Trends in Parasitology

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Opinion

Emerging methods in noninvasive parasite surveillance in wildlife disease ecology

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Noninvasive approaches are increasingly reshaping parasite and disease surveillance by reducing stress and harm to hosts while expanding opportunities for ecological and epidemiological research. In this opinion article, we discuss these emerging approaches, which rely on molecular, citizen-science, and computational methods, for monitoring parasites, vectors, and hosts. These tools can improve spatial and temporal coverage, support the surveillance of rare or threatened hosts and parasites, and contribute to the understanding of transmission pathways and disease dynamics. However, their reliability depends on careful validation, standardized protocols, and awareness of methodological limitations. While not direct substitutes for invasive methods, these approaches lift a considerable burden from wildlife. Integrating noninvasive approaches thus provides a strong basis for advancing disease ecology, wildlife health monitoring, and biodiversity conservation.

Highlights

Noninvasive approaches are reshaping disease and parasite surveillance, creating new opportunities in disease ecology research.

Combining multiple methods improves reliability, although standardization remains limited and appropriate validation is needed.

Noninvasive surveillance approaches are particularly valuable for threatened host and parasite populations.

Both strengths and limitations must be considered when selecting noninvasive methods.

Noninvasive methods most often serve as complementary tools, not replacements for traditional surveillance.

Emergence of nontraditional parasite and disease surveillance methods

Parasites (see Glossary), whether pathogenic or nonpathogenic, are ubiquitous and play essential roles in regulating ecosystems, host populations, and evolutionary processes [1,2]. Despite their ecological, epidemiological, and evolutionary importance, research on both **microparasites** and **macroparasites** has traditionally relied on invasive or destructive methods, such as host dissection, lethal or stressful sampling, and clinical testing. These methods can be operationally difficult, practically limited, and ethically challenging, particularly for rare or protected species. **Noninvasive sampling** strategies have emerged as effective alternatives, supporting the goal of data accumulation and advancing knowledge in disease ecology while reducing the impact on hosts [3–5].

As the related methodology advances, a growing toolkit is becoming available for noninvasive sample collection and **pathogen** or parasite surveillance. However, a greater number of noninvasive sampling studies are needed to clarify the full potential of applying these approaches effectively across different taxa, geographic regions, and temporal scales. The use of these methods relieves pressure on vulnerable host populations and holds considerable promise for improving the detection and, ultimately, the conservation of threatened parasite taxa, an area of research receiving increasing attention [6].

In this opinion article, we present a wide range of emerging noninvasive approaches (Figures 1 and 2; Table 1) classified as follows: (i) molecular and observational sampling methods that rely on dedicated data collection and analysis, often combining genetic tools with systematic monitoring; (ii) participatory and community-based surveillance frameworks, which actively involve the public in data collection and reporting; and (iii) digital surveillance approaches, which use both professionally generated datasets and opportunistic information derived from public search

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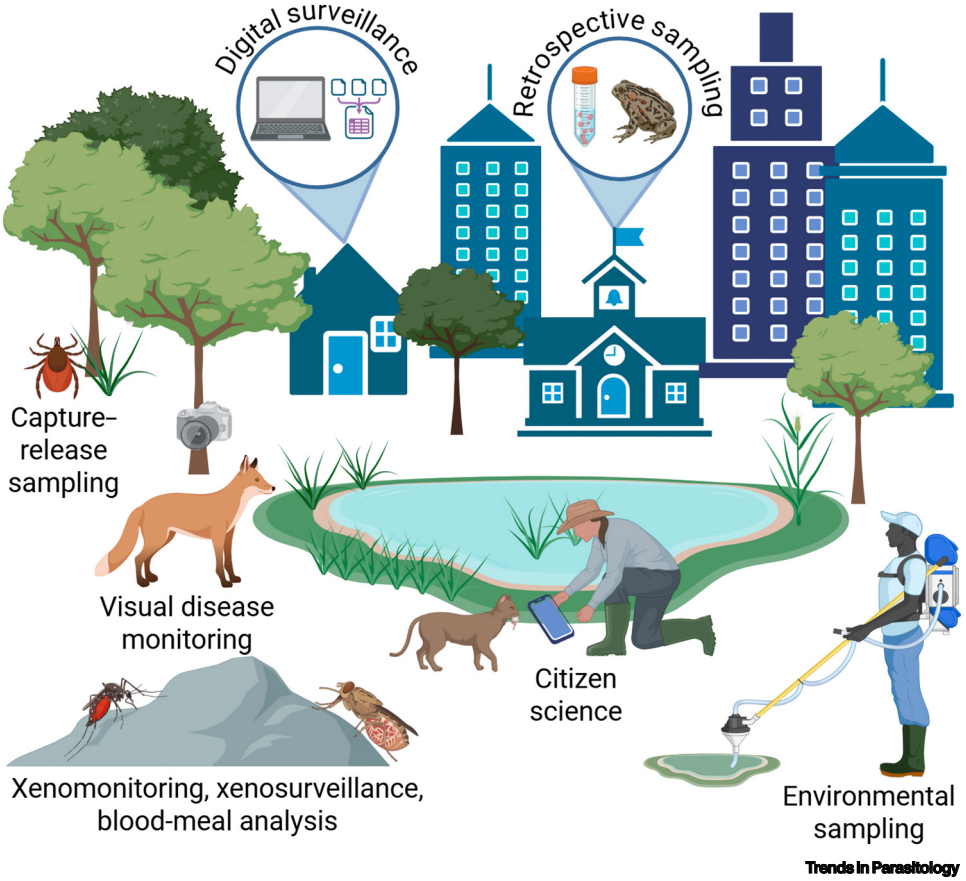

