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Overcoming the limitations of wildlife disease monitoring

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Abstract

Integrated wildlife monitoring (IWM) combines infection dynamics and the ecology of wildlife populations, including aspects defining the host community network. Developing and implementing IWM is a worldwide priority that faces major constraints and biases that should be considered and addressed when implementing these systems. We identify eleven main limitations in the establishment of IWM, which could be summarized into funding constraints and lack of harmonization and information exchange. The solutions proposed to overcome these limitations and biases comprise: (i) selecting indicator host species through network analysis, (ii) identifying key pathogens to investigate and monitor, potentially including nonspecific health markers, (iii) improve and standardize harmonized methodologies that can be applied worldwide as well as communication among stakeholders across and within countries, and (iv) the integration of new noninvasive technologies (e.g., camera trapping (CT) and environmental nucleic acid detection) and new tools that are under ongoing research (e.g., artificial intelligence to speed-up CT analyses, microfluidic polymerase chain reaction to overcome sample volume constraints, or filter paper samples to facilitate sample transport). Achieving and optimizing IWM is a must that allows identifying the drivers of epidemics and predicting trends and changes in disease and population dynamics before a pathogen crosses the interspecific barriers.

Introduction

Establishing, developing, and implementing wildlife health surveillance programs is a worldwide priority and a challenge within the One Health approach (Ryser-Degiorgis, 2013; OIE, 2019; Lawson et al., 2021; Machalaba et al., 2021; Giacinti et al., 2022; Mazzamuto et al., 2022; Delgado et al., 2023; Pruvot et al., 2023). Traditionally, wildlife health surveillance is considered to encompass general surveillance (also called scanning or passive surveillance) and targeted surveillance (formerly called active surveillance) (Ryser-Degiorgis, 2013; OIE, 2019). General surveillance is based on the detection of dead or visibly sick wildlife, while targeted surveillance relies on proactive sampling of dead or living wildlife to detect a selected disease or pathogen (Leighton, 1995; Artois et al., 2009; Leighton, 1995). While general surveillance better suits the investigation of disease or mortality outbreaks, particularly for new or emerging diseases in an area or population, targeted surveillance allows the detection of pathogens asymptomatically infecting the animals (Ryser-Degiorgis, 2013; OIE, 2019), monitoring prevalence trends (Barroso et al., 2020a, 2020b), and assessing the outcome of interventions (Boadella et al., 2012). Proposals to standardize and harmonize wildlife health surveillance at local, regional, and global scale have been and are currently being developed, with little success in achieving successful implementation up to date (Boadella et al., 2011a; Hanisch et al., 2012; Stephen, 2018; Tomaselli et al., 2018; OIE, 2019; Lawson et al., 2021; Machalaba et al., 2021; Giacinti et al., 2022; Mazzamuto et al., 2022; Pruvot et al., 2023).

Wildlife health surveillance aims at detecting, investigating, and monitoring disease in wildlife populations (Ryser-Degiorgis, 2013; OIE, 2019). However, achieving a precise knowledge of wildlife species abundance, density, and distribution is challenging, and establishing harmonized methodologies allowing exchange of information and comprehensive epidemiological studies across geographical regions has become an issue (Sonnenburg et al., 2017; Moussy et al., 2022; Barroso et al., 2023). As a result of such a challenge, most current wildlife health surveillance schemes lack integration with appropriate population monitoring (Stallknecht, 2007; Lawson et al., 2021). Efforts have been carried out to overcome the methodological and technical limitations and achieve harmonized wildlife population

monitoring (APHAEA 2023; Sonnenburg et al., 2017; EFSA, 2023; ENETWILD, 2023). This is even more complicated for multi-host pathogens, where the epidemiology and maintenance does not depend on a single-host species but on a host community network, which might include wildlife, domestic animals, and/or humans (Fenton and Pedersen, 2005; Godfrey, 2013; Portier et al., 2019; Stephen, 2023). While most approaches to assess and monitor wildlife abundance focus on a single species or taxon, determining and achieving knowledge on the host community network, including abundance and interspecific contact rates, must instead be the objective, allowing to fine-tune community interspecific pathogen transmission dynamics (Barroso et al., 2023; González-Crespo et al., 2023a, 2023b).

Combining epidemiological and community network approaches allows the classification of disease threats according to the risk of exposure and duration (Fenton and Pedersen, 2005; Triguero-Ocaña et al., 2020). Nevertheless, measuring wildlife population health, including demographics and the diversity and status of infectious and noninfectious diseases (Hanisch et al., 2012; Stephen, 2014), faces major methodological, technical, logistical, economic, and even political constraints (Wobeser, 2007; Ryser-Degiorgis, 2013). Developing and implementing integrated wildlife monitoring (IWM), merging wildlife health monitoring (WHM) and host community monitoring (HCM), is required to achieve integrated and harmonized disease and population monitoring (Cardoso et al., 2022; Barroso et al., 2023). The complexity of assessing and monitoring the complete range of hosts and pathogens in the community has led to the quest for indicator species (Gortázar et al., 2021; Mazzotta et al., 2023) as well as nonspecific health indicators (Ráez-Bravo et al., 2015; Vicente et al., 2019). Indicator host species should allow to detect pathogens due to their central role in the network of a system, while nonspecific health indicators would allow detecting changes in population health status once the baseline values are established for each system (Halliday et al., 2007; Glidden et al., 2018; Barroso et al., 2023).

