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FIELD+GENOMICS WORKSHOP: AN INITIATIVE TO BUILD NANOPORE SEQUENCING CAPACITY IN FIELD-BASED HOST-PATHOGEN RESEARCH

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Abstract. Wildlife disease surveillance has received considerable attention following recent emergence of high-consequence zoonotic pathogens in humans. Increased portability and affordability of sequencing technologies over the last decade have made real-time sequencing of wild animals and their pathogens a reality. Wildlife samples screened for pathogens, however, are rarely permanently archived in museum biorepositories, which limits potential for scientific validation and prevents extension by related disciplines (e.g., ecology, evolution, conservation). To better connect biodiversity and biomedical sciences, the *Museums and Emerging Pathogens in the Americas* (MEPA) network developed the Field+Genomics Workshop to build capacity for surveillance of wildlife and their pathogens in biodiverse countries. Here, we share workshop resources, in English and Spanish, to facilitate reproducibility and expansion of the workshop into the future. The workshop lasted 10 days, 6 days of fieldwork and 4 days of molecular lab and bioinformatic techniques. The field component emphasized the importance of holistic collecting—that is, permanently preserving many parts and symbionts from each sampled organism—as a critical step in wildlife and pathogen surveillance and to build foundational scientific infrastructure. The molecular component of the workshop used samples collected during the field portion to identify hosts and pathogens in real-time. For this component, we trained participants in methods of DNA extraction, library preparation, and Nanopore Adaptive Sampling (a software feature for real-time selective enrichment or depletion of target sequences). Bioinformatic training consisted of a basic introduction to computational genomics, a worked example to analyze a small sequence dataset, and an exercise using data generated from samples collected during the workshop. In total, the workshop cost ~$37K (~$3K per participant), however, ~25% of those funds are invested in basic equipment and infrastructure that is reusable in future workshops (e.g., sequencer, computer, etc.). This workshop highlights the effort and expertise required to conduct voucher-backed surveillance of wildlife and their pathogens and the many benefits of uniting biodiversity and biomedical sciences to build local capacity.

Keywords: bioinformatics, capacity building, Latin America, metagenomics, Nanopore Adaptive Sampling, open science

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Background

Wildlife disease surveillance has received considerable attention and funding following the recent emergence of high-consequence zoonotic pathogens in humans (e.g., Ebola virus, SARS-CoV-2, H5N1) (Watsa 2020; Lawson et al. 2021; Mazzamuto et al. 2022). Host and pathogen biodiversity are greatest in the tropics, potentially leading to increased risk of spillover and a greater need for regular, specimen-backed wildlife surveillance (Cook 2018). The microscopic nature of most pathogens (e.g., viruses, bacteria, fungi, protozoa) requires molecular diagnostic tools for detection and characterization (Aiewsakun and Simmonds 2018). Access to these tools, however, is uneven, posing significant challenges to scientists in regions with higher zoonotic risk who also face difficulties in securing and affording such technologies (Rodriguez-Morales et al. 2021). The increased portability and affordability of genomic sequencing technologies over the last decade—notably, Oxford Nanopore Technology's (ONT) MinION sequencer—has made real-time sequencing of wildlife hosts and their pathogens possible (Lu et al. 2016; Frank et al. 2023; Kipp et al. 2023; De Muelenaere et al. 2024). Pairing holistic sampling of hosts–that is, permanently preserving many parts from each sampled organism–with molecular screens for pathogens allows for the integration of ecological and genomic information to provide a more comprehensive One Health perspective on the ecology and evolution of emerging pathogens (Colella et al. 2023). In addition to health applications, real-time sequencing can further guide field-based sampling efforts through real-time identification of hybrids or detection of undescribed diversity.

Historically, wildlife samples screened for pathogens were rarely permanently archived in museum biorepositories (Colella et al. 2020; Thompson et al. 2021). That lack of sample preservation prevents validation of the original science and further hampers scientific extension by related disciplines (e.g., biodiversity, conservation). To bridge that gap between two otherwise complementary sciences—biodiversity and biomedicine—the *Museums and Emerging Pathogens in the Americas* network (MEPA[1]), a virtual Community of Practice and a branch of Project ECHO[2] (Extensions for Community Healthcare Outcomes), aims to better connect biorepositories with biomedical initiatives across the Americas and build capacity in surveillance of wildlife and their pathogens in biodiverse countries (Colella et al. 2021). To that end, we developed a Field+Genomics workshop, designed to train the next generation of molecularly-enabled field researchers and promote greater health equity through voucher-backed wildlife surveillance. The workshop values traditional specimen-based wildlife sampling as a means of building foundational in-country biodiversity infrastructure and pairs holistic sampling practices with cutting-edge molecular methods of species identification and pathogen detection.

