THE MILAN STATEMENT ON ENVIRONMENTAL DNA

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Environmental DNA, or eDNA — trace genetic material shed by organisms into the water, sediment, soil, and air around them[1] — has transformed biological monitoring. Over the past two decades, eDNA-based methods have grown from a set of novel research techniques into a validated, standardisable, and deployable toolset capable of detecting and characterising biodiversity often faster, more comprehensively, and at lower cost than conventional methods alone.

We, the undersigned participants in the International Workshops on Environmental Genomics[2], have witnessed the growth of these technologies over a decade of annual meetings, from experimental methods to scientifically mature tools with demonstrated utility. The evidence base is substantial: thousands of published peer-reviewed studies, international technical standards under ISO and CEN, validated protocols spanning freshwater, marine, and terrestrial environments, and deployment across sectors ranging from conservation and resource management to offshore industry, food safety, nuisance species surveillance, and selected regulatory contexts. Rather than asking whether eDNA works in principle, the priority is now to define where, how, and under what quality-assurance conditions validated eDNA methods can be used responsibly and consistently. We therefore support the broader, fit-for-purpose adoption of eDNA in operational monitoring and, where appropriate, regulatory decision-making.

Global decline in biodiversity and associated threats to food security, human health, and economic stability demand monitoring tools that can match their scale and urgency. Ambitious goals to protect nature set forth in agreements such as the Kunming–Montreal Global Biodiversity Framework and the EU Nature Restoration Law, as well as reporting requirements recommended by the Taskforce on Nature-related Financial Disclosures, necessitate expansion of the available toolkit for measuring biodiversity. Conventional monitoring methods remain essential, but when used alone they cannot always provide the spatial coverage, temporal frequency, taxonomic breadth, or cost efficiency needed for emerging biodiversity monitoring challenges. Importantly, because it enables non-destructive sampling, eDNA is also fully consistent with the ethos of protecting that which we study, in a way that many existing methods are not.

[1] While methods leveraging eDNA are varied, we here refer primarily to well-established approaches aimed at targeted species detection and/or broad biodiversity assessments utilizing amplicon-based species identification from nucleic acids recovered from environmental samples.

[2] IWEG participants include representatives from governmental, academic, and NGO-led research institutions, industry across multiple economic sectors, environmental managers, and the policy and regulatory communities.

Potential benefits extend well beyond those recognized in monitoring contexts. eDNA data, once generated, has multiple advantages for long-term storage and re-analysis, and methods are being developed intentionally to align with FAIR and CARE principles to promote equitable data sharing and sovereignty. Opportunities now exist to leverage advances in the field to drive public-private partnerships, including the creation of new professional opportunities and skilled jobs as well as the development of more transdisciplinary education and training pathways connecting molecular biology, ecology, bioinformatics, environmental management, and policy.

We conclude that validated eDNA methods should become a standard, complementary part of the biodiversity monitoring toolkit. We fully expect further improvements in the reliability and applicability of eDNA tools in the future, proportionate to those achieved by conventional methods. However, the importance of continued refinement should not preclude appropriate use of existing validated methods where they are fit-for-purpose.

We attest that many eDNA methods are ready for broader implementation, as they are now supported by appropriate validation, quality assurance, transparent reporting, and clearly defined decision contexts. The scientific foundation is strong. Standards exist—for instance, recently published ISO 17805:2026 for capture and preservation of eDNA from aquatic samples—and more are under active development. Quality assurance frameworks are increasingly available. Case studies demonstrate operational performance across diverse environments and applications. Regulatory experience is also growing, with eDNA methods already being used or accepted in specific licensing, assessment, and compliance-related contexts in many jurisdictions. There is no longer any principled scientific argument for broadly treating these methods as inherently experimental or even novel. For many important end-uses they are already mature and reliable, and their integration into existing biodiversity monitoring toolkits should be evaluated and pursued on a fit-for-purpose basis, with expectations appropriate to their intended use.

We call on regulatory bodies, government agencies, industry operators, and standard-setting organisations to recognise validated, quality-assured eDNA methods as legitimate tools ready for adoption in environmental monitoring, assessment, and, where appropriate, compliance frameworks.

The Milan Statement was adopted at the International Workshop on Environmental Genomics, Milan, Italy, 7–8 July 2026.

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