The objective of this article is describing the features, limitations, and biases of IWM and each one of their components (WHM and HCM) and how they affect the capability of IWM to understand the drivers, epidemiology, and impact of pathogen circulation.

Integrated wildlife monitoring

Figure 1 illustrates the components of IWM. It combines the study of the epidemiology of transmissible pathogens with the ecological knowledge of wildlife populations, including biodiversity and intra and interspecific contact rates and points defining the host community network. The detailed knowledge arising from such combination allows eco-epidemiologically characterizing the status of the pathogens present in a system as emerging, endemically maintained in a multi-host system, or spillover, as well as assessing whether the interaction of the host community with the pathogen(s) has a dilution effect or the multi-species host community exerts a density-dependent maintenance effect on the pathogen (Cortez and Duffy, 2021). IWM also allows defining the specific role of each host taxon, species, or population as maintenance, bridge, or spillover hosts (Fenton and Pedersen, 2005; Gervasi et al., 2017; Pepin et al., 2017; Triguero-Ocaña et al., 2020; Barroso et al., 2023).

The additional effort and cost of developing, implementing, performing, and combining the double monitoring (health and population) required for IWM, as well as the need to standardize

harmonized methodologies that can be applied transversally in countries and regions with different backgrounds and resources, call for the utilization of new noninvasive technologies, both for WHM and HCM. These new technologies should provide a wider and deeper monitoring while keeping efforts and costs within sustainable thresholds to allow long-term (ideally continuous) monitoring. Sampling and analytical methodologies such as environmental sampling (Martínez-Guijosa et al., 2020), use of filter paper (Santos et al., 2018), microfluidic PCR (von Thaden et al., 2020), and the establishment and determination of nonspecific health markers (Barroso et al., 2023) should contribute to improve the feasibility of WHM. Furthermore, noninvasive population monitoring using remote-sensing devices such as camera trapping (CT) or sound-recording would probably reduce the effort and field personal cost required for HCM (Toenies and Rich, 2021; Palencia et al., 2021a).

As aforementioned, IWM relies on WHM and wildlife HCM, each one of these components facing specific challenges, limitations, and biases. Moreover, the combination of WHM and wildlife HCM to achieve IWM creates additional challenges.

IWM limitations and biases

Section 1: WHM limitations and biases

WHM is critical given its relevance for public health, conservation, and food security. It generates benefits that range from early disease detection to the capacity to design and evaluate interventions and regulatory changes (Cano-Terriza et al., 2018; Gortazar et al. 2014; Mörner et al., 2002; Palencia et al., 2023a). WHM schemes should combine broad and inclusive general surveillance networks with targeted sampling schemes targeting priority hosts and pathogens, but flexible enough to adapt to emerging ones (Cardoso et al., 2022). However, multiple limitations constrain the implementation of WHM and bias our understanding of the epidemiology of shared pathogens at the human-domestic animals–wildlife interface. Funding the capacity building, infrastructure, and budget needs of a modern and complete WHM scheme is the obvious and most relevant concern.

General surveillance

General surveillance depends on heterogeneous actors with differential specific weights of wildlife rehabilitation centers and the eventual involvement of hunter and conservation associations, roadkill monitoring networks, or citizen science initiatives (Lawson et al., 2015; Schwartz et al., 2020). This generates two limitations: first, the scale and distribution of general WHM are heterogenous, non-stratified, and often do not match the distribution of the targeted sampling and monitoring networks; second, since most of these stakeholders are not directly linked to the human and animal health authorities, information is frequently lost or miscommunicated between the sources generating the data and the health authorities. Similarly, targeted WHM schemes are generally led by animal health authorities, who do not always communicate straightforward with human health authorities, environment and fish and game authorities, and the stakeholders involved in general WHM. Therefore, there is a need to improve and standardize general WHM data collection and communication bidirectionally, so the stakeholders participating in the basis of general WHM get a feedback of their involvement (Boadella et al., 2011a), as well as improving information sharing among authorities across administration compartments (Gortázar et al., 2016).
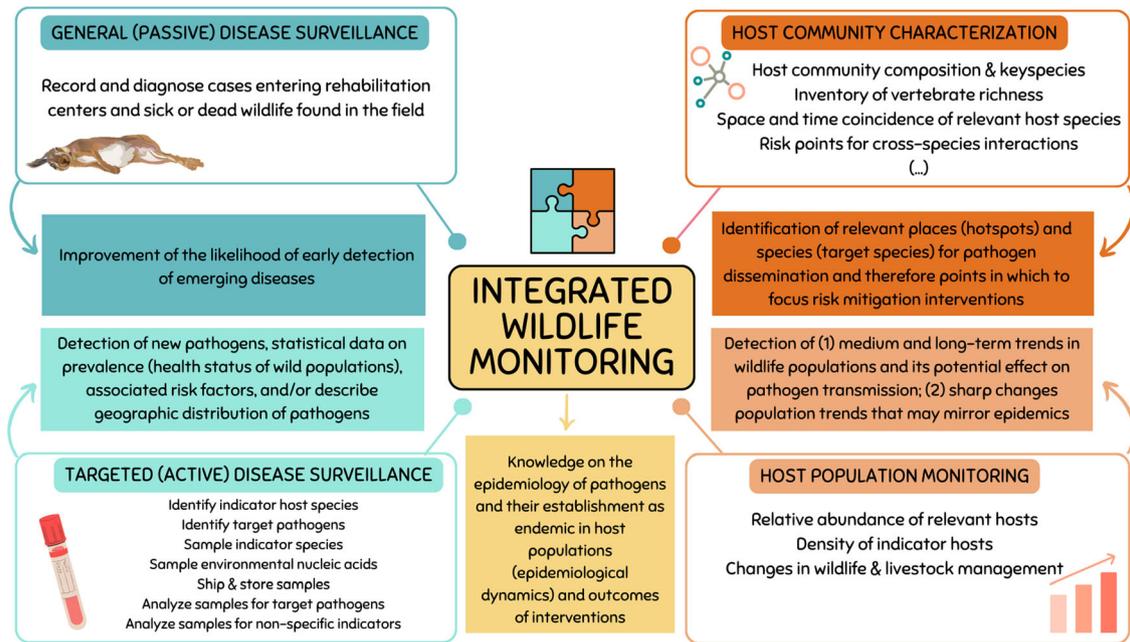
Figure 1. Components of Integrated wildlife monitoring (IWM) and main actions belonging to each component.