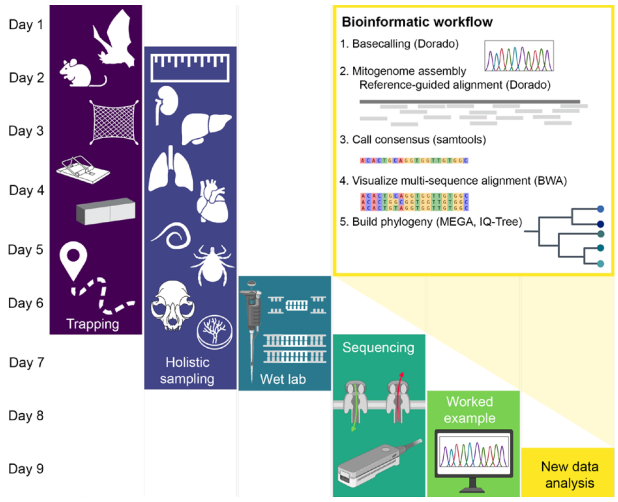

Figure 1. Schematic of the workshop workflow. Field collection of small mammals occurred during the first 6 days and utilized a variety of collection methods, followed by 4 days of wet lab and bioinformatic techniques.

Here, we summarize the 2024 MEPA Field+Genomics Workshop and provide links by which teaching resources can be accessed and adapted for future workshops. The 2024 workshop took place at the Reserva Otongachi Field Station, located close to Union del Toachi, on the border of the provinces Santo Domingo and Pichincha, in Ecuador and lasted 10 days, with 6 days of fieldwork and 4 days of molecular laboratory and bioinformatic techniques (Fig. 1). Twenty participants and instructors attended, representing 8 different countries across the Americas. The field component emphasized the importance of holistic collecting as an important first step in wildlife and pathogen surveillance that builds foundational scientific infrastructure for One Health applications. The genomic component of the workshop used samples collected during the first week of fieldwork to identify hosts and detect pathogens in real-time and train participants in methods of DNA extraction, library preparation, Nanopore Adaptive Sampling (NAS), and basic bioinformatics. All course materials are openly available online in English and Spanish to enable replication, adaptation, or extension of this workshop (see Data Availability).

[1] https://mepa-network.weebly.com/.
[2] https://projectecho.unm.edu/.

Figure 2. Baiting and setting a Sherman live trap in the field. Workshop participant Dr. Camila Acosta-López, Assistant Professor at Universidad Central del Ecuador, sets a trap in the cloud forest transect.

The Workshop

Field component

On Day 1, group introductions were followed by a tour of a local museum biorepository (Museo de Zoología de la Pontificia Universidad Católica del Ecuador [QCAZ]) and discussion regarding the role of museums in biomedical and biodiversity research. A brief welcome lecture (*Introduction to MEPA & Holistic Collecting*) introduced participants to the MEPA network and established expectations for the workshop. Then, the group traveled to the field station. That evening, 500 small mammal traps (live [Sherman box traps] and lethal [museum special, rat traps]; Fig. 2) and 6 mist nets (length = 12 m (2), 6 m (4); height = 3 m, gauge = 38 mm) were deployed, with nets monitored regularly following guidelines by Sikes et al. (2016) and then closed at the end of the night. Day 2 began early by checking traplines.

A morning lecture on *Specimen Preparation* introduced students to five assembly line-style "preparation stations": (1) measurements and data collection, (2) ectoparasites and fungal swabs, (3) tissue collection, (4) endoparasite necropsy, and (5) voucher specimen preparation. Captured small mammals were then processed holistically (Fig. 3, Galbreath et al. 2019), with tissues preserved in liquid nitrogen or DNA/RNA Shield (Zymo Research, Irvine, California, USA) within 15 minutes of euthanasia to maximize molecular quality. Euthanasia was performed by trained personnel (instructors) and followed approved IACUC procedures per Sikes et al. (2016) and the American Veterinary Medical Association (2020). The day concluded with each participant preparing a voucher specimen (e.g., study skin and skeleton), followed by a wrap-up lecture on the value of *Building Biorepository Infrastructure*.

