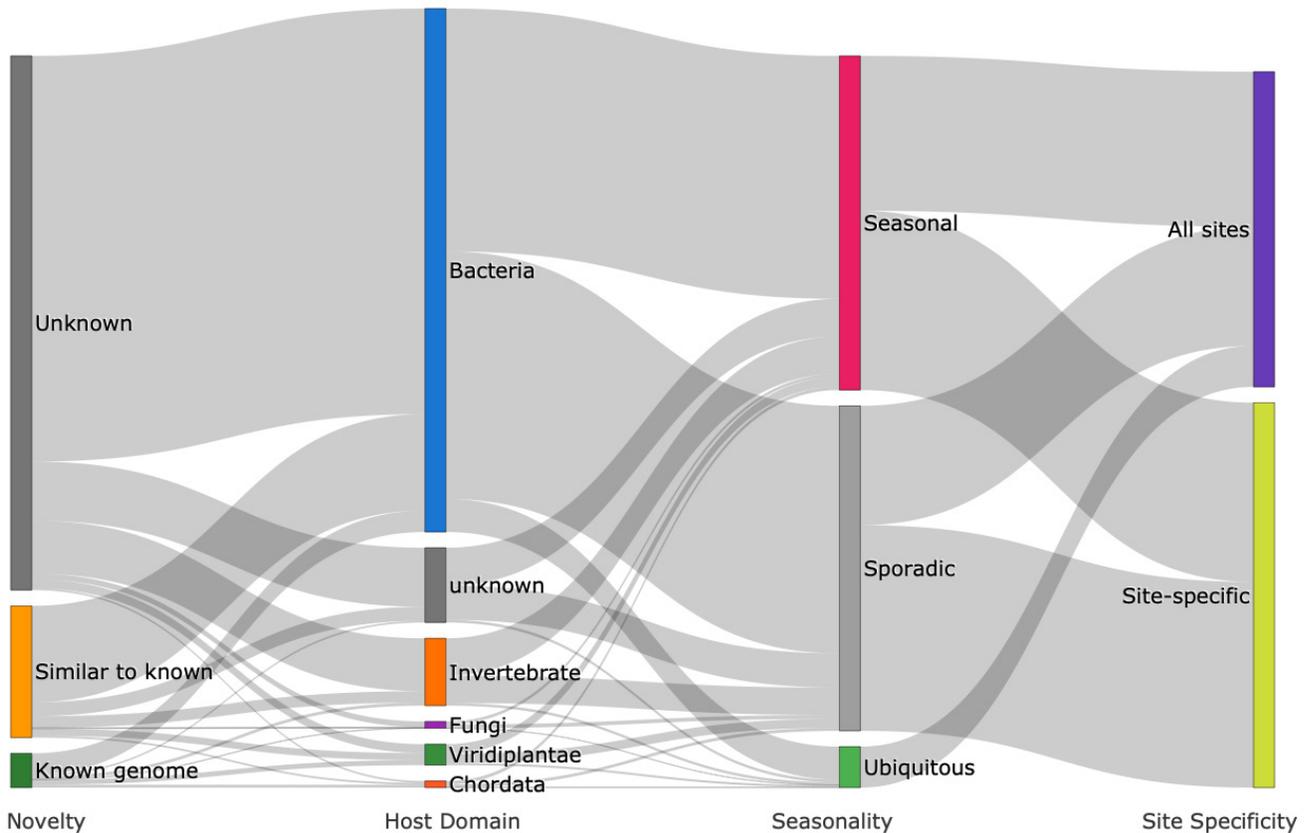


# THE LIBRARY OF WASTEWATER VIRUSES ('VIROME')

Understanding the dynamic viral landscape in sewage and the environment requires determining what viruses are typically present in wastewater itself. Our team is working with scientists at Lawrence Livermore National Laboratory in California and Los Alamos National Laboratory in New Mexico to build a comprehensive reference library of the wastewater virome: the complete collection of viruses typically found in sewage. Between 2023 and 2025, we performed intensive genetic sequencing on 321 samples from six cities in the United States, including Boston, Chicago, and Columbia, MO. We reconstructed complete genomes for more than 20,000 viruses, most of which had never been catalogued before. The host range of these viruses is enormous, with only a small fraction appearing capable of infecting humans. Additional work is being done to expand this catalog so that we have a complete reference of what is 'expected' from wastewater, so that we will be aware when something 'unexpected' is detected.