Targeted surveillance

The first limitation of targeted surveillance (sometimes also affecting general surveillance) is the impossibility to effectively monitor all the pathogens potentially present and/or emerging in all the potential host species in a system. Consequently, targeted WHM schemes have traditionally focused on wild ungulate and bird diseases known to have an impact on human and/or livestock health, giving less relevance to diseases mostly relevant for wildlife (Gortázar et al., 2007; Martin et al., 2011; Miller et al., 2013; Wiethoelter et al., 2015; Hassell et al., 2017; Wiethoelter et al., 2015). However, this approach ignores the potentiality for pathogens to jump the taxon barrier and becoming zoonotic or eventually pandemic, as repeatedly shown by different pathogens (Dudas et al., 2018; Dhama et al., 2020; Gortazar et al. 2014; Riedel, 2006). Adaptive protocols have been suggested for early detection of diseases newly introduced in a system (Miller et al., 2022).

By comprehensively and holistically monitoring the whole system, including pathogens, hosts, and their networks and relationships, IWM should achieve a better capability of monitoring known pathogens and detecting new ones. Once the host network has been analyzed, the most suitable indicator species and target pathogens can be identified. Ideal indicator species would be widespread, abundant, central in the host community contact network, easy to sample, and prone to get infected or develop antibodies against a broad range of relevant pathogens. While the Eurasian wild boar (*Sus scrofa*) matches these requirements in most of the systems where it is present (Figure 2), other hosts such as common and widespread rodents (e.g., genus *Apodemus* in Europe) or carnivores such as the red fox (*Vulpes vulpes*) can also be potentially good indicator species (Barroso et al., 2023; Mazzotta et al., 2023). Bats have been reported as reservoir of zoonotic diseases at the wildlife livestock–human interface, particularly in tropical regions, and are often forgotten by WMH schemes (Calisher et al., 2006; Allocati et al., 2016; Serra-Cobo and López-Roig, 2016), so they probably are a worthy target host for IWM.

As for the key shared pathogens to target through WMH for IWM, those present or endemic in the system are generally known,

although focusing WHM on the zoonotic aspect, the conservation approach, or the animal health perspective will drive the prioritization of such pathogens differently (ENETWILD consortium et al. 2022; Gortázar et al., 2016). However, the potential emergence of new pathogens (Miller et al., 2022) warrants nonspecific search through nonspecific sampling and analysis for pathogen groups, allowing the early detection of different and emerging pathogens and not only those already present in the system.

Since several transmission cycles can occur simultaneously in a system, more than one indicator host species and pathogen should be targeted to achieve a complete WHM. In industrialized countries, the scope of targeted WHM is limited by funding and logistic limitations, whereas in less studied regions with more limited resources the identification of both suitable indicator species and target pathogens remains challenging (Table 1).

Another technological and budgetary limitation of targeted WHM emerges from sampling, shipping, and storing representative numbers of biological materials such as blood, serum, lymphoid tissues, and ectoparasites. While collecting a representative sample size of the indicator species in each system can already be challenging and time- and effort-consuming, particularly for small species such as rodents, bats, or carnivores as compared to game species (Maaz et al., 2022; Mazzotta et al., 2023), methodologies allowing the identification of shared pathogens through environmental sampling could create a whole new wide range of possibilities for IWM (Martínez-Guijosa et al., 2020).

Regarding analyses, antibody detection tests are originally designed and validated for domestic species and diagnosis in wildlife consequently faces specific challenges (Michel et al., 2021). Nevertheless, reliable antibody detection tests have been well-established for most of the relevant host-pathogen combinations (e.g., Godfroid et al., 2010; Boadella et al., 2011b; Elmore et al., 2016; Raez-Bravo et al., 2016; Thomas et al., 2021; Luo et al., 2023). Additionally, pathogen molecular detection tests are equally valid in domestic animals and wildlife and readily available, at least in industrialized countries.

Figure 2. Wild boar as indicator species: main characteristics and examples of pathogens which can be monitored through wild boar serology.