Figure 1. Examples of noninvasive approaches used in wildlife disease surveillance. Molecular and observational sampling strategies include xenomonitoring, xenosurveillance, and blood-meal analysis of hematophagous invertebrates; environmental sampling using eDNA, eRNA, or iDNA to detect infectious agents; camera trapping to identify visible signs of disease in wildlife; retrospective investigations using archival material to assess historical parasite and pathogen occurrence; and capture–release methods to examine parasite and vector movement and lifespan. Citizen science-based surveillance frameworks include participatory monitoring, such as photo-based documentation of host behavior or visible parasitism, as well as biological sample contributions, including the public collection of parasites and potential vectors. Informational and digital surveillance rely on indirect information sources, in which patterns of human online activity (e.g., search behavior) and predictive modeling may indicate emerging pathogen dynamics in companion animals and wildlife hosts. eDNA: environmental DNA; eRNA: environmental RNA; iDNA: invertebrate-derived DNA.

queries or online activity. In practice, these digital approaches often overlap with both professional sampling and community-based surveillance, integrating elements of field monitoring and public participation.

Molecular and observational sampling strategies for noninvasive surveillance

Invertebrate-based sampling: xenomonitoring, xenosurveillance, and blood-meal analysis

Both molecular **xenomonitoring** and **xenosurveillance** typically refer to the detection of parasite (or pathogen) DNA/RNA within blood-sucking arthropods or mollusks [7–9]. In parasitological research, the distinction between the two approaches lies primarily in their focus. Xenosurveillance primarily targets parasitic organisms, such as microparasites, that are present in blood meals derived from hosts and is therefore considered more host centered, whereas xenomonitoring refers to parasite screening in arthropods that are known or suspected vectors

Glossary

Blood-meal analysis: a molecular approach used to identify the host species on which a blood-feeding invertebrate has fed.

Camera-trap surveys: involve the use of motion- or heat-triggered cameras in the field to passively record wildlife presence or behavior.

Capture–release sampling: a method in which animals are captured, sampled, or marked and then released to study movement, population dynamics, or host–parasite interactions with minimal long-term impact.

Citizen science or community science (CS): involves nonprofessional volunteers in scientific data collection, reporting, or analysis, often contributing large-scale observations of species occurrence or behavior.

Environmental DNA (eDNA) and environmental RNA (eRNA): forms of genetic material shed by organisms into the environment (e.g., water, soil, and air) that can be collected and analyzed to detect species or pathogens without direct observation; eRNA may indicate more recent biological activity.

Invertebrate-derived DNA (iDNA): host or pathogen DNA obtained from invertebrates (e.g., leeches and flies) that have fed on or interacted with vertebrates, enabling indirect detection of host species and associated pathogens.

Macroparasites: multicellular parasitic organisms, including helminths (e.g., nematodes, cestodes, and trematodes) and ectoparasites (e.g., ticks and leeches).

Microparasites: microscopic infectious organisms, typically including viruses, bacteria, fungi, and protozoan parasites. In this work, the term refers exclusively to eukaryotic parasitic organisms, such as protozoans.

Noninvasive sampling: refers to surveillance approaches that collect biological, observational, or environmental information while minimizing disturbance to target hosts or parasites and without necessarily requiring their capture, handling, injury, or death.

Parasite: a eukaryotic organism that lives in or on another organism (the host), obtaining resources from the host. Parasites may be pathogenic, meaning they are capable of causing disease in their hosts, or nonpathogenic, meaning they typically do not cause disease,

of parasite transmission and is therefore considered more parasite centered. Arthropod vectors such as mosquitoes, sandflies, and ticks can be collected using various trapping methods, after which specimens are analyzed for infection markers using techniques such as quantitative PCR (polymerase chain reaction), conventional PCR, or high-throughput sequencing. Both xenomonitoring and xenosurveillance have proven particularly effective for monitoring vector-borne parasites and pathogens, including filarial nematodes, bacterial pathogens, and arboviruses [4,8–10].

