Received: 5 August 2022 | Revised: 13 September 2022 | Accepted: 14 September 2022

DOI: 10.1002/edn3.364

Environmental DNA
Open Access
Dedicated to the study and use of environmental DNA for basic and applied sciences
WILEY

COMMENTARY

UK DNA working group eDNA week, January 2022

Lori Lawson Handley[1] | Tabitha Blackwell[2] | Holly A. Broadhurst[3] | Katie Clark[4] | Phil I. Davison[5] | Judy England[6] | Stefano Mariani[7] | Allan D. McDevitt[3,8] | Kirthana Pillay[9] | Dan Read[10] | Kerry Walsh[11] | Andy Nisbet[4] | Simon Creer[12]

[1]Department of Biological and Marine Sciences, University of Hull, Kingston upon Hull, UK

[2]School of Geography, University of Nottingham, Nottingham, UK

[3]School of Science, Engineering and Environment, University of Salford, Salford, UK

[4]Natural England, Horizon House, Bristol, UK

[5]Centre for Environment, Fisheries and Aquaculture Science (Cefas), Lowestoft Laboratory, Suffolk, UK

[6]Environment Agency, Red Kite House, Howbery Park, Crowmarsh Gifford, Wallingford, UK

[7]School of Biological and Environmental Sciences, Liverpool John Moores University, Liverpool, UK

[8]Department of Natural Sciences and the Environment, School of Science and Computing, Atlantic Technological University, Galway, Ireland

[9]School of Natural Sciences, Bangor University, Bangor, UK

[10]UK Centre for Ecology & Hydrology (UKCEH), Benson Lane, Wallingford, UK

[11]UK Environment Agency, Rotherham, UK

[12]Molecular Ecology and Evolution Group, School of Natural Sciences, Bangor University, Bangor, UK

Correspondence
Simon Creer, Molecular Ecology and Evolution Group, School of Natural Sciences, Bangor University, Gwynedd, UK.
Email: s.creer@bangor.ac.uk

Andy Nisbett Natural England, Horizon House, Deanery Road, Bristol, UK.
Email: andy.nisbet@naturalengland.org.uk

Funding information
Natural Environment Research Council, Grant/Award Number: NE/N003756/1 and NE/N006216/1

Abstract

Here, we report on eDNA week, an international conference held online as a five-day series of webinars from January 17, 2022, to January 21, 2022. The conference was organized by the UK DNA working group, which has witnessed considerable growth and application of eDNA research since its founding and first conference in 2014. The 2022 event, held online due to the COVID-19 pandemic, provided an opportunity to invite international researchers who are leading the field, without the usual constraints of conference location. Compared with the previous UK-based in-person conferences, there was greater international participation amongst the 514 people who registered to attend the event. To emphasize the importance of collaboration between sectors in driving forward DNA monitoring, a session was devoted to presentations by participants from governmental agencies, and another to those from commercial companies developing and utilizing DNA tools. The industry and stakeholder sessions were accompanied by state-of-the-art presentations delivered by a global group of DNA/eDNA researchers from 11 countries. These sessions were complemented by an open forum session for reflection and discussion.

KEYWORDS
biodiversity, ecosystem biomonitoring, eDNA, environmental DNA, UK DNA working group, webinar

1 | INTRODUCTION

The UK DNA working group (WG) is a forum that brings together government agencies, academics, industry, and other stakeholders. Established in 2014, it aims to improve end user awareness and usage of DNA-based applications for environmental monitoring and assessment, by focusing research priorities and sharing best practice. Established within the UK Environmental Observation Framework (UKEOF), the WG is a coordinating body for the public sector, with a mission to work collaboratively to maximize the value of the UK's environmental observations.

Working toward this mission, the WG holds meetings and annual conferences. Our last face-to-face conference was hosted by the Natural History Museum in London in January 2020, just before such events became impossible due to the COVID-19 pandemic. In January 2022, we held a week of webinars showcasing advances in environmental DNA and RNA (eDNA and eRNA) research, featuring presentations from UK stakeholders and industry representatives, and from invited international researchers (topics included bulk/community DNA, eDNA, and eRNA analyses). Registration was free and 514 people registered, with the number of attendees at individual webinars varying from 170 to 263.