National and international regulations for sample collection, transport, storage, and analyses for infection diagnosis are an additional constraint to achieve the comprehensive WHM required for IWM. For instance, only public laboratories or reference laboratories might be allowed to perform certain techniques, and some authorities might be reluctant or even prohibit taking or analyzing samples from their territory. Intranational differences in regionalized countries such as Belgium, Germany, Italy, and Spain add complexity, difficulties, and bureaucratic issues hampering the effective establishment of WHM and the adequate preventive or management measures (Uchtmann et al., 2015). At each level, racing against each other and betting on being the last one to notify a disease seems sometimes the goal rather than collaborating in establishing comprehensive, holistic, and harmonized WHM and IWM. The perspective of low- and middle-income countries (LMICs) is synthesized in Table 1.

Section 2: HCM limitations and biases

Epidemiological evidence derived from observational and experimental studies suggests that shared multi-host pathogens are rarely best described as single or two-host systems, where only certain species are regarded as maintenance (Nugent, 2011). Rather, most multi-host pathogens thrive in complex and dynamic "maintenance communities" where different wild and domestic species and the environment contribute to build networks facilitating pathogen transmission and survival (Gortázar et al., 2023).

Assessing wildlife population abundance and density is challenging, and new methodologies are increasingly being proposed and contrasted against traditional methods (APHAEA Consortium, 2023; ENETWILD consortium et al. 2018; Iijima, 2020). The objectives of wildlife population estimations can be (1) censusing all the animals; (2) estimating the population abundance/density without seeing all the animals; or (3) obtaining population indices (Lancia et al., 1994; Witmer, 2005). Censusing or counting all the animals is generally unfeasible and habitat-dependent, thus such methods are difficult to standardize,

harmonize, transfer among different locations, and apply on wider scales (ENETWILD consortium et al. 2020). Each population monitoring method has pros and cons, but in general it should be reliable (accurate and precise to allow time trend analysis), with the potential to be used as a reference to validate and calibrate other methods, and provide density estimates rather than relative abundances (ENETWILD consortium et al. 2020; Palencia et al., 2021a). The methods could vary for different target species, but they should also be well-established, repeatable, suitable for a broad range of settings and species, and accessible to all actors including, for example, hunters and private gamekeepers or fish and game officers (Acevedo et al., 2007; Sobrino et al., 2009; Palencia et al., 2021b; Ruiz-Rodriguez et al., 2022; Sobrino et al., 2009). However, all these methods to estimate wildlife population abundance and/or density usually focus on a single species, while pathogens are usually maintained in a multi-host network community (Fenton and Pedersen, 2005; Godfrey, 2013; Portier et al., 2019). This single-host approach can be useful for the selected key indicator species in the network, but it fails to capture the biodiversity and its potential effect on pathogen epidemiology dynamics (Barasona et al., 2019; Keesing and Ostfeld, 2021; Barroso et al., 2023). Such biodiversity assessment is a key added value of IWM, and integrative methodologies capable of assessing and monitoring multi-species populations are required to capture the epidemiological complexity of multi-host systems (Robinson et al., 2014; Barroso et al., 2023).

Advanced IWM schemes such as that implemented in Spain consider two aspects of the host populations, namely (1) host community characterization and (2) host population monitoring (Barroso et al., 2023). Host community characterization describes the host community composition and identifies through network contact analysis the key species considering the regionally relevant diseases, which can be used as indicator species. However, since all vertebrate species are potentially relevant as indicators, victims, reservoirs, or bridge hosts for either known or emerging disease agents (Gortázar et al., 2021), an inventory of vertebrate richness is advisable. Species richness is also an index of biodiversity and can

Table 1. The perspective (limitations and challenges) on integrated wildlife monitoring (IWM) development in industrialized countries and in low- and middle-income countries (LMICs)