Despite the apparent potential, relatively few studies have evaluated detection success rates in both hosts and hematophagous arthropods simultaneously. One example is a study on bats, where blood-associated microparasites, including *Trypanosoma* spp. and *Polychromophilus* spp., have been successfully detected in both host blood and blood-sucking ectoparasites [4]. Importantly, this approach primarily allows estimation of blood-associated parasite prevalence at the population level, since some ectoparasites may switch hosts multiple times [11]. Furthermore, distinguishing between parasites ingested only during a blood meal and those truly infecting or completing their life cycle within the vector remains challenging [12]. Consequently, while indicating vector potential, these methods alone are insufficient to confirm vector competence.

Integrating xenomonitoring and xenosurveillance with **blood-meal analysis** can further explain pathogen–parasite–host networks and uncover previously unrecognized transmission pathways among wildlife species [13]. For instance, bat-associated ticks, often considered highly specialized on bats, have been shown by various studies using blood-meal analysis to feed on a broader range of hosts, including other wildlife, domestic animals, and even humans [13,14]. Combining blood-meal analysis with xenomonitoring has also shown that bat ticks, which previously fed on domestic dogs, harbor bacterial pathogens, such as *Candidatus* Neoehrlichia mikurensis [13]. These findings, which combine various surveillance methods, suggest that pathogen transmission may occur through occasional host switching by tick vectors [13]. Such data also contribute to assessing zoonotic disease transmission risks to humans by clarifying both the host range and the diversity of zoonotic pathogens involved [13]. Additionally, combining blood-meal data across populations can provide insights into niche occupancy and invasion dynamics [15]. Nevertheless, methodological limitations remain, as host DNA may degrade rapidly after blood feeding, and mixed blood meals can complicate interpretation. However, a prior study demonstrated the accurate determination of the vertebrate blood meals of bat-associated soft tick species even 1.5 years after feeding, showing that, in certain circumstances, blood-meal analysis can be reliably conducted retrospectively over remarkably long timescales [16].

Environmental sampling: environmental DNA and RNA and invertebrate-derived DNA

Environmental DNA (eDNA) and **environmental RNA (eRNA)** analyses have become essential tools for noninvasive biodiversity and micro- and macroparasite monitoring [3]. Environmental nucleic acids are genetic material obtained directly from environmental samples (e.g., water, soil, sediment, and air) and include not only extracellular DNA and RNA but also gametes, spores, and whole microorganisms. Thus, parasites, their vectors, and their hosts can all be detected from environmental samples, either independently or simultaneously, using molecular techniques. Environmental nucleic acids support diverse molecular applications, including studies of parasite diversity, distribution, phylogeny, and life-history traits, and have substantially advanced several research fields, particularly aquatic parasitology [3,17]. For instance, these approaches have been successfully applied to detect trematodes and schistosomes in aquatic environments [18,19], monitor mosquito larval distribution [20,21], and identify waterborne protozoa [22]. Environmental nucleic acid approaches also support semitargeted and untargeted molecular

although they may still influence host physiology, fitness, behavior, or ecological interactions. Although mosquitoes and leeches are not always traditionally classified as true parasites, they are included in this work because of their longstanding importance in parasitological research.

Pathogen: an infectious biological agent, including parasites, viruses, bacteria, and fungi, capable of causing disease in its host, although infection may not always result in visible clinical signs.

Predictive modeling: the use of computational and statistical models to analyze biological data, identify underlying drivers of natural processes, and forecast patterns under changing conditions, such as species distributions, population dynamics, and ecosystem responses.

Remote imaging: the use of imaging technologies (e.g., drones and camera traps) to monitor wildlife or their habitats without direct contact with the organisms.

Search–query surveillance: the use of aggregated online search data to analyze patterns in user queries, which may reflect real-world changes or emerging trends.

Xenomonitoring: the detection of parasite or pathogen DNA or RNA in vector organisms (e.g., mosquitoes and ticks) to assess the presence of infection and vector potential.

Xenosurveillance: the use of blood-feeding invertebrates as 'sampling tools' to detect pathogens present in their blood meals, providing indirect information about host infections.