Days 3 through 5 involved checking traps at least twice daily, morning and evening, and holistically preparing collected specimens. Participants rotated among preparation stations each day, such that they were able to learn each skill. As time permitted, lectures focused on *Local Species Ecology*, *Mammals and Disease Ecology, Field Parasitology*, *Natural History Collection Databasing,* and *Holistic Specimen Research Applications.* The time and order of lectures varied based on the number of animals collected each day to accommodate required processing time. During downtime, participants gave a 3–5 minute informal, oral presentation about their background, research interests, and future plans for the application of information learned in the workshop.

The number of field days included in the workshop will depend on the scientific goals of the expedition and capture success. For training purposes, we recommend no less than 3 to 4 days of fieldwork but, minimally, specimen yields must be sufficient for strategic genomic sequencing during the second half of the workshop. All lecture slides are available in English[3] and in Spanish[4].

Genomic component

Wet-lab.—Day 6 began the genomic component of the workshop with DNA extractions. Our DNA extraction procedure takes approximately 4 h (3 h active, 1 h wait time), followed by a concentration step of variable duration depending on extraction yields[5]. We started extractions in the morning to ensure sufficient time for concentrating in the afternoon. Lectures occurred during breaks in the extraction procedure and included an *Introduction to Genomic Sequencing Methods* and *Applications of Nanopore Sequencing*. On Day 7, hands-on Nanopore library preparation began at 08:00 h. A maximum of 24 samples can be multiplexed with the ONT Native Barcoding Kit (SQK-

[3] https://doi.org/10.6084/m9.figshare.28736396.v2.

[4] https://doi.org/10.6084/m9.figshare.28736417.v2.

[5] https://doi.org/10.6084/m9.figshare.28744844.v1.

Figure 3. Demonstration of a holistic specimen preparation assembly line that included five stations: (1) species identification and measurement, (2) ectoparasite examination and fungal swab collection, (3) tissue necropsy, (4) endoparasite examination, and (5) voucher specimen preparation. On Day 2, workshop participants observed the process. On Day 3, participants started rotating through each station.

NBD114.24) and sequenced simultaneously. The number of samples selected for sequencing will vary depending on the scientific goals of the expedition, trap success, desired sequencing depth, and diversity of species sampled, among other variables (e.g., Frank et al. 2023, Kipp et al. 2023). Limited by the size of our heat block (n = 12) and number of pipettes available to the group (n = 8), we divided participants into two groups and processed 24 samples in two batches of 12.

That structure allowed Group Two to watch each step of the procedure performed by Group One, before trying it themselves. Day 7 culminated in loading the flow cell (≥ R10.4.1) and starting sequencing, ideally around 18:00 h (Fig. 4). Duration of sequencing depends on the scientific goals, with longer run times yielding more data. Adaptive sampling is a software-based enrichment or depletion method unique to ONT that selectively sequences a targeted subset of genetic material from a genomic sample (Martin et al. 2022). Here, we performed two sequencing runs: (1) an enrichment run for host and cestode mitochondrial genomes to confirm host and cestode species identity, and (2) a depletion run to recover potential pathogens and microbial symbionts. Adaptive sampling of mitochondrial genomes, which are commonly used for species identification, requires less time than adaptive sampling of a larger part of the nuclear genome (Wanner et al. 2021; Kipp et al. 2023) for two reasons: (1) the mitochondrion is smaller (~16 kbp) and (2) there are many more copies of mitochondria per cell compared to the nuclear genome (Naue et al. 2024). To adaptively sequence mammalian mitochondrial genomes, we budgeted 24 h of run time. During mitogenome sequencing, we iteratively checked output data volume and flow cell health (e.g., number of available pores), and performed test assemblies to estimate sequencing depth.

We then performed a depletion experiment, using the genome assembly of a common vampire bat (*Desmodus rotundus,* NCBI RefSeq assembly: GCF_022682495.1) to deplete host DNA, thereby enriching the metagenomic community for downstream pathogen identification. We ran the depletion experiment until <10% of pores on the flow cell were producing sequence data (~32 h).