	Limitations in countries with ongoing IWM (e.g., Spain)	Additional challenges for LMIC countries without IWM (e.g., DRC)
Passive (scanning) wildlife disease surveillance		
Record and diagnose cases entering rehab centers and sick or dead wildlife found in the field	Passive WDS distribution and scale do not match the distribution of active sampling and monitoring Need to improve information exchanges between rehab centers and other actors and animal and human health authorities Need to secure stable funding	Very limited funding Few rehab centers, scarcity of qualified personnel, poor communications Relevant actors' awareness and involvement (hunters, local communities, animal and human health authorities, rangers) Political instability and insecurity hinder routine field activities
Active (targeted) wildlife disease surveillance		
Ensure funding		
Identify indicator host species	Few well-characterized indicator species (wild boar)	Need to identify suitable indicator species Need for capacity building
Identify target pathogens	No significant limitations: Key shared pathogens are known	Need to identify the target pathogens
Sample indicator species	Relatively easy in hunter-harvested species	Almost no legal hunting → sampling requires capturing Limited sampling skills
Sample environmental nucleic acids	Only proof of concept	Potentially transferrable
Ship and store samples	Few significant limitations: Relatively short distances and good communications, stable energy supply, facilities available Occasional regulatory constraints	Longer distances and poor communications, unstable energy supply, limited facilities Need for standardized records and permits
Analyze samples for target pathogens	No significant limitations: Well-established antibody detection (most species) and pathogen detection tests	Antibody detection tests need adaptation to new host species Need to use other pathogens detection tests (culture, PCR, NGS . . .) - limited facilities
Analyze samples for nonspecific indicators	Only proof of concept	Conceptualization
Host community characterization		
Ensure funding		
Host community composition and key species	Only proof of concept Large body of literature	Potentially transferrable if CT grids can be deployed
Inventory of vertebrate richness	Needs improvement, e.g., combining CTs and AI-based bird audio ID	Potentially transferrable if CT grids can be deployed and bird audio ID works Need to consider the variety of habitats
Space and time coincidence of relevant host species	No significant limitations: Running, based on CT grids	Potentially transferrable if CT grids can be deployed
Risk points for cross-species interactions	Identified based on resource distribution (water, food)	Can be identified but will depend on species and habitat
Host population monitoring		
Ensure funding		
Relative abundance of relevant hosts	Hunting data for game species, transect counts and point counts for birds and terrestrial mammals, frequency based on CT grids	No hunting data available Some transect counts might be challenging (safety) Frequency is doable if CT grids can be deployed
Density of indicator hosts	Species or group-specific techniques + REM as a multi-species technique based on CT grids	Needs adaptation to target the chosen indicator species
Changes in wildlife and livestock management	Need to be aware of significant changes in regulations, catastrophic events (wildfires, diseases) or sudden changes in livestock distribution and abundance. This requires inter-agency information exchange	Changes are less predictable due to catastrophic events and political unrest. Difficult to identify changes due to insufficient information
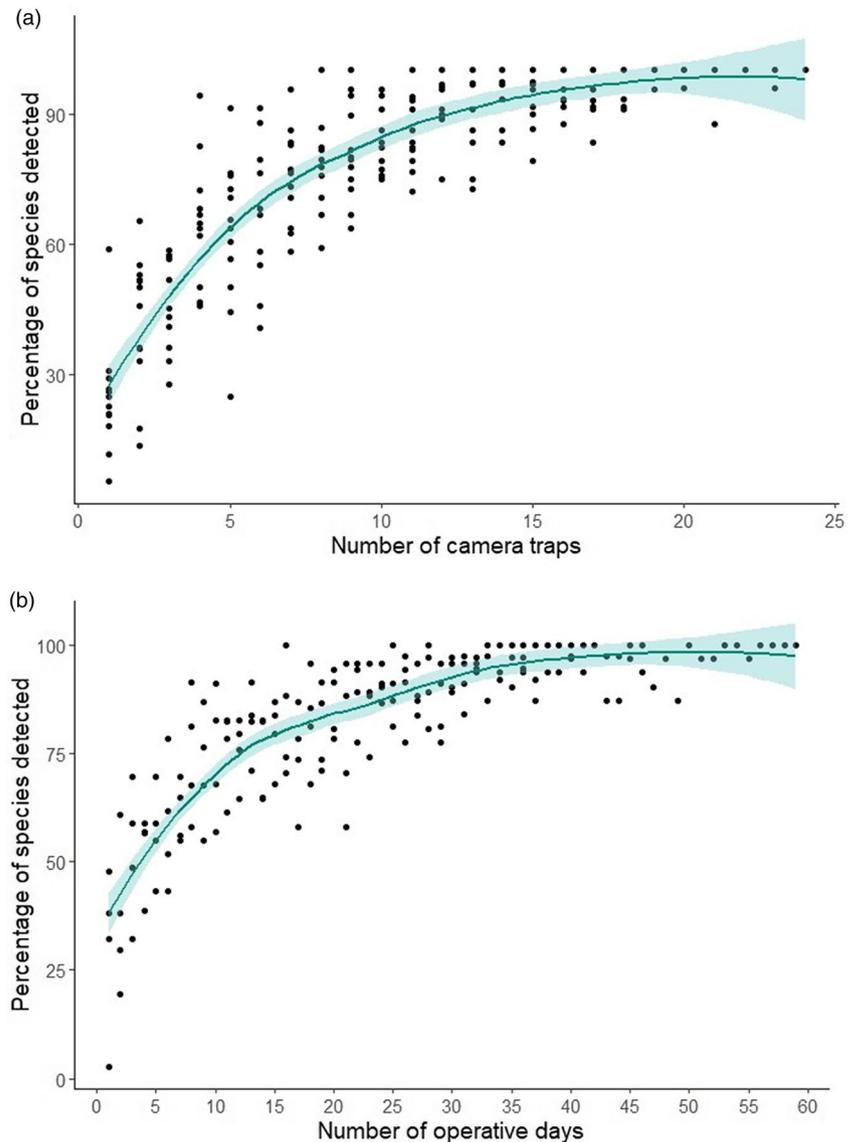
Figure 3. Percentage of species detected depending on the number of camera traps deployed in the field and the effort in days (number of operative days). Data was obtained from a nationwide pilot trial on integrated wildlife monitoring in Spain.

generate information to tackle the debate on the dilution effect or an increase in the circulation of at least certain pathogens due to higher host availability (Barasona et al., 2019; Keesing and Ostfeld, 2021; Barroso et al., 2023). The quantification of both direct and indirect contacts of relevant host species achieved through the network analysis should allow an understanding of pathogen transmission and circulation dynamics, as well as identifying the role of key host species in infection maintenance. Furthermore, the host community characterization should include identifying the main risk points for cross-species interactions, such as baiting sites or waterholes (Barasona et al., 2014a; Payne et al., 2017; González-Crespo et al., 2023a, 2023b).