Having become accustomed to online meetings and conferences after 2 years living and working through the COVID-19 pandemic restrictions, we understand their strengths and weaknesses. The major disadvantage of holding the online webinars was the lack of opportunities to network, build partnerships, and socialize with colleagues. However, compared with our previous conferences, our outreach was much wider and included international presenters and attendees from around the world. More people participated, it was cheaper and associated carbon emissions were fewer. The format of 2–3 h of webinars every day over 5 days (compared with the usual event held over two full days) was attractive to attendees but more demanding on organizers. It is likely we will alternate face-to-face and online events in the future.

2 | METHODOLOGICAL AND CONCEPTUAL ADVANCES, OBSTACLES AND SOLUTIONS

In 2014, at the first meeting of what would become the UK DNA working group, at the Food and Environment Research Agency (Fera) York, the focus was very much on single species monitoring, whether we could trust eDNA data, and if the technology was going to put people out of a job. 8 years later, the message from the UK agencies is that DNA-based technologies are now sufficiently established to massively upscale our ambitions: from reliable and cost-effective monitoring of single species, to performing habitat scale monitoring across the Tree of Life. Whether we can indeed detect *everything* with eDNA was addressed with optimism by Michael Stat (University of Newcastle, Australia; Stat et al., 2017) and Rosetta Blackman (EAWAG, Zurich), who demonstrated how multimarker metabarcoding across bacteria, macroinvertebrates and fish detected seasonal and spatial changes in community assemblage in a large river system (Blackman et al., 2022). Agreeing that systematic biodiversity surveillance using eDNA is within our grasp, Mike Bunce (Institute of Environmental Science and Research, New Zealand) cautioned that eDNA-based monitoring is still undervalued and underfunded relative to the magnitude of the threats to our environment.

A significant proportion of talks were focused on fishes in freshwater and marine environments, reflecting the enormous body of work that has been focused in this area. For example, Masaki Miya (Natural History Museum, Chiba, Japan) talked us through the history of eDNA metabarcoding for monitoring marine fish biodiversity (Miya, 2022). Louis Bernatchez (Université Laval Québec, Canada) discussed, amongst other things, how eDNA was now providing meaningful measures of relative abundance and tracking spatial and temporal dynamics of whole communities in comparison with traditional surveying methods (Boivin-Delisle et al., 2021). Abundance was a theme that was featured in several talks, with Ryan Kelly (University of Washington, USA; Shelton et al., 2022) and Naiara Rodriguez-Ezpeleta (AZTI, Spain; Fraija-Fernández et al., 2020) reporting similar findings in different systems, showing that eDNA data are now clearly moving beyond presence-absence only data. Naiara Rodriguez-Ezpleta also showed that eDNA is vertically structured and can be used to study fish migratory behaviors (Canals et al., 2021). Switching to the terrestrial environment, Sarah Bourlat (Museum Koenig Bonn, Germany) demonstrated that nondestructive methods of DNA extraction from bulk arthropod samples performs equally as well as destructive methods (Kirse et al., 2022) and Kristine Bohmann (University of Copenhagen, Denmark) demonstrated exciting new developments in the application of airborne eDNA to detect terrestrial vertebrates kept in a zoo (Lynggaard et al., 2022).

In order for a more complete understanding of how useful and reliable eDNA will be for biomonitoring, there is a return to focus more on the "ecology of eDNA." Kristy Deiner (ETH Zurich, Switzerland) gave us insights into her group's work on the persistence of eDNA in its multiple states, and how we need a greater understanding of these properties is needed under different environmental conditions (Mauvisseau et al., 2022; Figure 1). Beyond eDNA, Melania Cristescu (McGill University, Canada) showed how eRNA, despite a more rapid decay rate than eDNA (Kagzi et al., 2022), performs equally well as eDNA in species detections (Littlefair et al., 2022).