Bioinformatics.—Day 8 opened with an *Introduction to Bioinformatics* lecture. While the sequencer ran, we used a "worked example" to practice a basic bioinformatic workflow for processing NAS data. Kipp et al. (2023) published a straightforward example of how NAS can be used to selectively sequence DNA-based bacterial pathogens in black-legged ticks (*Ixodes scapularis*). For this exercise, we used Kipp et al.'s depletion dataset, which was adaptively sequenced such that tick sequences were selectively removed (depleted), increasing the probability of

Figure 4. Demonstration of Nanopore Adaptive Sampling, molecular lab, and bioinformatic protocols. Alexander Hey, University of Kansas graduate student, shows workshop participants details of Nanopore sequencing.

Table 1. Sequencing results for two Nanopore Adaptive Sampling (NAS) experiments conducted during the 2024 *Museums and Emerging Pathogens in the Americas* (MEPA) Field+Genomics Workshop. The pathogen depletion run, rejected reads that matched the host (e.g., common vampire bat, *Desmodus rotundus*; NCBI RefSeq assembly: GCF_022682495.1). The mitogenome enrichment run sequenced reads that matched mammalian and cestode mitogenomes with at least 70% sequence identity.

NAS Summary Statistics	Pathogen "depletion" run	Mitogenome "enrichment" run
Total Data Produced (pass + fail)	58.4 GB	57.57 GB
Estimated Bases	4.85 Gb	4.83 Gb
Reads Generated	1.5 M	1.7 M
Estimated N50	5.69 kb	5.34 kb
Passed Bases Called	4.5 Gb	4.51 Gb
Failed Bases Called (Q < 9)	418.46 Mb	372.54 Mb
Run Duration	18 hrs, 24 mins	18 hrs, 24 mins

detecting pathogen sequence information. We then guided participants in how to use BWA (Li 2013) and minimap2 (Li 2018) to map reads to a reference sequence, samtools (Danecek et al. 2021) to filter out residual host sequences, and NCBI's Basic Local Alignment Search Tool (BLAST[6]) to perform basic homology searches against known pathogen sequences. On Day 9, we terminated the mitogenome sequencing run and initiated the pathogen depletion run. While the sequencer ran, participants and instructors explored the sequencing output of the mammal mitogenome run.

We aligned raw reads to a local bat (*Sturnira bakeri*, QCAZ-M18241) reference mitogenome (GenBank: ON357724.1) with BWA MEM (-x ont2d), and called consensus in samtools. Consensus sequences were imported into MEGA v. 4.0 (Tamura et al. 2007) for alignment and visualization as a neighbor-joining phylogeny. While for publication purposes we recommend using alternative alignment and phylogenetic estimation software, this workflow is simple, even for those without bioinformatic experience, does not require access to high-powered computers, and provides an initial assessment of evolutionary relationships that can be used to direct field sampling in real-time or guide future analyses.

[6] https://blast.ncbi.nlm.nih.gov/Blast.cgi.

Overall, the pathogen (depletion) and host mitogenome (enrichment) experiments generated 58.40 GB and 57.57 GB of sequence data, respectively. Table 1 provides summary metrics output by the sequencer at the end of each run. After filtering for reads that mapped to the mitochondria, phylogenies were generated from 5.20 GB of data.

At the end of the workshop, participants were asked to complete an optional evaluation survey to gauge learning outcomes and identify opportunities for improvement. Survey results and ideas on how to overcome challenges identified during the workshop are detailed in the "Lessons Learned" section below.

How to Replicate This Workshop

Putting this workshop together and making the materials available online required significant funding and collaborative participation. We have compiled a package of materials for researchers and instructors aiming to extend this workshop or create similar training opportunities. These materials include a public website[7] with detailed directions for software installation, downloading data for the worked example, and step-by-step bioinformatics. Additional materials are available on FigShare[8], and include: (1) Workshop Resources (field waiver, code of conduct, pre-workshop emails, equipment list and budget, workshop application and evaluation forms[9]), (2) eight lectures in English[10] and Spanish[11], (3) template datasheets used by the University of Kansas Biodiversity Institute's Division of Mammals (specimen datasheets, gazetteer, ancillary datasheets, trapline datasheets, and bat net datasheets[12]), and (4) protocols used during the workshop (DNA extraction, flow cell wash, library preparation, and concentration and dilution procedures[13]). The materials are openly available and free to use with appropriate acknowledgement and attribution.

