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Research Article

Centering accessibility, increasing capacity, and fostering innovation in the development of international eDNA standards

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Abstract

Environmental DNA (eDNA) includes a set of rapidly emerging technologies that have the potential to support environmental monitoring and biodiversity conservation through novel, non-invasive, cost-effective and democratic methods and tools. Meanwhile, eDNA researchers are developing international standards for eDNA technologies, methods and data outputs. For eDNA technologies to be accessible, useful and appropriate, we must ensure that any standards developed include a broad conception of users from around the world, a diversity of ecological contexts and locations and, most importantly, a realistic outlook on research capacities and infrastructure. In this article, we assemble perspectives on international standardisation of eDNA from a diverse and global group of users and experts from Africa, South America and the Pacific Islands. The authors of this article collaborated by answering and discussing a set of open-ended questions aimed at eliciting hopes, concerns and experiences regarding eDNA standards. The result is a set of emergent themes and a generative consensus to highlight the need for the creation of adaptable standards, the development of regional capacity, increased sensitising to data sovereignty and the viewing of standardisation as a global capacity-building activity.

Key words: biodiversity, capacity-building, conservation, eDNA, environmental DNA, innovation, international standards, monitoring, standardisation

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Introduction

Researchers have demonstrated the utility of environmental DNA (eDNA) technologies and methods for detecting biodiversity, estimating species distributions, locating endangered or invasive species, detecting wildlife microbiota and disease and monitoring conservation across spatio-temporal scales and ecosystems (Kelly et al. 2014; Pedersen et al. 2014; Thomsen and Willerslev 2015; Valentini et al. 2016; Deiner et al. 2017; Taberlet et al. 2018; Beng and Corlett 2020). These methods and tools are rapidly transforming non-invasive and comprehensive biomonitoring on a variety of taxa and ecosystems around the world and supporting science to understand nuanced impacts of climate change (Thompson et al. 2023). However, many of the technologies available to sample, process and collect eDNA are still emerging and have not yet converged into a single, widely applicable workflow. Further, in terms of application, the field is shifting from a more developmental stage of assessments using eDNA to a more applied stage of biomonitoring using eDNA (Bani et al. 2020; Schenekar 2023). At the same time, efforts to barcode the entirety of life by building powerful reference databases and baselines for biodiversity have also been gaining speed over the last two decades through the International Barcode of Life and other global initiatives.

With these shifts in the maturity of eDNA and the potential application of these technologies, researchers using and developing eDNA methods and technologies are increasingly discussing the need for and importance of standards (Weigand et al. 2017; Helbing and Hobbs 2019; Bruce et al. 2021; De Brauwer et al. 2023; Lee et al. 2023), which include best practices, minimum requirements, protocols and certifications (Wilson-Wilde 2018). Scientific standards are an important aspect of ensuring quality and reliability and are often essential for developing trust in a scientific enterprise. They are also valuable because they help advance eDNA research tools and services and make them available, appropriate and trustworthy for institutional uptake for regulatory purposes (Kelly et al. 2023; Lee et al. 2023). They can range from ad hoc informal best practices to those developed by official standards bodies such as the International Organisation of Standardisation (ISO) and include both national and international perspectives.

As of 2024, there are several national efforts aimed at creating standards for eDNA in aquatic environments, including those in Europe, Australia, New Zealand, Canada, China and Japan. There are also nascent efforts to develop international standards for some eDNA methods through the ISO, as well as through the Ocean Biomolecular Observation Network (OBON). The standardisation effort has been largely driven by researchers in the Global North, from countries with the greatest access to state-of-the art technologies, laboratories and funding, such as those in Europe and North America, as well as Japan and Australia (De Brauwer et al. 2023; Sharaf et al. 2023; Shea et al. 2023). This means that some of the most biodiverse locations of the world are also the regions that are not currently being included in efforts to create global standards (Tydecks et al. 2018). This skewed access to the standardisation process, while originating from inherent inequalities in access to infrastructure, funding and technology, could perpetuate unequal participation in eDNA research in the future (von der Heyden 2022). For eDNA technologies to be accessible, useful and appropriate, we must ensure that any standards developed include the