As the field of eDNA research continues to grow and becomes more established as a biomonitoring method, there are still technical challenges in implementation for routine monitoring and surveying. Michael Stat discussed how eDNA analysis should be a complementary method to existing biomonitoring methods (rather than a replacement of these) and highlighted the importance of using multiple assays to capture fully the biodiversity within an ecosystem (Cole et al., 2022). A consistent problem in DNA-based monitoring is incomplete reference databases (and this was highlighted in several presentations), but Tristan Cordier

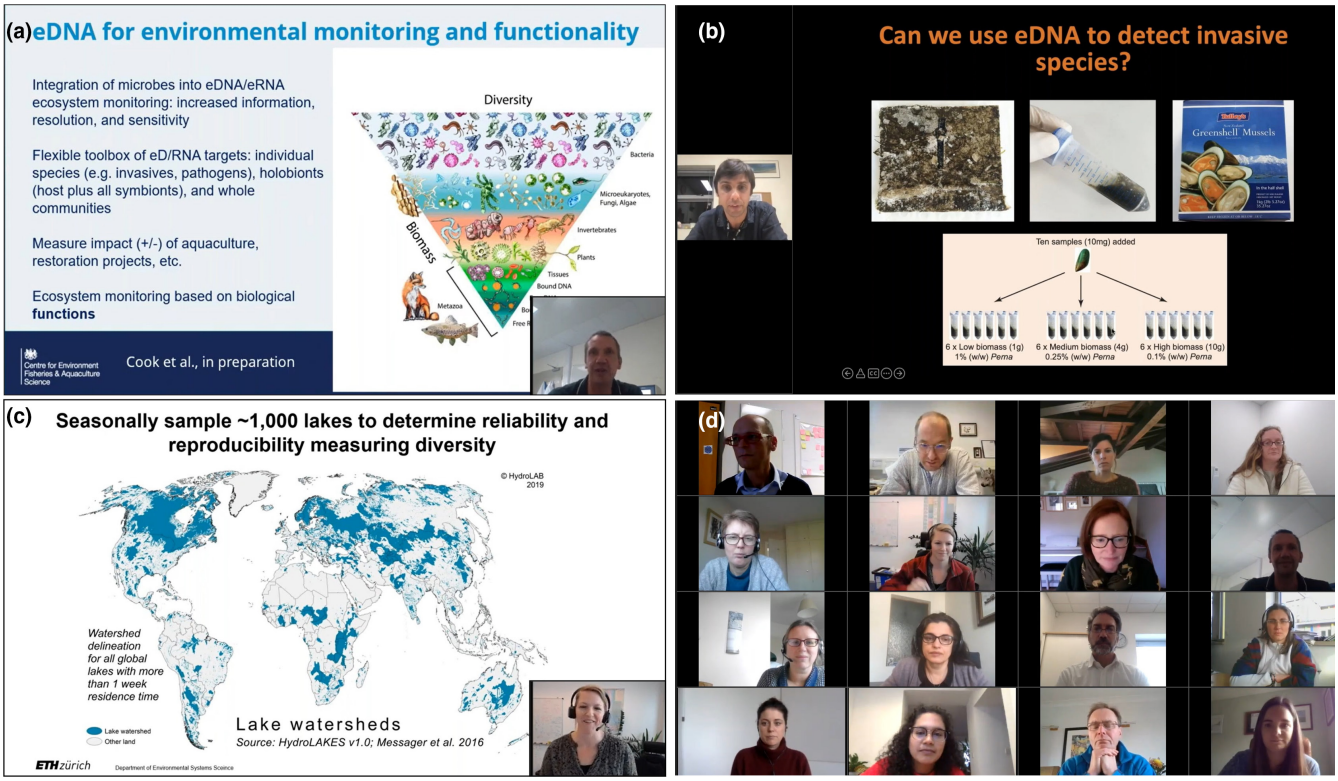

FIGURE 1 Screenshots from the recorded sessions of the UKDNA eDNA webinar series 2022 (a) Phil Davison presenting on behalf of Cefas, during the end user session; (b) Michael Stat presenting his work with industry using eDNA to detect invasive species on day two; (c) Kristy Deiner presenting as part of the academic sessions; and (d) speakers and hosts answering questions from the audience as part of the final summary and Q&a session on day five

(NORCE Climate, Norway) talked us through how supervised machine learning approaches can compensate for this in biodiversity assessments (Cordier et al., 2018).