The graph below shows the characteristics of the top 20,000 assembled genomes by novelty, host domain, seasonability, and site specificity. The conclusion is that most viruses present in wastewater have not been characterized previously, and that the viruses in wastewater are not consistent or static. The composition of viruses in wastewater changes substantially over time and across locations, with many viruses showing strong seasonal patterns and others appearing specific to individual sewersheds. Our lack of familiarity with the majority of viruses underscores the need for environmental surveillance. In the future, we hope that understanding the dynamics of these viral populations will unlock meaningful information about communities they are derived from.

Characteristics of top 20,000 assembled genomes



new virus found in a community, particularly a new influenza strain, we can identify which species are found in that area that could serve as a host for the pathogen.

- [SARS-CoV-2 Cryptic Lineages](#): Wastewater can reveal infections that never show up in nasal swab samples collected at hospitals or clinics. “Cryptic lineages” are

evolved COVID strains shed by people with long-term infections whose cases are unknown to public health officials. These rare lineages offer scientists a unique window into how the virus changes during prolonged infections. This dashboard compiles all the cryptic lineages we detected (published and unpublished) and updates as new lineages emerge. It is intended for a technical audience.

## RESPIRATORY ILLNESS DASHBOARD

With support from the University of Wisconsin-Madison team, Public Health of Madison and Dane County developed its publicly available Respiratory Illness Dashboard. This dashboard provides the community with information for a number of respiratory illnesses, including COVID-19 and influenza. The dashboard is updated weekly and describes various trends including number of new infections, hospitalizations, and school absences among others. One user commented, “We are seniors and it is a marvelous service to help us to keep healthy and wear a mask when and where needed. Also, it encourages us to get vaccinated. Thank you.” Another dashboard user stated: “I am the administrator of a childcare center and I appreciate being able to stay up to date on illnesses in the community to better help our children, staff, and families.”