HCM should at least include monitoring the relative abundance and spatial distribution of relevant hosts through time. Ideally, densities of indicator hosts should also be monitored, although this significantly increases the associated costs and efforts (Acevedo et al., 2008; Barroso et al., 2023; ENETWILD consortium et al. 2020). Moreover, since disease and associated mortality often affect differently host sex and age classes (López-Olvera et al., 2013; Garrido-Amaro et al., 2015, 2023), population estimation methodologies that permit identifying age and sex in indicator host species

should allow the establishment of population structure as an early nonspecific index of morbidity and mortality, thus contributing to general WHM.

Finally, population assessment methods, effort, and hence the quality and quantity of the information generated face the same territorial, political, and bureaucratic issues as aforementioned for WHM, varying not only among countries but even within countries (Ruiz-Rodríguez et al., submitted). Relevant changes in wildlife or livestock management should also be recorded as these will influence host populations.

Advances in population monitoring methodologies

Newer techniques to estimate wildlife population abundance and/ or density are traditionally validated against the formerly existing ones, considered the reference methodology. Methodology-biased indices can significantly affect wildlife population abundance and/or density estimations and consequently HCM and IWM (ENETWILD consortium et al. 2020; Norvell et al., 2003; Moore and Kendall, 2004; Le Moullec et al., 2017; Palencia et al. 2021a,2021b). The availability of low-cost electronic devices has led to their consideration as tools to assess and monitor wildlife populations, including unmanned aerial

Table 2. Main limitations found in the development of each component of integrated wildlife monitoring (IWM) systems and solutions proposed

IWM component	Reference	Main limitations constraining IWM	Proposed solutions
All components	1	Funding for capacity building, infrastructure, and budget	Establish IWM as a priority
All components	2	Methods and efforts are not uniform across regions and countries	Harmonize methods and efforts
Host community characterization and population monitoring	3	Time budget: finding the balance between field and deskwork effort and information yield	AI-based data treatment, R&D
Host community characterization and population monitoring	4	Methods still need development to broaden the host spectrum and optimize the information yield	AI-based sound identification, oriented R&D
Host community characterization and population monitoring	5	Unawareness of changes in regulations, catastrophic events (wildfires, diseases) or in livestock distribution and abundance	Improve inter-agency information exchange
Passive (scanning) WHM	6	WDS distribution and scale may not match the distribution of active sampling and monitoring networks	Acknowledge this limitation and merge results at larger scales
Passive (scanning) WHM	7	Motivation loss of non-government actors due to lack of feedback	Favor transparency and promote collaborative and inclusive workflows
Active (targeted) WHM	8	Need to identify the most suitable indicator species and target pathogens (mainly in LMICs)	Oriented R&D on indicator species and nonspecific disease indicators
Active (targeted) WHM	9	Limitations emerging from sampling, shipping, and storing large quantities of biological materials	Find the balance between optimal sample banking and keeping the budget stable - filter papers and environmental nucleic acid detection sponges facilitate field sampling and sample transport, and might help to overcome storage limits
Active (targeted) WHM	10	Regulatory constraints on sample collection, transport, and storage for infection diagnosis	Favor transparency and promote collaborative and inclusive workflows
Passive and active WHM	11	Misunderstandings due to insufficient information exchange	Improve information exchanges between agencies (human health, animal health, environment) and between agencies, rehab centers, and other relevant actors

vehicles, CT, genetic analyses, and sound detection (Gardner et al., 2010; Luikart et al., 2010; Trolliet et al., 2014; Barasona et al., 2014b; Linchant et al., 2015; Hodgson et al., 2016; Lyons et al., 2019; Beaver et al., 2020; Yip et al., 2020; Palencia et al., 2021a; Mason et al., 2022). However, when considered for HCM as a part of IWM, the methodologies used for population estimation must not only be reliable and validated, but also accomplish the requirements, particularly regarding capability of use in different habitats, multi-species detection, and reasonable cost (Acevedo et al., 2008; Barroso et al., 2023; ENETWILD consortium et al. 2020; Hofmeester et al., 2019). Genetic assessment of wildlife population is far too costly and restricted in species scope, while unmanned aerial vehicles, even if coupled with infrared sensors, cannot be used in all kinds of habitats (e.g., forests) and do only detect a limited variability of potential hosts. Therefore, CT is probably the new technology with the highest potential to become a useful tool for IWM, not only overcoming the mentioned limitations but also adding value and capabilities in the detection of host species beyond those identified through the traditional population estimations methodologies. Although less developed and still being tested as a proof of concept, sound detection of species can be relevant, particularly for the taxa more difficult to detect with other methods (including CT) and traditionally underestimated or ignored in HCM and WHM, such as birds, small mammals, and bats.

CT provides advantages as compared to other methods, since it generates information regarding both aspects of the host populations. Occasionally, camera traps deployed for population monitoring will generate wildlife disease surveillance data for diseases with visible signs, such as mange (Oleaga et al., 2011). However, the financial and logistical barriers for CT at broad geographical scales are a concern (Steenweg et al., 2017). One limitation to including HCM on IWM systems is the initial cost associated with camera purchase. The number of camera traps deployed and the time these cameras remain in the field determine our capability to (i) obtain reliable estimates of population density (Palencia et al., 2022), and (ii) characterize host communities in terms of composition and structure (Barroso et al., 2023).