Logistical considerations

A field site where electricity and a classroom are available nearby is ideal. Room and board accommodations for participants and instructors can also make this workshop more accessible and inclusive. Accommodations can be made individually or for the group by the lead organization. It is possible, however, to lead this workshop in more remote settings, by using a generator to support a sequencing and informatics-capable computer and camping outdoors. The list of resources made available in the next section facilitates the replication of this workshop, regardless of local amenities, but a generator would be required if electricity is not available. The area (size) of the field site should be adjusted based on the planned sampling methods, target taxa, and number of participants.

The lead organization must obtain the appropriate national, international, and institutional permissions and approvals to legally and ethically work with wild animals. That may include but is not limited to: an approved Institutional Animal Care and Use Committee (IACUC) protocol, in-country collecting permits (state, federal), and, if specimens are to be moved across international borders, a Material Transfer Agreement (MTA) outlining Mutually Agreed upon Terms (MAT) and Prior Informed Consent (PIC) negotiated under the Nagoya Protocol for Access and Benefit-Sharing. If the lead organization intends to sample wildlife in a foreign country, we strongly encourage them to partner with an in-country biorepository (i.e., a natural history museum or similar entity) early in the planning process to facilitate in-country permitting, logistics, and equitable specimen sharing (Ramírez-Castañeda et al. 2022). Permit documentation differs for each country, government, and institution, and can take more than 6 months to process.

Workshop participants should be selected at least 3 months in advance, and ideally 6 months ahead of the workshop. Depending on the country of origin, participants may require a visa to enter some countries. A sponsored invitation letter may speed up that process and should be considered when possible.

Safety considerations

Safety is critical to the success of this workshop. Although fieldwork has inherent risks, organizers can take steps in advance to set their team up for success (Campbell et al. 2025; Ramírez-Castañeda et al. 2022). Field safety includes *a priori* consideration of potential hazards, including environmental and interpersonal risks, as well as identifying the actions, resources, and responses to be undertaken in case of an adverse event (Kuebbing et al. 2021; Rudzki et al. 2022). Biosafety is another dimension of field safety that not only protects participants but also helps prevent the unintentional introduction of new pathogens into fragile ecosystems (Islam et al. 2025). Biosafety requirements differ across institutions, countries, and for different taxa (e.g., Sikes et al. 2016; Shapiro et al. 2024). We recommend advanced development of a Field Safety document tailored to the context of each workshop. Each

[7] https://alexanderhey.github.io/MEPA_Field-Genomics/.

[8] figshare.com/projects/MEPA_Field_Genomics_Workshop/243968.

[9] DOI: 10.6084/m9.figshare.28744208.v1.

[10] DOI: 10.6084/m9.figshare.28736396.v2.

[11] DOI: 10.6084/m9.figshare.28736417.v2.

[12] DOI: 10.6084/m9.figshare.28744412.v1.

[13] DOI: 10.6084/m9.figshare.28744844.v1.

participant must read and sign the Field Safety document to confirm understanding of the risks associated with fieldwork, acknowledge available resources in the event of an emergency, and limit liability of the lead organization.

Additional waivers or health documentation (e.g., proof of vaccination) may be required depending on the location of the workshop, lead or hosting institutions, and taxa to be sampled. As an example, proof of vaccination against yellow fever virus may be required in yellow fever endemic areas and rabies vaccines are generally required prior to handling carnivores or bats (Aguilar-Setién et al. 2022). The lead organization is responsible for collecting and maintaining digital and print copies of emergency contact information for instructors and participants in advance of the workshop. At a minimum, emergency contact information should include a contact name, phone number with country code, email, and mailing address, as well as pertinent medical information (e.g., allergies, medications, conditions, etc.). Additional emergency phone numbers and maps to health services (e.g., hospital, urgent care center, etc.) nearest the field site should be included in the emergency response packet compiled and maintained by the lead organization. A Code of Conduct should be developed, shared with, and agreed upon by all participants in advance that outlines standards for professional behavior, steps to prevent harassment, and appropriate contacts and links for reporting.