## Air Sampling as of December 2025

Multi-site Respiratory Pathogen Surveillance

**2,410**

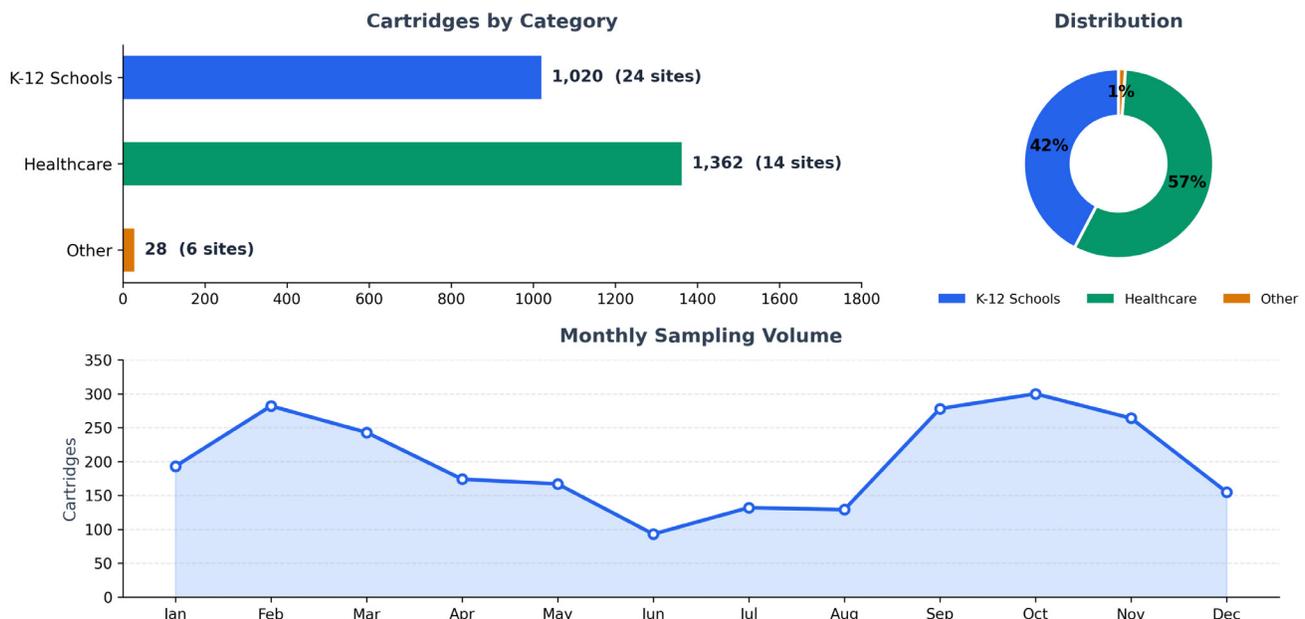
Unique Cartridges

**44**

Collection Sites

**61,533**

Individual Assay Results





**A Lungfish Air Sampler at a Healthcare Facility in Wisconsin**

Wisconsin, our school air sampling results are shared weekly as part of a respiratory illness dashboard maintained and shared publicly by Public Health Madison and Dane County, in addition to data shared on our own Lungfish dashboard. This transparency enables families to make informed decisions about their health and helps officials allocate resources where they're needed most.

**Air sampling proves equally valuable in clinical settings and facilities serving vulnerable populations.** In emergency departments and clinics, detecting viruses in the air can help healthcare professionals design effective infection control measures. In long-term care facilities and other congregate living settings, where residents face elevated risk of severe illness from respiratory infections, air samplers can detect viruses as they are introduced, providing an early layer of protection that individual testing alone cannot offer. The detection of viruses in the air may help clinicians anticipate an outbreak or when staff are at a higher risk for falling ill with a respiratory illness, allowing facility managers to adjust staffing plans to cover sick personnel and ensure that patient care is not interrupted. A major accomplishment of Lungfish in the last year is closing the timing gap between air sampling and virus detection. At four healthcare facilities in Madison, Wisconsin, air samples from healthcare facilities were tested on the same day that the air was collected using Cepheid GeneXpert and Biofire instruments purchased by Inkfish.

## Seeing the Invisible The Impact of Lungfish's Air Sampling Program

Air is essential to life, yet it also serves as the primary transmission route for respiratory infections like influenza, RSV, and COVID-19. **Lungfish's air sampling program captures the genetic material of unseen pathogens circulating in shared spaces, identifying health threats before they lead to widespread illness and giving communities a critical head start.**

Because children in schools have developing immune systems, frequent close contact with their classmates, and may bring infections home to their families, we have prioritized air sampling in schools to help families understand the viruses circulating in their local communities. **We continue to sample air in K-12 schools across Wisconsin and Missouri, testing for up to 30 different targets simultaneously.** In Dane County,



**Dave O'Connor prepares an air sampler at a site in Wisconsin**



The success of our domestic programs has generated interest from partners across the country and around the world. We have established partnerships with sites in several cities beyond Wisconsin and Missouri, providing varying levels of support depending on local needs and capacity. Some programs operate with deep involvement from our team, while others run independently with Lungfish guidance. This expansion helps track regional and national trends while providing municipal governments with actionable data about circulating pathogens, such as influenza, RSV, enterovirus, and adenovirus among others.