3 | TACKLING REAL-WORLD NEEDS

To emphasize the importance of translating progress in research to advances in real-world applications, the first day of the webinar series was devoted for UK public sector end users and regulatory agencies to present their work and experiences in the field.

Some applications are ready for regulatory use, and indeed, England was one of the first places to introduce an eDNA-based method into its land use planning system with the eDNA assay for great crested newts (*Triturus cristatus*; Biggs et al., 2014). Judy England (Environment Agency, UK) discussed future challenges including the need for better approaches to understand how climate change could manifest in future river ecosystems and how community dynamics shape ecosystem functioning and resilience in response to pressures. Moving methods from research into practice, regulators need to be confident that methods are reliable, repeatable, and robust enough to stand up to legal challenge. As Ryan Kelly from the University of Washington pointed out, regulators need researchers to make DNA boring! The "boring" analogy reflected on the need to make eDNA analyses routine, predictable, reliable, and repeatable for the purposes of widespread implementation in regulatory monitoring.

Other presenters described how DNA-based methods could meet different needs to monitor environmental change. Katie Clark (Natural England) outlined progress in how DNA technology is being incorporated into the UK Government's 25-year Environment Plan, contributing evidence to natural capital assessments, monitoring of protected sites and nature recovery networks, and on-going plans to integrate DNA technology into the Natural Capital Ecosystem Assessment (NCEA) program. Debbie Leatherland described Natural England's interest in using DNA to assess the condition of Protected Sites and to monitor the effectiveness of agri-environment agreements, and Willie Duncan (Scottish Environmental Protection Agency) described work being funded by the Scottish Government to develop habitat scale eDNA monitoring in four habitats in the Loch Lomond and Trossachs National Park. Applications to marine ecosystems were discussed by Phil Davison (Centre for Environment, Fisheries and Aquaculture Science (Cefas)), who featured projects by UK agencies (Cefas, Marine Scotland Science, Natural England, Joint Nature Conservation Committee [JNCC]) on the monitoring of inshore and pelagic fish assemblages, benthic macrofaunal communities, and invasive non-native species (Figure 1).

Public sector end users have largely focused on developing methods to detect single species (e.g., invasive or protected species) and

groups or assemblages that may be of conservation or economic value in themselves, or indicators of ecosystem quality. Katie Clark highlighted work supported by the Centre of Excellence (CoE) for DNA-based methods in the Department for Environment, Food and Rural Affairs (Defra) on developing new metrics to measure biodiversity and ecosystem function and resilience using DNA data. The CoE has also funded projects on developing guidance and standards, increasing data and analytical capability, and improving barcode reference libraries.

Public policy across the UK is increasingly focused on maintaining and improving natural resources, natural capital assets and ecosystems services. These policies need new ways of producing biodiversity and environmental data to provide insights into ecosystems and their function. Developing the skills and confidence of agency staff to use DNA methods is critical to achieve these public policy objectives.

4 | ENTERPRISE AND LEGACY: THE EVOLVING LANDSCAPE OF DNA RESEARCH AND APPLICATION

So where to next in the evolving landscape of DNA-based monitoring? Developing new metrics based on DNA-based tools for understanding ecosystem function and resilience was a priority theme repeated several times in the agency presentations. Debbie Leatherland highlighted the need to revisit habitat classification based on old metrics and to understand "what does *good* look like in terms of a DNA signature of a habitat"? Novel analyses, such as machine learning, highlighted by Tristan Cordier, will help to turn these aspirations into a reality (Cordier et al., 2018, 2019).