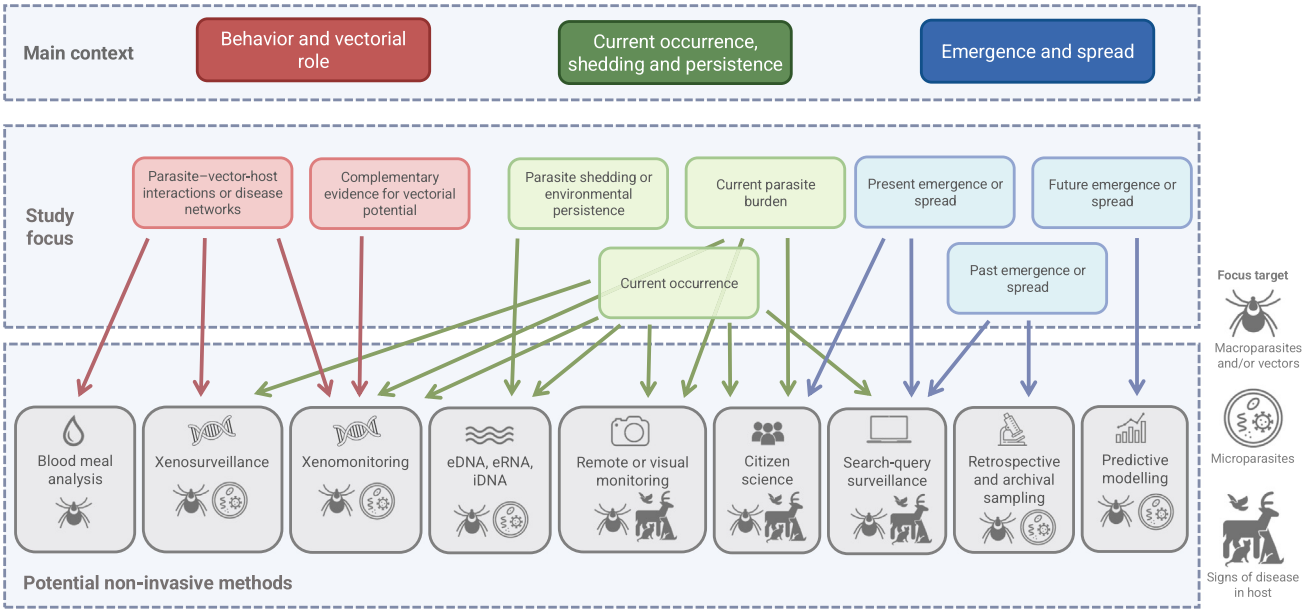

Figure 2. Framework illustrating the application of noninvasive methods in wildlife disease surveillance according to the primary ecological focus and research objective. The upper panel represents the main ecological focus of the research, including (i) behavior and vectorial role, (ii) current occurrence, parasite shedding, and environmental persistence, and (iii) parasite emergence and spread. The middle panel presents specific research objectives associated with each ecological focus, from which potentially suitable noninvasive methods can be identified. Icons indicate the primary surveillance target of each method, including parasites and/or vectors, microparasites, or visible signs of parasitic disease in wildlife hosts. The figure is intended as a conceptual guide to help researchers select appropriate noninvasive methods based on their research questions, recognizing that many approaches are complementary and can be combined within integrated surveillance frameworks.

methods, including metabarcoding, metagenomics, and metatranscriptomics, aiding the discovery, characterization, and surveillance of parasites and pathogens while also facilitating comprehensive assessments of parasite communities [3]. Since eRNA degrades more rapidly than eDNA, it is often considered a potential indicator of recent or ongoing infection or organismal activity [3]. Despite their high sensitivity and broad applicability, eDNA and eRNA assays are subject to limitations, including contamination risks, PCR inhibitors, and biases related to DNA persistence; hence, careful validation, replication, and appropriate controls are essential for reliable inference [23].

Invertebrate-derived DNA (iDNA) represents another noninvasive molecular tool for detecting foreign DNA in invertebrates. The approach has proven particularly effective in terrestrial and aquatic leeches, as they may retain host blood for several months. For example, one study found that leeches had fed on multiple vertebrate species and simultaneously detected several distinct lineages of trypanosomes [24]. Nevertheless, interpreting iDNA data poses several challenges, as the precise source of detected parasitic organisms often remains uncertain and the dispersal ranges of many invertebrate taxa are poorly known, complicating spatial attribution of transmission pathways.

Observational sampling: remote or visual parasitic disease monitoring

In addition to molecular and direct sampling methods, **remote imaging** has emerged as a valuable noninvasive approach for monitoring wildlife diseases, particularly those with visible clinical signs. High-resolution images obtained from **camera-trap surveys** have been successfully

Table 1. Overview of noninvasive methods used in parasite and vector surveillance, summarizing their main advantages and limitations