perspectives of a broad conception of users from around the world, consider different ecological contexts and locations and, most importantly, different research and infrastructure capacities available to eDNA researchers everywhere. Further, the social and ethical implications of eDNA standardiation should also be considered (Shen et al. 2023). As a step towards engaging the standardisation process more fully with voices from around the world, we assemble perspectives on international standardisation of eDNA from a diverse group of users and experts from Africa, South America, Asia and Pacific Islands. The authors of this article collaborated by answering a set of open-ended questions aimed at eliciting hopes, concerns and experiences regarding eDNA standards. The result is a set of emergent themes, which highlight the need for the creation of adaptable standards, the development of regional capacity, sensitising to data sovereignty and viewing standardisation as a global capacity-building activity.

Methods

This is a collaborative manuscript, written by scientists from around the globe. The goal of the project was to understand how efforts to develop international standards (including laboratory protocols, workflows and certifications) might support, or raise concerns for, researchers using eDNA methods and technologies in the Global South and remote (difficult to access) areas. To accomplish this goal, the eDNA Collaborative at the University of Washington engaged with a group of 18 researchers to elicit their perspectives on eDNA standardisation.

An initial set of eDNA researchers and practitioners from South America, Africa, Asia and Pacific Islands (n = 54) were gathered through online research and previous contact with the eDNA Collaborative. From this initial set of contacts, a group of researchers were invited by email to participate in this manuscript as co-authors (see Fig. 1). The group was chosen intentionally: to provide a range of participant locations, career stages (all stages of career from early career to institutional leadership), career types (research, management, university, non-profit, government), eDNA application (biodiversity assessment, invasive species, water, air, soil) and taxa. Some contacts were made through snowball sampling, with the intention of creating a diverse list of 18 participants/co-authors.

Figure 1. Co-Author affiliatiations and research locations.

This research draws on a rich tradition of qualitative social science methodology. As such, quantifying perspectives or encompassing a representative sample size is not the aim. This mode of qualitative research is common in fields, such as science and technology studies (Collins 2009; Ribes 2014), innovation studies (Edwards 2013) and many other social science fields in which the study population is large, dispersed and complex, such as global scientific and expert communities like environmental science (Borie and Hulme 2015). These methods are often used to represent diverse voices through feminist, post-colonial and de-colonial qualitative research that centres on situated perspectives (Haraway 1991).

The research here uses the interpretive qualitative method of grounded theory (Charmaz 2005), using expert interviews as a data source. Grounded theory is an advantageous method in social settings where there are no previous data or observation and it can reflect the lived realities of individuals who may not often be studied, especially in large-scale—in this case global—situations (Clarke 2005; Ribes 2014). To gather data, each co-author was provided with a set of open-ended questions about their research and expertise related to eDNA, their current use of standards, their perspective on the development of international standards, the resources available to them to conduct eDNA research and the clarity of their own eDNA research in the future. Co-authors were asked to think broadly in terms of standards, including any parts of a workflow from equipment and technology selection, to study design, sample collection, sample processing, PCR, metabarcoding, sequencing, bioinformatics and reporting. Co-authors were given the option to respond to the questions in writing or during a 30–45-minute semi-structured interview, based on the open-ended questions. All the co-authors responded via virtual interview. The interviewer took notes and asked follow-up questions during the interview.

The notes were then analysed and coded for themes using a standard grounded-theoretical approach (Charmaz 2005; Clarke 2005). As opposed to a hypothesis-driven deductive research approach, grounded theory is an inductive research approach in which the conclusions (theory) are based on the data (Charmaz 2005). A grounded theory approach relies on an iterative process of coding in which categories and themes are developed by the coder. With large datasets, this is sometimes accomplished using software; however, this small dataset was “hand-coded” using an Excel spreadsheet. The coding was done by an experienced coder, who identified themes, categories and sensitising concepts (Bowen 2006), which were iteratively developed in three subsequent coding sessions until what is called “saturation” was reached. That is, the codes became aligned into a conclusion and no new information is being generated. In this case, the iteration was accomplished through the direct input of the interview subjects, who are the co-authors of this manuscript. This is a common approach in smaller-scale grounded-theoretical studies such as this one and iteration with the research participants is the ideal because it avoids preconceptions and bias, but cannot always be accomplished due to the size of some studies (Clarke 2005). The size of this study, however, allowed for this iterative approach to be fully used, avoiding researcher and coding bias through direct triangulation.

