



Conference Abstract

# A pilot for implementing environmental DNA (eDNA) based methods into environmental and biomonitoring

Tiina Laamanen<sup>‡</sup>, Veera Norros<sup>§</sup>, Sanna Suikkanen<sup>§</sup>, Mikko Tolkkinen<sup>‡</sup>, Kristiina Vuorio<sup>§</sup>, Petteri Vihervaara<sup>§</sup>, Päivi Sirkkiä<sup>§</sup>, Kirsten Jørgensen<sup>§</sup>, Pirkko Kortelainen<sup>§</sup>, Anna Reunamo<sup>§</sup>, Marko Järvinen<sup>§</sup>, Kristian Meissner<sup>l</sup>

<sup>‡</sup> Finnish Environment Institute, Oulu, Finland

<sup>§</sup> Finnish Environment Institute, Helsinki, Finland

<sup>l</sup> Finnish Environment Institute, Jyväskylä, Finland

Corresponding author: Tiina Laamanen ([tiina.laamanen@syke.fi](mailto:tiina.laamanen@syke.fi))

Received: 22 Feb 2021 | Published: 04 Mar 2021

Citation: Laamanen T, Norros V, Suikkanen S, Tolkkinen M, Vuorio K, Vihervaara P, Sirkkiä P, Jørgensen K, Kortelainen P, Reunamo A, Järvinen M, Meissner K (2021) A pilot for implementing environmental DNA (eDNA) based methods into environmental and biomonitoring. ARPHA Conference Abstracts 4: e64800.

<https://doi.org/10.3897/aca.4.e64800>

## Abstract

Environmental DNA (eDNA) and other molecular based approaches are revolutionizing the field of biomonitoring. These approaches undergo rapid modifications, and it is crucial to develop the best practices by sharing the newest information and knowledge. In our ongoing project we:

1. assess the state-of-the-art of eDNA methods at Finnish Environment Institute SYKE;
2. identify concrete next steps towards the long-term aim of implementing eDNA methods into environmental and biomonitoring;
3. promote information exchange on eDNA methods and
4. advance future research efforts both within SYKE and with our national and international partners.

## Scientific background

Well-functioning and intact natural ecosystems are essential for human well-being, provide a variety of ecosystem services and contain a high diversity of organisms. However, human activities such as eutrophication, pollution, land-use or invasive species, are threatening the state and functioning of ecosystems from local to global scale (e.g. Benateau et al. 2019; Reid et al. 2018; Vörösmarty et al. 2010). New molecular techniques in the field and in the laboratory have enabled sampling and identification of much of terrestrial, marine and freshwater biodiversity. These include environmental DNA (eDNA, e.g. Valentini et al. 2016) and bulk-sample DNA metabarcoding approaches (e.g. Elbrecht et al. 2017) and targeted RNA-based methods (e.g. Mäki and Tirola 2018). The eDNA technique uses DNA that is released from organisms into their environment, from which a signal of organisms' presence in the system can be obtained. For example, in aquatic ecosystems, eDNA is typically extracted from sediment or filtered water samples (e.g. Deiner et al. 2016), and this approach is distinguished from bulk DNA metabarcoding, where organisms are directly identified from e.g. complete biological monitoring samples (e.g. Elbrecht et al. 2017). Despite the demonstrated potential of environmental and bulk-sample DNA metabarcoding approaches in recent years, there are still significant bottlenecks to their routine use that need to be addressed (e.g. Pawlowski et al. 2020).