Methods	Ecological focus	Sampling type	Advantages	Limitations	Validation requirements
Xenomonitoring and xenosurveillance	Parasite occurrence and vector potential	Direct sampling	• Nonlethal and minimally disruptive to vertebrate hosts • Can detect multiple parasites and pathogens from pooled samples • Suitable for large-scale surveillance	• Dependent on vector abundance and trapping success • Pathogen detection may reflect transient blood meals rather than active infection or vector role • DNA and RNA degradation can reduce detection sensitivity	• Compare detection results with conventional host or vector surveillance • Assess sensitivity and specificity across vector species and environments • Validate whether detected pathogens indicate active transmission rather than incidental exposure
Blood-meal analysis	Parasite and vector behavior, and disease networks	Direct sampling	• Provides direct information on host-feeding preferences • Can be combined with xenomonitoring and xenosurveillance • Useful for studying transmission pathways and host contact rates • Useful for rare, elusive, or protected species	• Blood-meal origin may be difficult to resolve in partially digested samples • Determining the host origin can be challenging when multiple host species sources are present	• Validate host associations using reference databases or independent host observations • Compare molecular identifications with known host distributions and vector behavior • Test reproducibility across digestion stages and sample preservation conditions
Capture–release sampling		Direct sampling	• Gives data on movement patterns and host use • Useful for studying host contact rates • Can support parasite conservation of rare and threatened parasite species	• Capture–release studies can be labor intensive and affected by low recapture rates • Behavioral observations may not fully represent natural conditions due to disturbance	• Evaluate whether capture and handling alter behavior • Assess recapture reliability and sampling bias
eDNA, eRNA, and iDNA	Rate of parasite shedding and survival in nature	Direct sampling	• Allows pathogen or parasite detection without direct observation of hosts • Sensitive for low-density or cryptic species • Useful in aquatic and terrestrial habitats • eRNA may provide evidence of recent biological activity • Enables broad biodiversity assessment from a single sample	• Environmental contamination and DNA persistence may lead to false positives • Difficult to estimate infection prevalence or host abundance • Degradation rates vary across environments • Lack of standardized sampling and interpretation protocols • Detection probability may be inconsistent	• Compare detections with conventional trapping or surveillance • Validate persistence and degradation rates under local environmental conditions • Replicate sampling across space and time to evaluate detection consistency
Remote or visual parasitic disease monitoring	Estimating disease burden	Indirect sapling	• Enables repeated monitoring over large geographic areas • Useful for observing visible disease symptoms, or behavioral abnormalities • Cost-effective for long-term surveillance	• Limited to diseases with externally visible and disease-specific symptoms • Observer bias and image quality can affect accuracy • Asymptomatic infections remain undetected • Species identification and diagnosis may be uncertain	• Compare visual diagnoses with laboratory-confirmed infections • Evaluate observer agreement and image classification accuracy • Determine detection probability under different environmental and image-quality conditions
Retrospective and archival sampling	Disease and vector emergence and spread	Direct sampling	• Enables long-term ecological analyses • Allows reconstruction of historical pathogen emergence and spread • Valuable for identifying past	• Archived samples may contain degraded DNA/RNA • Sampling biases in historical collections may limit representativeness • Metadata are often	• Compare historical detections with known parasites and pathogen records when available • Assess effects of preservation methods on

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Table 1. (continued)

Methods	Ecological focus	Sampling type	Advantages	Limitations	Validation requirements
			host–pathogen associations • Using museum collections or preserved specimens helps avoiding additional wildlife disturbance	incomplete • Preservation methods may affect molecular analyses	DNA/RNA recovery
Citizen science		Direct and indirect sampling	• Expands geographic and temporal coverage • Cost-effective large-scale data collection • Useful for rapid detection of parasite occurrence, invasive species, or unusual mortality events • Valuable for rare or sporadic observations	• Data quality and accuracy may vary among participants • Uneven spatial sampling effort • Species misidentification is common • Reporting biases may affect interpretation • Verification and standardization can be challenging	• Implement training, standardized protocols, and quality-control procedures • Assess participant accuracy and sampling bias • Use expert verification
Search-query surveillance		Indirect sampling	• Rapid and inexpensive source of large-scale temporal data • May provide early warning signals for parasite or vector emergence • Useful for identifying seasonal or geographic trends	• Search activity may reflect public concern rather than true parasite presence • Highly sensitive to media coverage • Limited applicability in regions with low internet use • Difficult to distinguish wildlife-specific patterns from human health concerns	• Compare search trends with epidemiological or ecological surveillance data • Test whether signals precede confirmed outbreaks or vector detections • Assess effects of media events and public attention on search activity
Predictive modeling		None (results can be used both in direct and indirect sampling)	• Can identify environmental drivers and forecast parasitic disease emergence or vector spread • Integrates ecological, climatic, and surveillance datasets • Supports risk mapping and management planning • Useful for scenario testing under climate or land-use change	• Model accuracy depends heavily on data quality and assumptions • Uncertainty may be high in data-poor systems • Predictions may not translate directly into field conditions • Requires substantial computational expertise and validation	• Validate predictions using independent field or surveillance datasets • Perform cross-validation and sensitivity analyses • Quantify uncertainty and predictive performance metrics

*Direct sampling involves the collection of biological material or organisms, whereas indirect sampling relies on observational, remote, or digital data sources.

used to identify and quantify the prevalence of conditions such as sarcoptic mange, caused by the parasitic mite *Sarcoptes scabiei.* This condition produces characteristic lesions and hair loss in various mammal species that are readily detectable in photographs. For example, camera-trap surveys have revealed mange prevalence in red fox populations by visually scoring disease-compatible lesions from extensive image datasets [25]. Such remote photographic monitoring can improve understanding of parasitic disease emergence from visual data [26]. Similarly, although evidence for its application remains more limited, sound-based remote monitoring, for example, of mosquito species, may offer an effective alternative for detecting the presence of disease vectors and can likewise be considered a form of observational sampling that may also be combined with citizen science (CS) initiatives (see later) [27–29]. Beyond species detection, passive acoustic monitoring may also provide valuable information on wildlife health. Vocalization characteristics, including song complexity, frequency, rate, and temporal structure, can reflect an individual's physiological condition, immune function, and even parasite burden.