Our international work extends air surveillance to settings where it may have the greatest impact. In partnership with Macha Hospital in southern Zambia, we initiated air sampling in July 2025. During an outbreak, we consistently detected influenza A in the air, and we also identified ongoing SARS-CoV-2 circulation that surprised the local clinical team. **In a low-resource setting, the detection of respiratory viruses in the air of well-ventilated rooms demonstrated that air sampling can reveal pathogen circulation that could otherwise go unnoticed.** It could also create a new paradigm for respiratory virus monitoring, since air sampling is dramatically less expensive than comprehensive individual testing. Much like many companies “skipped” landline phones and jumped directly to cellular communications, air sampling for viruses could similarly **provide virus awareness without the cost and resources needed for individual testing.**

In Nepal, we are partnering with the Birat Nepal Medical Trust to address one of the world’s most pressing infectious disease challenges: Tuberculosis (TB). TB remains a leading cause of death globally, killing approximately 1.24 million people in 2024 according to the World Health Organization. Multidrug-resistant TB poses particular challenges for diagnosis and treatment. We are sampling air in TB hostels, facilities that house individuals undergoing treatment for drug-resistant disease, to evaluate whether air monitoring can improve detection of TB in clinical settings. **Success here could transform how high-burden countries approach TB surveillance in clinics, hospitals, and communities.**



**A Lungfish air sampler at a local site in Wisconsin**



# INNOVATION

ENVIRONMENTAL SEQUENCING REIMAGINES VIRUS DETECTION, ENABLING ANYWHERE, ANYTIME SURVEILLANCE BEYOND TRADITIONAL LABORATORIES



## Detecting Viruses in the Environment From Samples to Sequences

Our air and water are full of tiny organisms we cannot see. Most standard tests only look for specific, already-known germs. If we could identify all viruses in an environmental sample at once, we could transform public health by spotting new threats before dedicated tests exist, tracking how viruses change over time, and catching pathogens that routine testing can miss. **This year, we took major steps toward making this kind of broad, practical viral sequencing a reality.**

## The Challenge Finding Needles in Haystacks

The fundamental obstacle is that viruses represent only a tiny fraction of genetic material in any environmental sample. While metagenomics sequencing techniques have existed for some time, the proportion of sequences derived from viruses is much smaller compared to bacteria, fungi, and human cells. This makes it tricky to extract the information about viruses from each sample, so we use two approaches to improve the detection of viruses among this huge pile of genetic data.

The first approach, **unbiased metagenomic sequencing**, captures all genetic material in a sample without discrimination. This generates massive datasets where viral

sequences are needles in a haystack, but the advantage is powerful: it can identify *any* virus present, including novel pathogens no one is specifically looking for.

The second approach, **targeted enrichment**, uses molecular probes to amplify specific viral genetic fragments before sequencing. This method is more technically demanding and requires about two days of laboratory work, but it dramatically increases the proportion of viral sequences detected. The tradeoff is that it cannot detect viruses that do not match existing probes.

## Metagenomic Sequencing Catching Threats Before They Are Recognized

The power of comprehensive sequencing becomes clear when considering emerging diseases. When a new virus appears, targeted diagnostic panels cannot detect it because no one knows to look for it yet. **Metagenomic sequencing has no such limitation.**



Consider what might have been possible in late 2019 and early 2020 if environmental sequencing had been widely deployed. Sampling air at airports and wastewater nationwide could have detected SARS-CoV-2 in the United States within days of its arrival and several weeks before PCR testing became available. The viral sequences themselves would have provided molecular fingerprints showing how the virus was spreading across the country, information that took months to piece together through clinical surveillance.

While generating sequence data is now straightforward using modern Illumina instruments that produce billions of genetic letters in a single run, the real challenge lies in analysis. **We developed computational pipelines that rapidly sift through enormous datasets to identify sequences matching known human viruses, eliminate redundant information, classify specific pathogens, and verify detection accuracy.** For wastewater samples, which represent the collective viral output of entire communities, they have established processing capabilities for more than 20 sites nationwide.



**ISCO Automatic Water Sampler at the Eagle Bluffs Conservation Area in Missouri**

## Environmental Sampling Across Ecosystems

Our long-term vision extends far beyond fixed monitoring sites. **We aim to make viral sequencing possible anywhere, at any time.** In February 2025, we demonstrated this potential by collecting and sequencing air and water samples aboard



**MKT Wetlands in Missouri**

a marine vessel in Panama. After shipping twenty boxes of equipment internationally, we established a complete workflow outside a traditional laboratory and successfully sequenced samples including seawater and indoor air. From seawater, we identified over sixty fish species. From air collected in the ship's kitchen, we detected numerous plant viruses.