### Methods and implementation

The project is divided into three work packages: WP1 Gathering existing knowledge, identifying knowledge gaps and proposing best practices, WP2 Roadmap to implementation and WP3 eDNA monitoring pilot. Please see more details in the Fig. 1

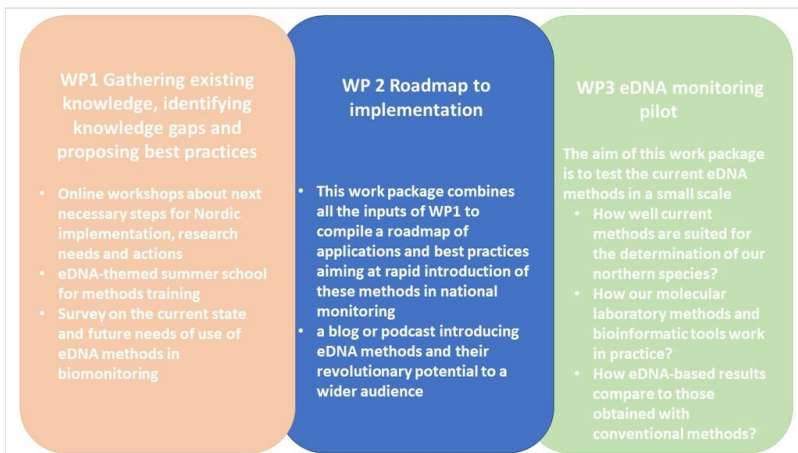


Figure 1. [doi](#)

The work packages of the "A pilot for implementing environmental DNA (eDNA) based methods into environmental and biomonitoring" -project.

### Keywords

eDNA, biomonitoring

## Presenting author

Tiina Laamanen

## Presented at

1st DNAQUA International Conference (March 9-11, 2021)

## References

- Benateau S, Gaudard A, Stamm C, Altermatt F (2019) Climate change and freshwater ecosystems: impacts on water quality and ecological status. Federal Office for the Environment (FOEN) & Eawag <https://doi.org/10.5167/uzh-169641>
- Deiner K, Fronhofer E, Mächler E, Walser J, Altermatt F (2016) Environmental DNA reveals that rivers are conveyor belts of biodiversity information. *Nature Communications* 7 (1). <https://doi.org/10.1038/ncomms12544>
- Elbrecht V, Vamos EE, Meissner K, Aroviita J, Leese F (2017) Assessing strengths and weaknesses of DNA metabarcoding-based macroinvertebrate identification for routine stream monitoring. *Methods in Ecology and Evolution* 8 (10): 1265-1275. <https://doi.org/10.1111/2041-210x.12789>
- Mäki A, Tiirola M (2018) Directional high-throughput sequencing of RNAs without gene-specific primers. *BioTechniques* 65 (4): 219-223. <https://doi.org/10.2144/btn-2018-0082>
- Pawlowski J, Apothéloz-Perret-Gentil L, Mächler E, Altermatt F (2020) Environmental DNA applications for biomonitoring and bioassessment in aquatic ecosystems. Bundesamt für Umwelt (BAFU) <https://doi.org/10.5167/uzh-187800>
- Reid A, Carlson A, Creed I, Eliason E, Gell P, Johnson PJ, Kidd K, MacCormack T, Olden J, Ormerod S, Smol J, Taylor W, Tockner K, Vermaire J, Dudgeon D, Cooke S (2018) Emerging threats and persistent conservation challenges for freshwater biodiversity. *Biological Reviews* 94 (3): 849-873. <https://doi.org/10.1111/brv.12480>
- Valentini A, Taberlet P, Miaud C, Civade R, Herder J, Thomsen PF, Bellemain E, Besnard A, Coissac E, Boyer F, Gaboriaud C, Jean P, Poulet N, Roset N, Copp G, Geniez P, Pont D, Argillier C, Baudoin J, Peroux T, Crivelli A, Olivier A, Acqueberge M, Le Brun M, Møller P, Willerslev E, Dejean T (2016) Next-generation monitoring of aquatic biodiversity using environmental DNA metabarcoding. *Molecular Ecology* 25 (4): 929-942. <https://doi.org/10.1111/mec.13428>
- Vörösmarty CJ, McIntyre PB, Gessner MO, Dudgeon D, Prusevich A, Green P, Glidden S, Bunn SE, Sullivan CA, Liermann CR, Davies PM (2010) Global threats to human water security and river biodiversity. *Nature* 467 (7315): 555-561. <https://doi.org/10.1038/nature09440>