For these ambitions to become a reality, comprehensive reference databases and DNA-based biodiversity records need to be globally accessible. Katie Clark highlighted how Natural England had identified massive gaps in reference databases and initiated the UK Barcode of Life project (UKBOL, ukbol.org) to fill in gaps in reference libraries, supported by the DNA CoE. Given the millions of DNA biodiversity records already generated by our community, improving the accessibility of DNA records could potentially revolutionize our understanding of the distribution of biodiversity at a global scale (Berry et al., 2021), but making DNA biodiversity records globally accessible is something that only a small number of research projects have so far achieved. Inspirational examples of this came from Rachel Meyer (University of California, Santa Cruz) from the CALeDNA project (Meyer et al., 2021, ucedna.com) and Mike Bunce, who leads the Open Waters Aotearoa Programme. Both speakers discussed the importance of working with citizen scientists to undertake large-scale sampling to be undertaken and to engage local people of all ages in conserving biodiversity (Meyer et al., 2021), and highlighted the importance of making DNA data/results more accessible beyond just specialists in the field (Berry et al., 2021). Projects such as eBIOAtlas and Vigilife, spearheaded by NatureMetrics and SpyGen, respectively, are also striving toward making DNA records publicly accessible. It is clear that a number of different research groups and organizations (governmental, nongovernmental, and commercial) recognize this need, but a global partnership is urgently needed to streamline the process, to avoid duplication of effort and to address the ethics of releasing data, for example, of protected species. Where possible, efforts should be made to align the new global recording ventures with established, large-scale initiatives, such as the International Barcode of Life (iBol).

The commercial sector has rapidly evolved to accommodate the needs of government agencies and other end users for cost-effective biodiversity monitoring. This was reflected in the inspirational talks from companies developing and offering DNA-based monitoring solutions: SpyGen, NatureMetrics, Applied Genomics, ADAS, and SimplexDNA. The growth of the commercial sector is offering exceptional opportunities for postgraduate researchers to find employment outside of academia, and to foster collaboration between sectors.

It is also important to emphasize the importance of the UKDNAWG and international initiatives, in particular DNAqua-Net, in promoting dialog between researchers and the end user community and facilitating the uptake of DNA-based methods. Florian Leese (University of Duisberg-Essen, Germany) highlighted the incredible progress made by DNAqua-Net in terms of developing DNA-based workflows and software solutions (Buchner et al., 2021; Macher et al., 2021) and producing practical guides to DNA-based methods for biodiversity monitoring (Bruce et al., 2021; Pawlowski et al., 2020) that are indispensable introductions to the field for both researchers and end users alike. Florian acknowledged the openness and international perspective of several national working groups. A positive next step would be to continue the legacy of DNAqua-Net to formally address formally the uptake of DNA-based methods into international directives.

From our perspective, the UK DNA WG eDNA week was a tremendous success, and we thank all organizers and participants for a rewarding week of knowledge mobilization between the academic, industry, and stakeholder communities. The global reach of the event signified the maturation of the UK DNA WG network from its beginnings as a small and informal collaboration between stakeholders and academics in 2014. 8 years on, widespread development and adoption of novel methodologies are enabling both targeted monitoring of single species, to ecosystem scale assessments of biodiversity across the tree of life. Accompanied by novel statistical analyses and links to functional ecological understanding, DNA/RNA-based bioassessment approaches are now powerful and complementary tools to existing biodiversity monitoring, with demonstrative opportunities to enhance the spatial and temporal frequency of biodiversity data acquisition. Importantly, much of the work has been enabled by the network's postgraduate researchers, who are now succeeding as early career postdoctoral researchers, fellows, industry representatives, and faculty members, forming the next generation of highly qualified and trained eDNA scientists. We would encourage visits to the talk recordings and engagement with the network, so that we can collectively codesign the next decade of impactful, globally significant and relevant DNA-based monitoring (Table 1).