This proof of concept showed field sequencing is achievable. We now aim to simplify every step from sample preparation to data analysis to make the process more accessible. Building on this fieldwork capability, we have also conducted weekly monitoring of groundwater at two ecologically important wetland sites in Missouri. The first, Eagle Bluffs Conservation Area, is a restored floodplain wetland sustained primarily by treated effluent from the Columbia Wastewater Treatment Facility and supplemented by seasonal river inputs. Located at the halfway point on the Mississippi Flyway, Eagle Bluffs provides critical habitat for nearly 300 species of migrating and wintering birds.

The second site, the 3M Flat Branch–Hinkson Creek Wetland (also known as the MKT Wetlands), serves as crucial habitat for hundreds of freshwater-dependent animals including migratory birds and endangered amphibians and reptiles. Unlike Eagle Bluffs, this is a natural, stormwater-fed ecosystem.





### Eagle Bluffs Wetlands in Missouri

By sampling both sites in parallel, we can directly compare human-influenced versus wildlife-driven viral signatures. Eagle Bluffs reflects downstream viral diversity linked to municipal wastewater, while MKT Wetlands captures the baseline viral community of a natural ecosystem. Together, they provide a powerful framework for investigating viral persistence, ecological transport, and the boundary between engineered and natural microbial systems. The first year of data established a baseline for future monitoring, enabling the detection of changes, threats, and trends in subsequent years.



**A Lungfish Air Sampler at a Healthcare Facility in Wisconsin**

## Beyond Viruses Monitoring Community Well-being

The applications of wastewater analysis extend beyond infectious disease surveillance. In 2025, we improved our analyses of chemical traces in wastewater. By detecting chemical traces in wastewater, we can reveal stress levels and the use of antidepressant and anti-anxiety medications across the population.

**In 2025, we successfully developed methods to identify more than 25 different chemical markers in wastewater samples.**

The types of chemical markers include stress biomarkers, antidepressants, attention-deficit/hyperactivity disorder medications, antibiotics, analgesics and antipyretics, cough suppressants, buspirone, codeine, oseltamivir and COVID-19 treatment (Paxlovid). These markers provide a community-wide health snapshot, offering up-to-date information about residents' well-being. We are developing an interactive online dashboard that displays this information in visual formats.

In the future, we would like to assess markers related to happiness and mood, such as dopamine and serotonin metabolites, along with other medications. By comparing this data with economic conditions, local events, and health statistics across different communities, we hope to gain a deeper understanding of the factors that affect community well-being.





**Apollo Air Sampler in Pediatric Ward at Macha Hospital**

## Defining the Future of Air Sampling

Bioaerosol sampling, or collecting, biological organisms including viruses from the air, is a field with a century of history that often feels like it is still in its infancy. From Charles Lindbergh collecting Arctic spores in 1933 to the groundbreaking studies by William and Mildred Wells on airborne disease transmission in the mid-20th century, scientists have long known that sampling the air is possible. The challenge has always been determining how to do it effectively across different environments and for different purposes.

No perfect air sampler currently exists. **Our goal is not necessarily to manufacture a new device, but to rigorously test the concepts and mechanics that define what makes a sampler effective for pathogen detection.** We are investigating the difficult engineering trade-offs this work requires: a sampler must be powerful enough to capture microscopic particles, yet quiet and unobtrusive enough for daily use in occupied spaces, all while remaining affordable enough for broad deployment.

To better understand these variables, we recently conducted a controlled chamber study with InnovaPrep. Their Cub instrument proved superior at capturing inactivated SARS-CoV-2 in a laboratory setting, but we have learned that lab performance doesn't always predict field success. This year we showed that \$500, whisper-quiet InBio Apollo instruments successfully captured viral genetic material in real-world sites in Wisconsin. Encouraged by this result, we deployed



**Macha Hospital, Zambia**



**Apollo Air Sampler at Macha Hospital, Zambia**



**Shelby O'Connor Air Sampling Demonstration in Nepal**

these samplers to Zambian clinics and detected an influenza A outbreak, showing that **these simple devices can provide useful pathogen data even in challenging real-world conditions**. This also highlights that effectiveness is not a single metric. What works best depends on whether you are optimizing for a sterile laboratory or a busy clinic, a loud auditorium or a quiet room, or for maximum sensitivity or practical deployment at scale.