In birds, for example, parasitic infections and immune status have been associated with changes in song characteristics, suggesting that acoustic signals can serve as honest indicators of host health and infection status [30]. Similar relationships have also been reported in bats, where vocalizations vary with ectoparasitic infestation [31].

Retrospective and archival sampling: museums as sources for parasite surveillance

The infrastructure of integrated specimen and parasite archives in museum collections is recognized as an essential component of disease ecology and biodiversity research [32]. These archives allow host, parasite, and pathogen materials (including tissues, ecto- and endoparasites, blood smears, etc.) to be linked with spatiotemporal metadata, thus enabling high-resolution retrospective analyses of emergence, host switching, and ecosystem change [32]. While traditional museum collections have historically relied on invasive sampling methods, such as whole-animal specimens and voucher collections, more recent efforts increasingly incorporate DNA samples and other noninvasive materials [33]. Furthermore, molecular techniques that enable the recovery of specimen DNA directly from preservation media (e.g., ethanol) [34] may also provide a nondestructive means of investigating historical host–parasite interactions without additional sampling of preserved specimens. These collections provide valuable resources for reconstructing historical and current distributions of parasites and for investigating their emergence dynamics [35,36]. In a notable example, museum-archived amphibian specimens were used to investigate the historical distribution of the myxozoan parasite *Myxidium immersum*. Retrospective examination of specimens collected over more than a century revealed that the parasite was absent from Australian frogs before the introduction of the cane toad (*Rhinella marina*) in 1935 but became widespread thereafter, supporting the theory that the parasite was introduced alongside its invasive host rather than being native to Australia [37]. In addition to emerging disease detection, museum-based sampling can help track long-term ecological change affecting parasite communities. For instance, a global analysis combining more than 50 000 parasite-occurrence records from museum and collection databases projected that climate-driven habitat loss alone could drive up to approximately 30% of parasitic worm species to extinction by 2070 [38].

Capture–release sampling of parasites

A rarely applied approach is the **capture–release sampling** of parasites, which enables the assessment of parasite presence and abundance on or near hosts while minimizing harm to both hosts and parasites. One notable example is that of the kiwi tick, *Ixodes anatis*, an endemic species that is likely co-threatened with its kiwi hosts. Although the primary aim of the study was not parasite conservation, the authors used a nondestructive sampling protocol in which ticks were collected from host burrows, examined, marked, and subsequently released rather than being lethally sampled [39]. This approach represents an important pioneering example of how capture–release sampling of parasites can be carried out while minimizing impacts on both hosts and their associated parasite fauna, demonstrating the potential of noninvasive methods to support the emerging field of parasite conservation. Yet capture–release methods can be justified without a focus on parasite conservation, as in the case of studying bat flies, which are highly specific hematophagous ectoparasites of bats. Using mark–recapture techniques with UV-fluorescent dyes, it is possible to quantify host choice and switching behavior among bat hosts under laboratory conditions [11]. These methods can also be applied to other hematophagous invertebrates under natural field conditions to understand dispersal movements of mosquitoes [40], to assess survival time of tsetse flies [41], or to estimate the abundance of tick populations [42]. Capture–release approaches can thus serve conservation purposes and provide a framework for exploring ecological and behavioral aspects of parasite biology in both natural and controlled settings.

Participatory and community-based surveillance frameworks

Citizen science in observational monitoring: public photographic and sound documentation and data provision

Citizen science or community science (CS), where volunteers contribute diverse forms of data, significantly extends the reach of noninvasive wildlife monitoring and can provide valuable insights into threats and disease dynamics affecting wildlife populations. Although CS has a long history, the widespread availability of smartphones has opened new opportunities for near-continuous, spatially extensive data collection, the scale of which would be insurmountable for professional researchers alone. Targeted CS initiatives can improve knowledge of vector populations relevant to human and animal health. For instance, CS projects have mapped mosquito and tick distributions, using either photographic documentation or acoustic recordings (in the case of mosquitoes), providing critical insights into species emergence, spread, and human exposure risk. Such occurrence data can additionally inform our understanding of ecological and environmental drivers of vector population dynamics, which is essential for designing effective control strategies [43–47]. CS observations can also reveal behavioral risk factors that influence parasite transmission and spillover events. A recent study used iNaturalist (inaturalist.org) observations of domestic cats preying on bats that are known reservoirs of several potentially zoonotic parasites and pathogens [48]. Several bat species preyed upon by cats have been documented to harbor parasites relevant to both wildlife and human health, revealing potential predation-related spillover risks [48].