The results and discussion below represent the collected views of the participant/co-authors, but do not propose a singular perspective or voice. In

keeping with qualitative research, the results are not described numerically[1]. The "Results and discussion" section describes this diversity of opinions, which may or may not agree with one another. We highlight several themes that were identified and aligned across the interviews and are described in the "Conclusions" section of the article.

Results and discussion

Current use of standards

There is no universal definition of a "standard." In this context, we use the ISO definition: "a document, established by consensus and approved by a recognised body, that provides, for common and repeated use, rules, guidelines or characteristics for activities or their results, aimed at the achievement of the optimum degree of order in a given context" (ISO 2019, p. 24). Standards are used in almost all fields and industries to facilitate communication, interoperability of tools or methods and comparability of results. A good standard will ensure reliability and trust. Almost all participants used some form of standard in their work. These range from ad hoc or informal standards such as best-practices and guidelines to more formal protocols such as methods and data requirements to fully formalised standards for lab accreditation or quality assurance or certification, such as those curated by the ISO.

Several participants have adapted national standards to meet their own needs, such as guidelines for PCR analysis and reporting from the Department of Fisheries and Oceans Canada (Abbott et al. 2021), the Japan eDNA Society's guidelines for sampling and analysis (The eDNA Society 2019) and Genome Canada's iTrack Program's standardised methods (Gagné et al. 2021; Abbott et al. 2023). Many participants reported using standards for data reporting, especially when interfacing with international repositories and consortiums such as Ocean Biomolecular Observing Network (OBON) and its Ocean Biodiversity Information System (OBIS) data protocols, the Global Biodiversity Information Facility (GBIF) protocols or the International Barcode of Life (IBOL) BOLD System. Some researchers have developed regional protocols, such as the Ocean Info Hub's (OIH) Ocean Data and Information Network for Africa and the Latin American and Caribbean Region. These standards differ in their purpose, scope, range from methods, protocols, workflows and data requirements. Only three participants mentioned ISO standards and those that did had relied on the ISO forensics standards (ISO/TC 272) or lab certification standards (ISO/IEC 17025).

Perspectives on benefits of standards

Every participant identified benefits (either from existing standards or potential ones) emerging from the creation of international standards. These include several points which centre around reproducibility and collaboration, guidance for research, increasing credibility of eDNA and meeting end goals.

1 Descriptive words align roughly to the following when describing proportions of participants/co-authors (n = 18): "few" = 3–4, "several" = 5–7, "many" = 8+, "almost all" = 16–18.

International standards are broadly seen to increase international collaboration by ensuring the results are comparable, reproducible and accurate. When asked how standards currently support their eDNA research or may in the future, almost every participant highlighted the importance of reproducibility or replicability of results. Although reproducibility and replicability are different things (at least at the post-bioinformatics stage), the terms were often used interchangeably. Regardless of the exact meaning and context, these concerns centre around the ability to conduct research in different locations that could be comparable and accurate across time and space. The perceived need to strengthen eDNA research to make it a more credible and trustworthy science that will be accepted by other scientists, decision-makers and resource managers is closely related to this need for reproducibility/replicability as well as interoperability. Several interviewees mentioned that that credibility was important to secure funding for eDNA research and related it to reproducibility and replicability. Some participants also discussed how laboratory certification would be easier with international standards. Realistic and achievable certification and standardisation were also viewed by some as a way to democratise eDNA science by allowing smaller, less well-funded laboratories to gain credibility and stand on par with more prestigious (often better resourced) laboratories and institutions.

In addition, many participants desired clarity and comparability of results across the world and recognised the difficulty of achieving this without standard methods and protocols. Some participants wished for a common nomenclature, clear guides and accepted workflows from sample collection through bioinformatics and data reporting, which would make eDNA methods more accessible to researchers across the world. This, too, was seen to facilitate international collaboration and uptake of eDNA research. Some participants mentioned open access data and software for clarity in workflows and provenance, such as the BioProv for bioinformatics workflows (Salazar et al. 2021), although others were wary of how data might be used if made public, which is explored in the next section.