**Looking ahead to 2026, we are excited to integrate the ORCHARDS research group into our team.** ORCHARDS (the Oregon CHild Absenteeism due to Respiratory Disease Study) is a long-running, CDC-supported surveillance program in the Oregon (WI) School District that pairs cause-specific

school absenteeism tracking with targeted home respiratory sampling of symptomatic students to identify influenza, SARS-CoV-2, and other common respiratory viruses. We will couple the detection of school index respiratory infections by ORCHARDS with both our ongoing school and growing household air sampling program in the coming year. This combination will help us quantify how reliably different air samplers capture known viruses from the air of households with ongoing transmission. **A future vision of Lungfish is to democratize air sampling so it is available for people in their homes; this is a key step on that path.**

Finally, **we are exploring the boundaries of molecular detection directly from air samples.** We have validated the use of point-of-care diagnostic platforms, including the Cepheid GeneXpert and Biofire Torch, with samples from healthcare facilities. We find these point-of-care tests yield results comparable to standard laboratory tests when applied to air samples. The prohibitive cost of these instruments and their consumables currently makes them impractical for widespread deployment. Despite this economic barrier, **we are utilizing them in targeted settings such as Tuberculosis hostels in Nepal, where rapid detection of airborne Mycobacterium tuberculosis bacteria, the causative agent of Tuberculosis, could transform infection control.** Our primary objective is not to solve cost issues or define integration specifications immediately, but to prove a fundamental concept: that rapid, point-of-care pathogen testing from air samples is scientifically viable and valuable for preventing and containing infections. Once we establish that the science works, the path toward more affordable implementation becomes clearer.

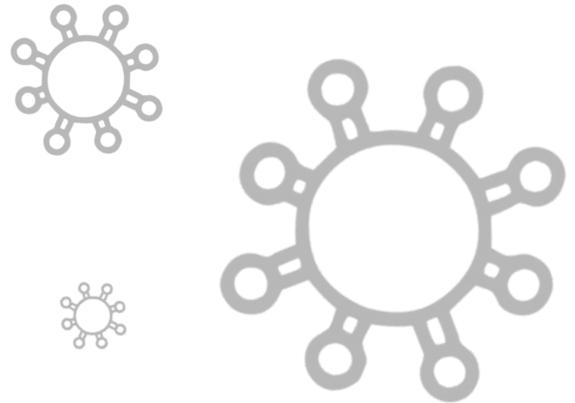


**Lungfish Leadership with Partners in Nepal**



# OUTREACH

BUILDING PARTNERSHIPS THAT SHARE KNOWLEDGE AND CONNECT COMMUNITIES THROUGH COLLABORATIVE ENVIRONMENTAL SURVEILLANCE



## Outreach for Shared Training and Next-Generation Collaboration

To ensure environmental surveillance benefits our communities more broadly, we put collaboration at the center of our approach. Over the past year, we reached out to potential partners across universities, government laboratories, industry, public health agencies, and community organizations. **The goal has been practical: to connect the right expertise, coordinate efforts, and build shared capacity and use for environmental surveillance.**

We are starting to build our most extensive partnerships close to home. By working largely with community-based organizations and schools in Madison, Wisconsin, we are **widening access to environmental surveillance education and creating more ways for people to participate meaningfully.** In previous years, we created activities with a local school and at the university. These types of educational artifacts are laying the foundation for expansions into more sophisticated programs with a greater reach, such as establishing new partnerships with Milwaukee public schools in 2026 and further opportunities at UW-Madison.