On a local scale (e.g., management units), CT is a method that can be conducted in different environmental conditions and at any time to collect robust data, taking advantage of the multi-species reliability (Palencia et al., 2022). In open areas, with high detectability, direct methods such as vantage points and linear transects could be recommended against CT, especially in areas in which high vandalism is expected increasing the cost of camera repositioning and reducing the data recorded. If direct methods are selected survey design and reference method should be adapted to each species.

Limitations will depend on the socioeconomic context and are listed in Table 1. One challenge is finding the balance between field and deskwork effort and information yield. As mentioned above, the number of camera traps deployed in the field and the number of days of camera trap activity influence the reliability of population density estimates and the accuracy of the host community characterization. In our experience in Spain, 70%–80% of the detectable species were detected after 18 days of functioning and 8.5 camera traps (Figure 3). Camera traps can generate tremendous amounts of image data, and thus, attention has been given to

A theoretic modeling approach to integrated wildlife monitoring: Combining wildlife health surveillance, species features and network analysis to disentangle the factors determining Rift Valley fever virus hosts in Africa and the Arabian Peninsula (Walsh and Mor 2018)

A modeling study including both host community (HCM) and wildlife health monitoring (WHM) variables obtained from literature review and publicly available databases not only identified the host species of Rift Valley fever virus, but also allowed to disentangle the factors driving a wildlife species to be such a host.

The theoretic, modeling, and literature-based nature of this study conditioned the data gathered in the study to complete the integrated wildlife monitoring (IWM) approach. Thus, species and population information for HCM consisted mainly in biological and life-history traits, namely adult body mass, gestation length, home range, sexual maturity age, social group size, neonate body mass, and weaning age. As for Rift Valley fever virus (RVFV), only species susceptibility was taken into account for WHM, considered as reported positivity by serology, polymerase chain reaction amplification and/or virus isolation. Interspecific interaction for network analysis was based on the pathogens shared by each species included in the model.

Despite the limitations, this study allowed not only to identify the most relevant host species for RVFV, but also to detect drivers for a species to be a RVFV host, namely interspecific network centrality, host range, and early-life development. The field application of IWM should allow to improve and refine the outputs by adding to the model two key aspects: host species population abundance for HCM and pathogen prevalence in each host species for WHM. Both variables should allow new network analyses leading to more specific host role assessments and driver identification.

Integrated wildlife monitoring in practice: Identifying wild boar as the key indicator species for integrated wildlife monitoring in Mediterranean ecosystems (Barroso *et al.* 2023)

A nation-wide pilot test combining HCM and WHM in eleven sites in Spain allowed the identification of the wild boar as the key target species for IWM.

Camera-trapping data were used to estimate wildlife and domestic animal abundance and interspecific interactions, which allowed to characterize the host community network, thus gathering the required information for HCM. Blood samples collected from wild boars hunted in all eleven study sites allowed the determination in serum of specific and non-specific health indicators for WHM. Environmental variables for each study site were additionally included in the modeling.

The combination of HCM, WHM, environmental variables and modeling allowed not only to identify wild boar as the key target species for IWM, but also to disentangle the host community and environmental factors driving pathogen circulation within the system, such as the number of host species in the system, the interaction between the two most abundant host species (wild boar and red deer), or the latitude.

Figure 4. Illustrative cases of integrated wildlife monitoring: a theoretical approach for Rift Valley fever virus in Africa and the Arabian Peninsula and a practical pilot study in Spain.

developing artificial intelligence approaches for processing images. These allow scientists to remove empty images, identify species, count individuals in an image, and individual recognition (Vélez et al., 2023). Photogrammetry tools are used to save time and gain precision in animal density estimation (Palencia et al., 2023b). Other aspects to consider include the variations between camera trap models (Palencia et al., 2021b), and choosing the right camera trap settings for a broad range of study species (Hofmeester et al., 2019). Finally, there is a need to identify biases in the detection of species and quantification of interspecies interactions due to differences in size, movement ecology, and habitat preferences (Hofmeester et al., 2021). Moreover, camera traps are not the universal solution as they face strong limitations in the biodiversity assessment of taxa other than terrestrial mammals (Ortmann and Johnson, 2021). Addressing bird diversity, for instance, implies involving trained ornithologists or, eventually, making use of AI-based sound identification devices (Toenies and Rich, 2021). Similar devices are used for bat monitoring (Russo and Voigt, 2016).

Proposed solutions

Table 2 lists the main limitations to IWM identified in the sections above, along with suggested solutions for each one. Of the two general limitations, funding, and harmonization, the second one would seem easier to solve. There is potential to overcome four of these 11 limitations through increased information exchange and transparency and promoting collaborative and inclusive workflows. A further three limitations need, at least partially, to be addressed through ongoing research, two of them possibly with the support of artificial intelligence. Furthermore, a few technical innovations might contribute to IWM optimization, namely sound identification artificial intelligence, nonspecific health markers, microfluidic PCR, filter paper samples, and environmental nucleic acid detection, as specified above.