Finally, questionnaire-based reporting and data provision can significantly improve epidemiological understanding of wildlife diseases when combined with veterinary diagnostic data [10]. This approach has proven particularly valuable for studying *Dirofilaria immitis*, the causative agent of heartworm disease in both wildlife and domestic animals, by providing insights into infection patterns and risk factors in domestic dogs while complementing xenomonitoring efforts targeting mosquito vectors [10]. These findings can also contribute to a broader understanding of ecological patterns of disease in wildlife hosts.

Citizen science in biological sampling: public specimen submission programs

CS initiatives have also become an increasingly valuable component of biological sampling strategies, particularly in parasite and vector-borne pathogen surveillance [49]. Public submission programs for ticks and mosquitoes, in which members of the public collect and submit specimens for subsequent morphological identification or molecular screening for pathogenic parasites, enable large-scale, geographically extensive sample collection with the potential for early detection of emerging pathogenic parasites. For instance, a study in which volunteers collected ticks for pathogen screening revealed considerable pathogen diversity and relatively high prevalence of some human-infective agents [49]. Furthermore, CS-based surveillance can help detect newly emerging or expanding vector species, such as *Hyalomma* spp., known vectors of Crimean-Congo hemorrhagic fever virus [46,50]. Additionally, CS sample collection may involve environmental sampling, for example, collecting pond water for eDNA analysis, which can help detect the presence of parasites, including those associated with amphibians [51]. Wildlife salvage programs represent another valuable form of biological sampling in CS. Some research institutions or museums encourage the public to report and submit animals killed by vehicles, buildings, power lines, or wind turbines. These specimens contribute to museum collections and provide valuable resources for investigations of host–parasite associations and parasite diversity (https://bellmuseum.umn.edu/salvage-wildlife/).

Overall, while CS approaches offer considerable reach and scope, they require rigorous validation and quality control methods and, in some cases, standardized sampling protocols and proper

training to ensure the reliability of the collected data [52]. Equally important, citizen scientists involved in biological sampling should also receive training in the ethical considerations associated with specimen collection and handling, as well as relevant local legislation, permitting requirements, and biosafety procedures, thus supporting responsible research practices, compliance with legal regulations, and animal welfare.

Digital surveillance and predictive modeling

Search-query surveillance: monitoring online search behavior to uncover shifts in disease ecology

Search-query surveillance, often referred to as digital 'infoveillance', uses aggregated online search activity to explore ecological or epidemiological trends. In this approach, publicly available datasets such as Google Trends are analyzed to identify temporal and spatial patterns in human search interest, which may be associated with environmental events, wildlife disease emergence, or changing human–animal interactions. Because these datasets are generated passively and continuously by large numbers of users, they provide a noninvasive, low-cost source of information that can complement traditional ecological monitoring methods. This approach has been widely used in public health surveillance but is increasingly being explored for applications in wildlife health, conservation biology, and animal disease monitoring [53,54]. For instance, recent studies have shown that Google Trends data can reflect the dynamics of vector-borne diseases, including Lyme disease [55]. Analyses of search queries related to the disease demonstrate a strong correlation with reported disease incidence and seasonal patterns [55]. Nevertheless, these patterns do not necessarily directly reflect disease dynamics in wildlife hosts, although they may indicate the presence of wildlife reservoirs and ongoing pathogen circulation. Findings suggest that digital search-query surveillance may serve as a simple, extremely low-cost complementary tool for the early detection and monitoring of vector-borne diseases across broad spatial and temporal scales, while also contributing to a better understanding of vector and disease ecology and corresponding human behavior.

Predictive modeling: artificial intelligence and machine learning in wildlife disease ecology

Predictive modeling, increasingly powered by artificial intelligence (AI) and machine learning (ML), represents a transformative approach to understanding and forecasting parasite and pathogen dynamics. These computational frameworks can integrate diverse datasets, including host traits, vector ecology, genetic information, and environmental variables such as remotely sensed environmental data (e.g., land cover, vegetation indices, climate, and habitat characteristics). This may aid in prioritizing surveillance efforts in high-risk populations or geographic areas. For instance, such models can predict previously unrecognized reservoir hosts, identify species likely to harbor zoonotic parasites, and highlight the biological traits and geographic hotspots associated with parasite maintenance and disease emergence [56].

Similarly, predictive models can identify previously unrecognized vector species by analyzing combinations of ecological, phylogenetic, morphological, and behavioral traits shared with known invertebrate vectors [57,58]. For example, ML analyses of *Ixodes* ticks have identified core biological traits associated with zoonotic vector status while also highlighting previously overlooked tick species with a high predicted probability of transmitting zoonotic pathogens [58].