There were a variety of opinions that participants expressed about how standards will help or hinder their work. For example, standards may help researchers understand where they can cut costs, making the technology more affordable and accessible, but at the same time, some fear that standards could make research more expensive by requiring particular materials or technologies. Several people discussed how standards could make eDNA tools more effective at developing a baseline understanding about biodiversity and view eDNA as a means to this end, but only if these standards are accessible to communities, managers and those working on the front lines of conservation.

Concerns about standards

Although there are differences in emphasis and opinion, many participants are aligned in their concerns about international standards. These concerns centre around resources, including 1) cost, accessibility and capacity; 2) data requirements and ownership; and 3) questions about the technical feasibility of standardisation.

Access and capacity

Access to the resources necessary to meet standards was a ubiquitous concern across all participants. These resources include finances, access to technologies, materials and equipment, as well as capacity (such as personnel for running a sequencing machine). Participants were concerned that, if the cost is too high, standards will be out of reach, impossible to achieve and elite. Concerns like these, around "setting the bar too high" were expressed by many participants. It is important to note that scientists desire to meet rigorous standards, but it may be physically impossible to access all the resources needed to meet them. Researchers in many parts of the Global South have a difficult time accessing laboratory supplies and when they are obtained, they can be 3–4 times as expensive as they would be when purchased in Europe or North America. They may also take many months to arrive due to customs and shipping delays because there are no regional suppliers. This barrier can make it difficult or impossible for researchers to meet stringent standards or to produce outputs in a timely fashion. In addition, this resource reality means that sending samples overseas for processing may be less expensive than trying to obtain materials and process samples in their labs, although this can be made more difficult by exchange rates, with many Global South currencies considerably weaker against the US Dollar or Euro. Further, shipping samples overseas can lead to potential or perceived issues around experimental and data control that will be discussed later.

Fundamentally, access to materials and technologies is a major barrier to meeting standards, especially if capacity and funding are already stretched. For example, if a high number of biological or technical replicates is required to meet a standard, this may mean that it is too costly to conduct a research project according to those standards. Other participants gave examples of their ongoing difficulties in obtaining reagents or other materials. For some, meeting Canadian or EU standards that include using synthetic DNA for calibration (as opposed to serial dilutions) or using probes in addition to primers for qPCR analysis, is not possible and so standards that require these cannot be met. This type of trade-off is a reality for many researchers in the Global South and remote areas and, in many cases, there is no option, but to adapt protocols and standards to what is available, although this may be problematic during the peer-review process.

Difficulty accessing technology and state-of-the-art equipment was also mentioned by many participants. Laboratory sterilisation was a particular problem identified by a few researchers. There are entire regions (e.g. polar regions, middle jungle and the Amazon Forest) and situations (on research vessels) with no sterile extraction lab and so any standard which requires one would be unattainable. While those doing genetic work aim to have sterile labs, standards that require best practices, such as separating workflows into dedicated and separate rooms, each with their own air sources, can be fundamentally cost prohibitive or physically infeasible. Similarly, researchers in many regions have limited access to sequencers and if they do, a human-centred genomics facility may be all that is available, which is not ideal for eDNA research. Additionally, challenges with access to refrigeration are common, especially when combined

with shipping delays. While some of these issues, such as sequencing, are becoming less of a challenge due to developments in portable and affordable sequencing technologies, such as the Oxford Nanopore, these technologies are far from being universally accessible, reliable or applicable. Still, the lack of access to computing power and specialised training necessary for bioinformatics work makes these technologies impractical for many researchers.

Some people pointed out that the goal of eDNA monitoring is to make monitoring more cost effective than traditional monitoring, but if standards require expensive materials, this is directly at odds with this goal. Fundamentally, researchers do not have access to all materials everywhere and this must be considered when developing international standards. There was a common worry that, if international standards are set by those in more developed countries, they will be unattainable by those in less-resourced and accessible areas. Finally, the cost of purchasing the actual standards or obtaining laboratory certification was discussed by some participants as also being a concern.

Technical concerns

The second most-common concerns were around the technical issues of creating useful standards. Many participants identified the difficulty of creating a "one-size-fits-all" standard method or protocol ranging from sampling design to data analysis, when it is used to research a wide variety of locations, ecosystems, taxa and applications. The material differences between many study sites are vast–from tropical forests to Arctic deserts and from soil to air to water–and people are concerned that a standard might not translate or be interoperable, across such physical and biological differences.