General discussion

Current wildlife health surveillance schemes present major flaws (Ryser-Degiorgis, 2013; OIE, 2019; Lawson et al., 2021; Machalaba et al., 2021; Giacinti et al., 2022; Mazzamuto et al., 2022; Delgado et al., 2023; Pruvot et al., 2023) and have not been able to forecast and prevent the onset of new epidemics jumping interspecific barriers and even becoming pandemics (Konda et al., 2020; Delahay et al., 2021; Sharun et al., 2021; Keusch et al., 2022). The combination of WHM and HCM to achieve effective IWM has the potential to overcome these limitations, but it also faces new

challenges and biases that must be considered and addressed when implementing IWM. Some of these limitations are inherited from conceptions of the former WHM schemes, as the restricted scope of host and pathogen monitoring biased to species phylogenetically related to and diseases shared with domestic livestock, respectively (Wiethoelter et al., 2015), which leaves aside potentially sources of new pathogens such as rodents or bats, as well as pathogens from out of the system (Mazzotta et al., 2023). Since monitoring all the vertebrate hosts and pathogens in a system is physically impossible, selecting indicator host species through network analysis (Godfrey, 2013; Gortázar et al., 2021; Barroso et al., 2023) and identifying key pathogens to investigate and monitor covering the main transmission pathways (Ciliberti et al., 2015; ENETWILD consortium et al. 2022) should allow IWM to overcome the limitations of previous schemes. Since host contact and interactions leading to potential disease transmission are heterogeneous, interspecific social network analyses are useful for wildlife disease ecology, epidemiology, and management beyond the traditionally assumed density-dependent models. The individuals (in intraspecific analyses) and species (in interspecific analyses, sometimes including pathogens) with higher and closer contact rates with other individuals or species are potentially more relevant for pathogen maintenance, transmission, and circulation (Craft and Caillaud, 2011; Craft, 2015; Silk et al., 2017, 2019; González-Crespo et al., 2023a; Silk et al., 2017). Thus, network analysis within the HCM component of IWM can contribute to identify the ideal target host species to monitor diseases in the most cost and effort-efficient way. Moreover, when coupling the information from network analyses with the information on disease susceptibility and prevalence obtained through targeted surveillance within the WHM, the selection can be further refined to specific host species-pathogen combinations. Such procedure has allowed, for example, identifying the wildlife hosts of Rift Valley fever virus (Walsh and Mor, 2018) or selecting wild boar as the most relevant host species for IWM in Mediterranean environments (Barroso et al., 2023; Figure 4). Once selected the ideal host species-pathogen combinations in each system, the correspondence between the prevalence and population trend of the indicator host species and the global prevalence and population dynamics of the hole system, as monitored through IWM, should allow the validation of such choice.

As compared to previous WHM schemes focused on limited host species and pathogens, the main step forward of IWM is adding HCM to WHM (Cardoso et al., 2022; Barroso et al., 2023). Within WHM, general disease surveillance generates reports of disease or mortality outbreaks to the corresponding national and international health authorities, thus improving the likelihood of early detection of emerging diseases. The periodic (usually annual) disease analyses obtained through targeted surveillance do not only allow the early detection of the targeted pathogens in areas where they were absent, but also, and more importantly, the monitoring of diseases already present in the system and identify their drivers. As for HCM, the spatial characterization of host community allows to identify both geographic hotspots and key species for disease maintenance and transmission, providing wildlife population managers and animal health authorities with specific targets to increase the efficacy and efficiency of mitigation measures. Finally, the regular monitoring of host populations allows the analysis of population trends, which wildlife managers and other can use both for quantitatively assessing the related disease-transmission risk and for the detection of potential epidemics onsets (Figure 1). By merging both HCM and WHM, IWM allows a comprehensive understanding of role of each species in pathogen transmission and

maintenance, transmission routes, and disease status in a system (Fenton and Pedersen, 2005; Pepin et al., 2017; Gortázar et al., 2021), requiring collaboration among health, wildlife, and livestock authorities and managers. Furthermore, achieving knowledge of the host community assemblage allows identifying the drivers of epidemiology and infection within the system (Martínez-López et al., 2009; Barasona et al., 2019; Triguero-Ocaña et al., 2020; Barroso et al., 2023), and monitoring the host network community and the population structure of the indicator host species provide additional early indicators of trends and changes in disease and mortality through network imbalances before the pathogen crosses the interspecies barrier (Craft, 2015; Espinaze et al., 2018; Garrido-Amaro et al., 2023).

Nevertheless, IWM has also drawbacks, limitations, and constraints beyond the restricted scope of each one of its components. Both WHM and HCM have associated costs and are labor-intensive, which raise funding constraints and logistic limitations, respectively. Such constraint and limitations are logically more difficult to overcome in LMICs without ongoing IWM (Table 1). This study proposes solutions aimed at addressing and overcome such limitations and constraints both in industrialized and LMIC countries (Table 2).

Additionally, methodological limitations are also challenging to achieve comprehensive IWM. Upcoming sampling and diagnostic techniques may contribute to increase and widen the pathogen range covered by WHM, new methodologies to estimate population density and abundance may allow a more complete assessment of biodiversity and the populations of the indicator species identified by the network analysis. However, the sampling and diagnostic techniques, the population estimation methodologies, and the network analyses performed will vary in their capability to identify pathogens, hosts, and indicator species, leading to biases that must be taken into account when assessing the actual performance of IWM schemes. Further characterization of such biases through comparative assessment of the aforementioned techniques, methodologies, and analyses will help to be aware of the limitations of the resulting IWM.

Conclusion

To summarize, IWM is the necessary step beyond to target the management of shared diseases from a One Health approach and preventing future pandemics. However, IWM must still face serious scope, funding, logistic, and methodological challenges to be implemented, particularly in LMIC countries. This study proposes solutions aimed at addressing and overcome such limitations and constraints both in industrialized and LMIC countries.

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