In Summer 2025, we launched an enrichment program which enabled 11 college and two high school students to develop technical skills in environmental surveillance while refining their ability to communicate their work to diverse



Lungfish Team in Madison, WI





audiences. They executed their own research projects and their program culminated in a symposium featuring 3-minute thesis presentations. We focused on having participants improve their scientific communication skills because most undergraduate curriculum lack training on how to discuss complex topics with general audiences. **In today's society, explaining scientific research to a general audience has become an imperative.** This activity provided them with an exercise in sharing research clearly and concisely for general audiences. We plan to continue this program in Summer 2026, and we hope to offer it to more students.

Our team is developing an undergraduate course that will be offered at UW-Madison beginning in January 2026. This course will teach advanced skills to prepare students to enter careers related to research and technology in environmental surveillance. We are also developing a 2-week program for high school students to engage in authentic environmental surveillance research in Summer 2026. This education program will then be modified for adult learners interested in exploring pathogen surveillance in their communities. Other activities include an expansion of our summer undergraduate enrichment program as well as educational activities and programming for our air sampling partners.

More globally, we are deepening and expanding our global partnerships. Through active participation and relationship-building, our first-year outreach helped launch several strong programs. Each one is designed to address whether air sampling can be used in different low resource settings to improve health care. For example, we initiated programs with health care facilities at Macha Research Hospital in Zambia and the Linkou Chang Gung Memorial Hospital in Taiwan where we can connect air sampling results to active surveillance projects. **Working with global partners gives us the opportunity to teach others how to develop environmental surveillance programs that could be valuable in their own communities.**

**Lungfish Staff Member Preparing Air Sampling Analysis**



# LUNGFISH TEAM



 University of Missouri



  
**WISCONSIN**  
UNIVERSITY OF WISCONSIN-MADISON



# THANK YOU!

The Lungfish team is grateful to the many partners who contributed their time, expertise, and collaboration during the project's first year, some of whom are listed below. This work would not be possible without the engagement and shared commitment of all our partners. We look forward to continuing these collaborations in the years ahead.

## Inkfish

Christopher Crnich, MD PhD, UW School of Medicine and Public Health

Robin L. P. Jump, MD, PhD, University of Pittsburgh School of Medicine

Catherine Sutcliffe, Johns Hopkins Bloomberg School of Public Health

Dan Shirley, MD, MS, University of Wisconsin School of Medicine and Public Health

Rachael Lancor, Madison County Day School

Andy Wright, EAGLE School of Madison

Amy Proal PhD, PolyBio Research Foundation, Icahn School of Medicine, Mount Sinai

Kari Stampfli, Dane County Schools

Sarah J Breon, Dane County Schools

Grant Higerd-Rusli, MD PhD, Stanford University

Seth Hoffman, MD, Stanford University

Lucas Beversdorf, City of Milwaukee Health Department

Shu-Hui Chen, PhD, Department of Emergency Medicine, Chang Gung Memorial Hospital, Keelung, Taiwan

Kuan-Fu Chen, MD, PhD, Department of Emergency Medicine, Chang Gung Memorial Hospital, Keelung, Taiwan, College of Intelligent Computing, Chang Gung University, Taoyuan, Taiwan

Maria E. Sundaram, Marshfield Clinic Research Institute

Lea Veltum, UW health clinics

University of Missouri-MU Student Center

Maria Cássia Mendes-Correa, Associated Professor, Infectious Diseases Department, São Paulo University Medical School

Sarah Dunstan, Associate Professor, Doherty Institute at the University of Melbourne

Maxine Caws

Raghu Dhital

Birat Nepal Medical Trust

Genetup Laboratory

NATA Morang

TB Nepal

Centre for Molecular Dynamics Nepal

Coalition for Agnostic Sequencing of Pathogens from Environmental Reservoirs (CASPER) partners including:

- Center for Predictive Bioresilience, Lawrence Livermore National Laboratory
- John Dennehy, Queens College, City University of New York
- Jeff Kaufman, Securebio
- Oklahoma Water Survey, University of Oklahoma
- Rachel Poretsky, University of Illinois Chicago
- Jason Rothman, University of California, Riverside
- Helena Solo-Gabriele, University of Miami
- Michael Tisza, Baylor College of Medicine