Different eDNA technologies are also at very different stages of technology readiness, depending on the application and some participants are concerned that standardising at this stage, when many researchers are troubleshooting and experimenting with different techniques, may stifle innovation and may make it difficult for the field to change in the future. People pointed out that the technology is developing at a rapid pace and methods and technologies are still in flux. Further, many locations also lack a local species DNA reference library, which was mentioned by many researchers in this study and has been documented by others (Perry et al. 2022; von der Heyden 2022; Schenekar 2023). The fundamental challenge of a lack of reference library was particularly highlighted by researchers working in biodiverse areas (such as the Tropics) where new species are being discovered weekly and conducting biodiversity inventories is expensive and difficult due to the nature of cryptic or rare species.

Data concerns

Data sharing and data standardisation were another set of concerns discussed by almost everyone. While participants regarded data standardisation as important, some also felt that it was costly and time consuming, partly due to the high cost of computing and lack of access to reliable internet connectivity and data servers in some locations, particularly remote islands. Beyond these technical aspects, however, many people discussed data standards in terms of data ownership and control, particularly in relation to genetics. The Nagoya Protocol,

which outlines the fair and equitable use of genetic resources, was named as both a difficulty for researchers wanting to ship eDNA samples across borders and recognised as an important consideration for ethical standards development. Some also think that the Nagoya Protocol does not go far enough in protecting genetic resources. While there was no precise consensus amongst participants, many people mentioned the legacy of genetic colonialism, issues with colonial science more generally, intellectual property rights and indigenous sovereignty as being important considerations for standards development, both in terms of genetic resources themselves and the data related to these resources.

Several people discussed the specific issue of data security, describing how eDNA-related data can be very culturally and personally sensitive, particularly in terms of unintentional geo-location of human DNA "bycatch" that could end up in public databases (Whitmore et al. 2023). This is especially true when it is related to cultural resources and threatened species, which could be subject to exploitation without community consent or overharvest and do not want their data to be geo-located.

Other concerns

Several other concerns around standards were also discussed by some participants. One of these is in relation to publication and that if standards become required for publishing in particular journals or receiving funding from particular sources, this could become a barrier for some researchers. Another concern related to development of standards themselves and that it may be inappropriate to adopt standards from one field and apply them to another. One example would be adopting genomic methods from museum collections or forensics labs, which might not be helpful for those trying to develop genomic methods to be used in the field. Finally, a few participants were concerned about the development of standards that favour private companies, either favouring one over another or stifling experimentation in academic settings by imposing strict, industry or regulatory standards in that context.

Resources required to foster eDNA research

In addition to being asked to discuss their perspectives on standards, participants were given an opportunity to talk about access to resources needed more generally. Many of the answers arose in the form of bottlenecks or gaps, in which a research workflow became difficult or impossible without developing alternatives.

One, almost universal concern, for those doing eDNA analysis in the Global South and remote areas was the high cost and difficulty of obtaining reagents, although other materials, such as filters and flow cells, were also mentioned. As discussed above, for some, even basic laboratory equipment is difficult to come by and sequencers were often regionally inaccessible or non-existent, although advances in rapid, *in-situ* metabarcoding are changing this (Doorenspleet et al. 2021; Egeter et al. 2022. Sterile environments for extraction are also difficult to access or build in many regions, making many eDNA methods out of reach. In some cases, focusing on extremely small DNA fragments (< 75 bp) might be unattainable and prone to cross-contamination, but targeting larger fragments (from more recent DNA deposits into the environment) is within reach even in field laboratories.

Shipping samples and materials across borders was identified by many participants as being a major, time-consuming and expensive hurdle. Without regional suppliers, shipping times can become prohibitive. There is a general acknowledgement across most participants that there are significant gaps to fill in funding, access and coverage of areas in terms of reference libraries and understanding species and baselines. This includes the High Seas and the Global South, but also many areas of the tropics more generally, where there has been little comprehensive genomic work done. The Barcode of Life Database (BOLD), for example, illustrates a concentration of data in the Global North. Several people discussed the need for experts in specific taxa working to develop rigorous databases on under-represented ecosystems or species. As one participant pointed out: "your sequences are only as good as your libraries".