TABLE 1 List of speakers and talk titles presented during the UKDNA eDNA webinar series, links for each recording, and the time of each talk within the recordings

Speaker:	Talk title:	Recording link:	Recording time:
Willie Duncan (Scottish Environmental Protection Agency)	The Scottish DNA Hub, Developing Habitat Scale DNA monitoring	https://youtu.be/ZVLDj2XAdb8	6:10
Judy England (Environment Agency)	Ecological Challenges.		24:35
Debbie Leatherland (Natural England)	Natural England's evidence needs for Protected Site and Agri-environment Monitoring		35:00
Katie Clark (Natural England)	Priorities, progress, and plans—Defra Centre of Excellence for DNA-based methods		52:20
Phil Davison (Centre for Environment, Fisheries and Aquaculture Science) and Iveta Matejusova (Marine Scotland Science)	DNA-based applications in marine ecosystems		1:07:50
Mike Bunce	Community Engagement, Biobanks, Accessible Data and Deterrents—how important are these elements in a rapidly developing eDNA landscape?	https://youtu.be/3VoNscj7WMw	2:45
Michael Stat	Working with industry to characterize biodiversity and survey for invasive species using eDNA.		32:00
Tristan Cordier	Harnessing environmental genomics and machine learning for routine biomonitoring.		1:03:35
Rosetta Blackman	Spatial–temporal patterns of biodiversity and food-web characteristics across a river catchment using eDNA.		1:30:30
Rachel Meyer	Sustaining a citizen science eDNA program in California: challenges and opportunities.		1:54:40
Sarah Bourlat	Challenges and possibilities for the assessment of terrestrial arthropod communities using DNA-based methods.	https://youtu.be/fymMjH3P-j8	4:15
Louis Bernatchez	Toward eDNA analysis as a globally accepted approach for fish management and conservation.		30:30
Ryan Kelly	Making eDNA Boring.		58:30
Melania Cristescu	Can eRNA pick up where eDNA fails?		1:26:20
Masaki Miya (recording)	Environmental DNA metabarcoding: A novel method for biodiversity monitoring of marine fish communities.		1:56:20
Sebastian Mynott (Applied Genomics)	Advancing eDNA-based survey technologies for improved biodiversity monitoring.	https://youtu.be/zzOvFFFr9qE	4:20
Alice Valentini (Spygen)	SPYGEN: 10 years of expertise in eDNA for biodiversity monitoring		23:50
Helen Rees (ADAS)	Development of eDNA assays for rare and invasive freshwater snails.		45:15
Kat Bruce (NatureMetrics)	Scaling up: Using eDNA to inform management and conservation of nature around the world		1:07:30
Florian Leese	Back to the future: National roadmaps (hopefully) pave the way for harmonized international biomonitoring 2.0.	https://youtu.be/xamlYloBUiA	3:28
Kristy Deiner	Measuring global biodiversity through understanding biogeochemical cycling of environmental DNA in lakes		24:20
Naiara Rodriguez	From estuaries to the deep ocean: diving into the potential of eDNA for assessing fish diversity		49:00
Kristine Bohmann	The sky is not the limit—detection of terrestrial vertebrates using metabarcoding of airborne environmental DNA	Recording not available.	NA
Si Creer	Wrap-up talk and Q&A	https://youtu.be/xamlYloBUiA	1:15:15

AUTHOR CONTRIBUTIONS

TB, SC, PD, LLH, ADM, SM, AN, DR, and KW involved in writing; TB, SC, PD, LLH, ADM, SM, AN, DR, and KW involved in webinar design; all authors involved in supporting contributions and editing manuscript drafts.

ACKNOWLEDGMENTS

We would like to acknowledge funding support from NERC grants NE/N003756/1 and NE/N006216/1, awarded to SC.

CONFLICT OF INTEREST

The authors have no conflicts of interest to declare. All coauthors have seen and agree with the contents of the manuscript, and there is no financial interest to report. We certify that the submission is original work and is not under review at any other publication.

DATA AVAILABILITY STATEMENT

The presentations from the event are available online: UK DNA Working Group eDNA Week - Webinar recordings - UKEOF.