Workshop resources and materials

A comprehensive list of physical equipment and materials required for this workshop is included as Supplementary Material and online via FigShare (Project #243968). Required field gear will vary depending on the geographic location, taxa being sampled, and the number of participants. In general, data sheets, tags, tubes, and specimen preparation supplies were provided by the museum biorepository that has agreed to accession and preserve the resulting specimens in perpetuity. In-country museum biorepositories may also have traps and specimen preparation gear that can support the field component of the workshop.

Participants were expected to bring their own laptop computers for the bioinformatic portion of the workshop. Prior to the start of the workshop, participants were instructed on how to independently download and install required software and data files to their local machine to allow the workshop to operate off-line, as needed. Detailed instructions for software installation on Linux, MacOS, and Windows operating systems are included on the workshop website and were emailed to participants two weeks in advance. We recommend that instructors also carry a backup digital copy of all required software and data files. To ensure that participants were able to perform the bioinformatic workflows during the workshop, the "worked example" exercise was designed to be reproducible on computers with medium- to high-computing capabilities (e.g., RAM => 8 GB, I5 or similar processor, no dedicated graphics card required). Given the nature and volume of NAS data, however, higher computing power may be needed to work with data generated during the workshop. In such cases, participants can work in small groups and take turns watching and completing steps on more capable computers.

Participants were responsible for bringing their own field gear. A list of required gear was provided in advance and included snake gaiters, tall rubber boots, long pants, long-sleeve shirts, leather gloves, headlamp, rain gear, a hat, and personal toiletries, including sunscreen, bug spray, and personal medications. The list of required gear will vary significantly depending on the season, duration, weather, lodging, and amenities at the field site.

Budget

Major workshop expenses included field gear, curatorial supplies, molecular equipment and reagents, airfare, transportation, and room and board for participants and instructors. In 2024, purchasing all workshop equipment and reagents from scratch required approximately $4500 for field gear and $13,500 for genomic lab equipment and reagents, totaling $18,000. While molecular equipment and reagents were the most expensive category, a large proportion of the required equipment and infrastructure only needs to be purchased once, and some could be borrowed from in-country collaborators.

For example: a MinION sequencer ($1000), pipettes (8 x $355 each = $2840), 4 TB hard drive ($280), portalyzer ($300, Peck et al. 2022), and M3 Macbook computer ($4000) with sufficient GPU to perform adaptive sampling, are one-time purchases, whereas, mammal traps may be provided by in-country collaborators. In 2024, round-trip airfare per person (home country to/from Ecuador) was approximately $1000 (12 international plane tickets); room and board at the Reserva Otongachi field

Table 2. High-level cost breakdown for the 2024 *Museums and Emerging Pathogens in the Americas* (MEPA) Field+Genomics Workshop (20 people). See Supplementary Materials for a detailed breakdown of expenses.

Item	Cost
Field equipment	$4500
Molecular equipment and reagents	$13,500
Airfare (~$1000 per participant)	$12,000
Lodging ($29/person/day)	$5800
Board ($6/person/day)	$1200
Transportation ($20/person)	$400
Total	$37,400

station were $35 per person per day ($7000 for a group of 20 people); and group transportation by bus was $20 per person ($400). In total, individual attendance for an international participant could be sponsored for about $1360, however, total costs will vary depending on local conditions and accommodations.

Lessons Learned

Need for partnerships that build in-country infrastructure

Partnering with an in-country museum biorepository is essential to the success of this type of workshop and directly supports the growth and long-term maintenance of in-country research infrastructure, as a form of benefit sharing. By permanently archiving materials in a local biorepository, the samples collected during the workshop can be made available to the local scientific community to address additional questions (Colella et al. 2020). Further, involvement of local participants, institutions, and community stakeholders in advance can help meaningfully shape the research focus and experiments to be conducted during the workshop (Hetu et al. 2019, Vilaça et al. 2024).

For example, although this workshop focused on DNA-based pathogens and host mitochondria, the methods could be extended to screen for RNA-based pathogens. Including local personnel in the workshop further fosters local network development and scientific capacity, ensuring the long-term transfer of knowledge and skills (Martin et al. 2022). By strengthening both infrastructure and workforce, this type of workshop can create a more equitable and sustainable framework for future research and empower local communities to address their own biodiversity and health challenges (Ramírez-Castañeda et al. 2022). Such partnerships also facilitate in-country logistics, international communication, and inform research priorities.