Finally, almost half of the participants discussed bioinformatics as being a major bottleneck in their work. The reasons are broad, from difficulties with accessing computing capacity and storage, to lack of expertise and a fast-moving field where pipelines and statistical packages are developing at a rapid rate. Several participants specifically identified the need for training in bioinformatic analyses and the difficulty of retaining people in the bioinformatics field.

Perspectives on future of eDNA research

A final interview question was related to perspectives on the future of eDNA research, both their own and the field as a whole. As might be expected when speaking to a group of eDNA researchers, everyone expressed a general sense of excitement and optimism for their research and expanding applications for eDNA in the future. People spoke about the fast rate of technological development, with decreasing time to obtain data, possibilities for quantification of organisms and a future where "everything is done in the field", due to the accessibility of real-time long-read sequencing (Doorenspleet et al. 2021; Egeter et al. 2022). The excitement was palpable as people spoke about the development of global genomics libraries, improved protocols, applications to conservation and regulatory contexts and scientific possibilities for understanding the world through RNA, ancient DNA and other evolving applications (Pedersen et al. 2014).

In terms of a cohesive vision for the field, participants discussed the need for people to really "dig in for the long term", develop expertise and refine methods and protocols. Several people think that this in-depth work is necessary to move the field forward and become more rigorous and trusted. A few participants described a difference in goals between those that are working to develop eDNA as a means to understanding and addressing the biodiversity crisis and those that want to make a profit from the technology, although most people discussed common values across eDNA researchers that is based on openness, collaboration, sharing and even democratic and egalitarian ideals.

Conclusions

It is important to remember that the purpose of this article is not to portray a unified perspective, but instead to describe a diversity of viewpoints, which may, or may not, always be in agreement. Therefore, the outcomes of this paper

should not be taken as a collective voice, but instead a collection of voices that offer to broaden scope and ideas in relation to international standards for eDNA.

Theme 1: Creating adaptable standards

Many people described the potential positive impacts that international standards could have on their work, but they also illustrated ways that these standards should be adaptable and flexible, having different options or protocols for different contexts and applications. Several examples were provided to illustrate this point, including alternative standards for: in-field (or on a boat or in a kitchen) vs. in-lab. This would include different standards for different processing and analysis goals and flexibility to consider different costs and materials or reagents (such as different Taq polymerases). A common perspective was the need to have pragmatic guidelines that can make research comparable, but that are not so stringent that research (or researchers) are left behind. While flexibility may seem at odds with standardisation, flexibility is actually a well-known property and even purpose for standards, which act as "boundary objects" to enable shared meaning and communication across different communities (Star and Ruhleder 1994). This is especially important to consider in terms of communication to regulatory bodies and developing a shared trust concerning this new form of environmental data. In this vein, standards can be created and reported in ways that ensure their adaptability taking into account those things that are minimum requirements ("need to have") vs. ideals ("nice to have"). This would allow more people to use standards and speak across locations, fields and applications and regulatory bodies especially as technologies are in flux.

Theme 2: Develop regional capacity

One overarching desire is the need to strengthen regional or in-country capacity for eDNA research. Increasing regional capacity will help avoid imbalances in "parachute" or colonial science (von der Heyden 2022; Shea et al. 2023) and enable researchers in the Global South to have more access to eDNA technologies and capabilities. This can be achieved by, for example, equitable, fair and open mentorship between individuals from the Global North and South.

A recent study by Shea et al. (2023) found that eDNA sample analysis is mostly done in the Global North, by researchers collecting and bringing back samples to process at their home institutions, including sampling without permits or involvement from local or regional researchers (von der Heyden 2022). Yet, this is also often the case for researchers in the Global South, who send their samples to the Global North to be processed because of a lack of access to laboratories or because of cost constraints. This issue can be addressed by building regional or local consortia that could help develop accredited laboratories, provide training to in-country researchers and support capacity-building locally. This must include increasing access to sequencing technology, as there are few sequencing machines in Africa and other regions also lack access to them (Ebenezer et al. 2022). The Open Institute of Africa BioGenome Project is an excellent example of this kind of consortium-building exercise, as it aims to build capacity by