ORCID

Lori Lawson Handley https://orcid.org/0000-0002-8153-5511
Holly A. Broadhurst https://orcid.org/0000-0003-3482-3374
Stefano Mariani https://orcid.org/0000-0002-5329-0553
Allan D. McDevitt https://orcid.org/0000-0002-2677-7833

REFERENCES

Berry, O., Jarman, S., Bissett, A., Hope, M., Paeper, C., Bessey, C., Schwartz, M. K., Hale, J., & Bunce, M. (2021). Making environmental DNA (eDNA) biodiversity records globally accessible. *Environmental DNA*, *3*(4), 699–705. https://doi.org/10.1002/edn3.173

Biggs, J., Ewald, N., Valentini, A., Gaboriaud, C., Griffiths, R. A., Foster, J., Wilkinson, J., Arnett, A., Williams, P., & Dunn, F. (2014). *Analytical and methodological development for improved surveillance of the great crested newt. Appendix 5. Defra project WC1067*. Freshwater Habitats Trust.

Blackman, R. C., Ho, H. C., Walser, J. C., & Altermatt, F. (2022). Spatio-temporal patterns of multi-trophic biodiversity and food-web characteristics uncovered across a river catchment using environmental DNA. *Communications Biology*, *5*(1), 1–11. https://doi.org/10.1038/s42003-022-03216-z

Boivin-Delisle, D., Laporte, M., Burton, F., Dion, R., Normandeau, E., & Bernatchez, L. (2021). Using environmental DNA for biomonitoring of freshwater fish communities: Comparison with established gill-net surveys in a boreal hydroelectric impoundment. *Environmental DNA*, *3*(1), 105–120. https://doi.org/10.1002/edn3.135

Bruce, K., Blackman, R. C., Bourlat, S. J., Hellström, M., Bakker, J., Bista, I., Bohmann, K., Bouchez, A., Brys, R., Clark, K., Elbrecht, V., Fazi, S., Fonseca, V. G., Hänfling, B., Leese, F., Mächler, E., Mahon, A. R., Meissner, K., Panksep, K., … Deiner, K. (2021). *A practical guide to DNA-based methods for biodiversity assessment* (Vol. *1*, e68634). Advanced Books. https://doi.org/10.3897/ab.e68634

Buchner, D., Macher, T. H., Beermann, A. J., Werner, M. T., & Leese, F. (2021). Standardized high-throughput biomonitoring using DNA metabarcoding: Strategies for the adoption of automated liquid handlers. *Environmental Science and Ecotechnology*, *8*, 100122. https://doi.org/10.1016/j.ese.2021.100122

Canals, O., Mendibil, I., Santos, M., Irigoien, X., & Rodríguez-Ezpeleta, N. (2021). Vertical stratification of environmental DNA in the open ocean captures ecological patterns and behavior of deep-sea fishes. *Limnology and Oceanography Letters*, *6*(6), 339–347. https://doi.org/10.1002/lol2.10213

Cole, V. J., Harasti, D., Lines, R., & Stat, M. (2022). Estuarine fishes associated with intertidal oyster reefs characterized using environmental DNA and baited remote underwater video. *Environmental DNA*, *4*(1), 50–62. https://doi.org/10.1002/edn3.190

Cordier, T., Forster, D., Dufresne, Y., Martins, C. I., Stoeck, T., & Pawlowski, J. (2018). Supervised machine learning outperforms taxonomy-based environmental DNA metabarcoding applied to biomonitoring. *Molecular Ecology Resources*, *18*(6), 1381–1391. https://doi.org/10.1111/1755-0998.12926

Cordier, T., Lanzén, A., Apothéloz-Perret-Gentil, L., Stoeck, T., & Pawlowski, J. (2019). Embracing environmental genomics and machine learning for routine biomonitoring. *Trends in Microbiology*, *27*(5), 387–397. https://doi.org/10.1016/j.tim.2018.10.012

Fraija-Fernández, N., Bouquieaux, M. C., Rey, A., Mendibil, I., Cotano, U., Irigoien, X., Santos, M., & Rodríguez-Ezpeleta, N. (2020). Marine water environmental DNA metabarcoding provides a comprehensive fish diversity assessment and reveals spatial patterns in a large oceanic area. *Ecology and Evolution*, *10*(14), 7560–7584. https://doi.org/10.1002/ece3.6482

Kagzi, K., Hechler, R. M., Fussmann, G. F., & Cristescu, M. E. (2022). Environmental RNA degrades more rapidly than environmental DNA across a broad range of pH conditions. *Molecular Ecology Resources*, *22*, 2640–2650. https://doi.org/10.1111/1755-0998.13655

Kirse, A., Bourlat, S., Lange, K., Zapke, B., & Zizka, V. (2022). Comparison of destructive and non-destructive DNA extraction methods for the metabarcoding of arthropod bulk samples. *Molecular Ecology Resources*. https://doi.org/10.1111/1755-0998.13694. Online ahead of print.