Workshop participants identified local access to equipment, resources, and infrastructure as the major barrier to scaling such workflows and technologies in lower-resourced countries. For example, field workflows require access to traps (mist nets, traps, etc.; >$2500), sampling media (250 ml DNA/RNA shield; $250), and consumables (data pages, tags, cryotubes, etc., ca $500), as well as space and storage infrastructure to maintain samples long-term. Similarly, adaptive sequencing requires access to both a MinION sequencer ($1000), flow cells ($700/ea.), laboratory consumables (e.g., pipette tips, tubes, etc., $1500), and a GPU-enabled computer (>$3000). Additionally, sequencing data and intermediary analysis files consume significant digital storage. Not all countries and institutions have access to liquid nitrogen for cryogenic tissue preservation in the field. Dry ice or shelf-stable buffers, like DNA/RNA Shield or RNA later, may be used as alternatives depending on in-country regulations.

During the workshop, we performed adaptive sampling and live base calling/demultiplexing simultaneously on a GPU-enabled Apple MacBook Pro M3 (2023) in MinKNOW v. 23.11.2. The latest software update (MinKNOW v. 24.02), however, disabled simultaneous base calling and adaptive sampling for MacOS due to strain on the Apple silicon processor (pers. comm. ONT). As a result, the sequence output generated during this workshop may not perfectly reflect results obtained in future workshop iterations. Future iterations should leverage recent software updates and perform adaptive sampling in real-time, followed by later base calling and demultiplexing if using MinKNOW v. 24.02 on MacOS.

Teaching new teachers

This workshop was designed to teach field and molecular techniques to the next generation of scientists in Latin America, however, an ideal extension of this effort would be to teach workshop instructors, such that in-country instructors are able to replicate the workshop. As with any skill, regular application and use are key to retention and adoption. Therefore, we recommend recruiting participants with a high probability of using these tools and skills in the near future.

Plan for post-workshop communication

Establish a plan for group communication after the completion of the workshop. Choose a platform that is accessible, informal, and multilingual, and, ideally, one that allows sharing of images and files. For the 2024 workshop, we established a WhatsApp group to continue discussion and problem-solving after the workshop. For collaborative writing to be successful, we identified co-leads and co-senior authors, representing pairs of North-South colleagues, to lead discrete products stemming from the data generated during the workshop. For manuscript development, we used Google Docs as it is freely accessible to all participants and allows multi-user editing, text change tracking, and commenting. Co-leads were tasked with data analysis, visualization, and writing of respective projects, and encouraged to reach out to other participants and instructors for help, as necessary.

Conclusion

Workshops that integrate complementary field and molecular skill development build new capacity in biodiverse countries to address critical societal questions related to emerging pathogens, biodiversity loss, climate

change, and food security, among others. By (1) developing and enhancing the skills, knowledge, and abilities of local scientists, (2) building international, multi-disciplinary collaborative networks, and (3) growing in-country biodiversity infrastructure by contributing samples to local biorepositories, such workshops can help stimulate solutions to the public health and biodiversity challenges of each region. By linking field-based collection and permanent specimen archival to real-time genomic surveillance of hosts and pathogens, workshops like this can improve detection of zoonotic pathogens while also aligning with global One Health initiatives.

This workshop aimed to demonstrate the level of effort, expense, and expertise involved in conducting voucher-backed surveillance of wildlife and their pathogens, coupling fieldwork for specimen collection with downstream molecular applications. Such training workshops are one mode of benefit sharing (Colella et al. 2023) under the Nagoya Protocol for Access and Benefit Sharing and will serve local communities beyond the duration of a single workshop, grant, or project. Such collaborations further contribute to in-country infrastructure in the form of natural history museum biorepositories (Colella et al. 2020), while exposing non-museum-based researchers to the benefits of long-term data and sample archival. Together, these outcomes highlight how collaborations that unite fieldwork, genomics, and museum science can advance both local capacity and global health preparedness.

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Data Availability

All supplementary materials are available on FigShare[14].

Declaration of Conflicts of Interest

The authors declare that no competing interests exist.

[14] https://figshare.com/projects/MEPA_Field_Genomics_Workshop/243968.

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