Although remote sensing has been an important component of disease ecology since the 1990s, recent technological advances (e.g., satellite imagery and geospatial technologies) have greatly broadened its applications, enabling large-scale predictive modeling and disease risk mapping by linking environmental conditions with vector distributions, abundance, and disease dynamics [59–61]. Additionally, predictive frameworks may also exploit publicly available molecular sequence repositories, including the Sequence Read Archive [62] and other genomic databases.

Reanalysis of these archived sequencing datasets using modern bioinformatics and ML approaches can reveal previously undetected pathogenic parasites, reconstruct historical distributions, infer host associations, and improve our understanding of parasite evolution and epidemiology without requiring additional field sampling. To date, however, these applications have been demonstrated primarily for viruses and pathogenic fungi [63,64]. These resources can provide large-scale training datasets for predictive models. Additionally, digital surveillance increasingly includes web-based epidemic intelligence platforms, such as PADI-web (Platform for Automated extraction of Disease Information from the web) and BEACON (Biothreats Emergence, Analysis and Communications Network) [65,66], that automatically collect and analyze information from news reports, social media, and other online sources to identify emerging disease events, potentially involving parasites of wildlife.

Predictive models are particularly valuable in regions where direct sampling is limited, allowing researchers to identify likely hotspots for disease emergence or spillover. The combined effort of data-driven predictions and noninvasive sampling provides a more comprehensive understanding of parasite–pathogen ecology and dynamics across ecosystems.

Concluding remarks

Noninvasive approaches are rapidly transforming parasite and pathogen research by supporting surveillance and ecological and epidemiological investigations without harming hosts or disrupting sensitive ecosystems. A growing toolkit, including eDNA and iDNA analyses, xenomonitoring, CS, and digital epidemiology, has greatly expanded the spatial and temporal range of wildlife parasitology and disease monitoring. Adding multiple complementary methods provides stronger evidence for parasite occurrence, transmission pathways, and host–parasite dynamics than any single approach alone (see Outstanding questions). Furthermore, these methods support the emerging ethical priorities in disease ecology and conservation biology. Conservation biology has traditionally focused on charismatic hosts of parasites, such as mammals and birds; however, parasites are increasingly being recognized as integral components of biodiversity, despite many facing coextinction risks alongside their hosts. Some noninvasive sampling strategies, therefore, offer important opportunities for documenting parasite diversity and monitoring populations while minimizing harm to vulnerable species. Whenever possible, researchers should prioritize the use of existing, well-curated biological collections, such as specimens deposited in natural history museums and other accredited biorepositories, rather than undertaking new collections that require invasive sampling of hosts or parasites. Wider adoption of digital repositories based on the FAIR Digital Specimen framework, making data Findable, Accessible, Interoperable, and Reusable, would improve the discoverability of these distributed collections, enabling collaboration and the reuse of archived specimens and their associated data by the broader research community. Such practices maximize the long-term scientific value of these samples, promote reproducibility, and reduce the need for repeated invasive sampling.

Furthermore, although considerable progress has been made, the replacement of invasive methods is only justified when alternative techniques have been sufficiently validated and shown not to introduce systematic bias. Without appropriate validation, noninvasive methods can provide distorted representations of parasite prevalence, pathogen diversity, host associations, or transmission dynamics due to differences in detection probability, environmental degradation of biological material, or sampling biases.

In addition, rapid advances in sensor technologies, automated sampling, and predictive modeling are shaping wildlife disease surveillance by improving the collection, processing, and interpretation of noninvasive data. As these technologies continue to develop, they offer ethical alternatives

Outstanding questions

How can standardized protocols and validation frameworks be developed to improve comparability across studies, ecosystems, and taxa?

What is the optimal way to integrate multiple complementary surveillance approaches (e.g., molecular, ecological, citizen science, and digital data) into unified disease monitoring frameworks?

How can the reliability of citizen science and digital surveillance datasets be assessed, improved, and validated for detecting wildlife disease emergence and predicting outbreak dynamics?

Can noninvasive methods accurately capture complex host–parasite interaction networks and cryptic transmission pathways in natural systems?

How can noninvasive surveillance approaches be adapted for use in understudied regions and data-poor ecosystems?

What role can noninvasive methodologies play in parasite conservation and the assessment of parasite coextinction risk?

to invasive sampling while also increasing sampling intensity, geographic coverage, and the speed and consistency of data acquisition. Their incorporation into surveillance could greatly improve parasite monitoring, biosecurity, and the early detection of emerging parasites. Wider adoption by governmental and international organizations could help achieve more cost-effective, ethical, and comprehensive surveillance, representing an important shift toward integrated approaches to wildlife disease ecology and management.

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Declaration of interests

The authors declare no competing interests.

Declaration of Generative AI and AI-assisted technologies in the writing process

During the preparation of this work, the authors used Grammarly in order to correct the grammar and improve the overall readability of the manuscript. After using this tool/service, the authors reviewed and edited the content as needed and take full responsibility for the content of the publication.

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