offering regional workshops for knowledge exchange in biodiversity genomics and bioinformatics. To date, the project has trained over 400 African scientists in hands-on molecular biology, genomics and bioinformatics techniques and engaged with over 3500 African participants in regional workshops (Sharaf et al. 2023, 2024). This was accomplished using a multi-institution, hybrid, regional workshop model and has the goal of the creation of an African-based biodiversity genome database, with sequences of over 100,000 endemic African species (Ebenezer et al. 2022). Another related example of success in the field of eDNA is the marine microbiome initiative to leverage bioeconomy across the Atlantic (Ortmann et al. 2023; Thompson et al. 2023, 2024).

Further, proficiency testing and obtaining reference materials can be an issue in certifying labs, but this could be done regionally. One example is the National eDNA Reference Centre being established in Australia which will facilitate standardisation, design assays relevant to the region and provide proficiency testing for labs on the continent (Trujillo-González et al. 2023). As such, regional hubs or consortia will likely help resolve issues relating to data and genetic property by keeping samples local, whilst regional networks can help produce libraries and methods that are relevant to particular localities and ecosystems.

Theme 3: Sensitise to data sovereignty

Standards should be developed in a way that provides options, realising that not all data can be geolocated and that some researchers and communities may want to opt-out of publishing sensitive data due to issues of sovereignty or security. Researchers engaging in these conversations in other fields, such as palaeogenomics (or ancient DNA), have identified ways to create more equitable participation of researchers in the Global South by attuning to local implications of research, taking time to develop and implement accountability measures and acknowledging the historical harms caused by scientific colonialism and other forms of exploitation (Ávila-Arcos et al. 2022). Beyond data, eDNA standards should consider ethical engagement with indigenous communities more broadly (Handsley-Davis et al. 2021). Attention should be given to existing frameworks, such as "The CARE Principles for Indigenous Data Governance," which address the tensions between the desire for open data and protecting indigenous and traditional knowledge (Carroll et al. 2020). These principles build on work by other data sovereignty efforts in the US, Canada, New Zealand/Aotearoa and Australia. The CARE Principles have been adopted by The Smithsonian Institution and others and could also be adopted by eDNA and genomics organisations and incorporated into standards development. Further, researchers should not privilege eDNA knowledge and consider local knowledge and expertise in equal value to genetic research (Shen et al. 2023).

Theme 4: View standardisation as global capacity building

Although international standards have no technical requirement to be attainable by all, if a standard is truly an international or "global" standard, eDNA practitioners everywhere should have the capacity to meet it. In other words: while it is important to have a standard, it is more important that everyone can use it within their own situations and contexts. This is especially true because

both the biological and social contexts for eDNA research vary across the world and also within locales. The goal of standardisation should be a process-based goal: standardisation itself should build capacity. If eDNA standards are open, accessible and affordable, they can become a powerful tool. Standardisation can help build a strong international network of researchers that rise together to face the biodiversity crisis. This will require the research community to work together to strengthen capacity and support training and mentorship on a global scale, for example, to study climatic and global changes. Importantly, rather than hindering development, dialogues taking place around standardisation of eDNA methods and technologies should act as catalysts and democratising exercises, but in order to do so, dialogue must take place across all hemispheres of the globe and invite a wide range of stakeholders into the conversation.

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Additional information

Conflict of interest

The authors have declared that no competing interests exist.

Ethical statement

No ethical statement was reported.

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Author contributions

Conceptualization: SLH, RPK, EA. Data curation: SLH. Formal analysis: SLH. Investigation: SLH. Methodology: SLH. Project administration: SLH. Writing - original draft: MLL, SH, RPK, GHBP, MLDL, NKDC, EA, SLH, NAP, PAA, JGMG, KKCH, NM, KNO, DAP, FT, MW, VYN, YR. Writing - review and editing: PAA, DAP, JGMG, YR, KKCH, FT, NM, EA, NKDC, VYN, SLH, MLDL, GHBP, RPK, SH, MLL, KNO, NAP, MW.

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Data availability

All of the data that support the findings of this study are available in the main text or Supplementary Information.

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Supplementary material 1

Interview questions

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Data type: docx

Explanation note: Contains the questions used in interviews for this research.

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