Littlefair, J. E., Rennie, M. D., & Cristescu, M. E. (2022). Environmental nucleic acids: A field-based comparison for monitoring freshwater habitats using eDNA and eRNA. *Molecular Ecology Resources*, *22*(8), 2928–2940. https://doi.org/10.1111/1755-0998.13671

Lynggaard, C., Bertelsen, M. F., Jensen, C. V., Johnson, M. S., Frøslev, T. G., Olsen, M. T., & Bohmann, K. (2022). Airborne environmental DNA for terrestrial vertebrate community monitoring. *Current Biology*, *32*(3), 701–707. https://doi.org/10.1016/j.cub.2021.12.014

Macher, T., Beermann, A. J., & Leese, F. (2021). TaxonTableTools: A comprehensive, platform-independent graphical user interface software to explore and visualise DNA metabarcoding data. *Molecular Ecology Resources*, *21*(5), 1705–1714. https://doi.org/10.1111/1755-0998.13358

Mauvisseau, Q., Harper, L. R., Sander, M., Hanner, R. H., Kleyer, H., & Deiner, K. (2022). The multiple states of environmental DNA and what is known about their persistence in aquatic environments. *Environmental Science & Technology*, *56*(9), 5322–5333. https://doi.org/10.1021/acs.est.1c07638

Meyer, R., Ramos, M., Lin, M., Schweizer, T., Gold, Z., Ramos, D., Shirazi, S., Kandlikar, G., Kwan, W.-Y., Curd, E., Freise, A., Parker, J., Sexton, J., Wetzer, R., Pentcheff, N., Wall, A., Pipes, L., Garcia-Vedrenne, A., Meija, M., … Wayne, R. (2021). The CALeDNA program: Citizen scientists and researchers inventory California's biodiversity. *California Agriculture*, *75*(1), 20–32. https://doi.org/10.3733/ca.2021a0001

Miya, M. (2022). Environmental DNA metabarcoding: A novel method for biodiversity monitoring of marine fish communities. *Annual Review of Marine Science*, *14*, 161–185. https://doi.org/10.1146/annurev-marine-041421-082251

Pawlowski, J., Apothéloz-Perret-Gentil, L., Mächler, E., & Altermatt, F. (2020). *Environmental DNA applications for biomonitoring and bioassessment in aquatic ecosystems*. Federal Office for the Environment

Bern. Environmental Studies. No. 2010. https://doi.org/10.5167/uzh-187800

Shelton, A. O., Ramón-Laca, A., Wells, A., Clemons, J., Chu, D., Feist, B. E., Kelly, R. P., Parker-Stetter, S. L., Thomas, R., Nichols, K. M., & Park, L. (2022). Environmental DNA provides quantitative estimates of Pacific hake abundance and distribution in the open ocean. *Proceedings of the Royal Society B*, *289*(1971), 20212613. https://doi.org/10.1098/rspb.2021.2613

Stat, M., Huggett, M. J., Bernasconi, R., DiBattista, J. D., Berry, T. E., Newman, S. J., Harvey, E. S., & Bunce, M. (2017). Ecosystem biomonitoring with eDNA: Metabarcoding across the tree of life in a tropical marine environment. *Scientific Reports*, *7*(1), 1–11. https://doi.org/10.1038/s41598-017-12501-5

How to cite this article: Handley, L. L., Blackwell, T., Broadhurst, H. A., Clark, K., Davison, P. I., England, J., Mariani, S., McDevitt, A. D., Pillay, K., Read, D., Walsh, K., Nisbet, A., & Creer, S. (2022). UK DNA working group eDNA week, January 2022. *Environmental DNA*, *00*, 1–7. https://doi.org/10.1002/edn3.364