

Comments on new guidelines for harbor monitoring using metabarcoding

Scientific note from DCE – Danish Centre for Environment and Energy

Date: 17 August 2026 | 45



AARHUS
UNIVERSITY

DCE – DANISH CENTRE FOR ENVIRONMENT AND ENERGY

Data sheet

Scientific note from DCE – Danish Centre for Environment and Energy

Category: Scientific briefing

Title: Comments on new guidelines for harbor monitoring using metabarcoding

Author: Rumakanta Sapkota

Institution: Department of Environmental Science,

Referee: Adam Leslie Koziol, Department of Ecoscience
Quality assurance, DCE: Kirsten Bang

External comment: No external comments

Claimant: The Danish Environmental Protection Agency

Please cite as: Sapkota, R. 2026. Comments on new guidelines for harbor monitoring using metabarcoding. Aarhus University, DCE - Danish Centre for Environment and Energy, 5 s. – [Scientific note no. 2026 | 45](#)

Reproduction permitted provided the source is explicitly acknowledged

Number of pages: 5

1 Introduction

The Danish Environmental Protection Agency has by 17-08- 2026 requested DCE – Danish Center for Environment and Energy to review and comment on the draft “Quality assurance guidelines for metabarcoding procedures associated with port surveys under the HELCOM/OSPAR Joint Harmonized Procedure (JHP)” by **Obst et al. 2026**. The Quality assurance guidelines for metabarcoding outline best-practice workflow from sample collection, laboratory work for sequencing, and bioinformatics to data management. The document provides general recommendations throughout the workflow, highlights the importance of transparent reporting of the steps involved, and encourages the publication or sharing of raw and processed data in open-access repositories. The document will serve as a key reference for monitoring or survey programmes.

With the submission of this memo, the Danish Environmental Protection Agency has been provided with the draft of the guidelines, including comments and revisions inserted through Track Changes.

2 DCE comments

The major and minor DCE comments on the Quality assurance guidelines for metabarcoding are presented in the table below.

Major comments

	Page/Section	Comment
1	page 6 G.1	This section covers the water, hard and soft bottom samples. However, marine sampling also includes settling plates and scraping samples. These sample types are used for NIS monitoring, as they capture the active settlement of organisms in the marine environment. We recommend acknowledging these additional sample types.
2	Page 6 and 7 Contamination and quality control (G.2)	We agree with the field negative controls, as it is vital for demonstrating the absence of no cross-contamination. However, the recommendation of positive control per sampling campaign can be challenging in practice. Monitoring programs often lack clarity on what is positive control. The document would benefit by providing clarity on the use of positive control during field sampling. For ex. mix or mock community or one species, and how do we include them in different samples (water, sediment etc).
3	Page 8, H.1	This section lacks a description of PCR replication as a factor for species detection.
4	Page 7, Positive and negative control (G.5)	We agree and support positive controls, where a mixture of DNA or a mock community can be included during PCR reactions. However, this section has more relevance in the laboratory work (H.1 and H.2) and may fit within the PCR or DNA extraction. Consider moving or merging the text in G.5 with the PCR-related text in the first paragraph of page 8 (section H.2).

Minor comments

	Page/Section	Comment
1	Page 2. Glossary	ASV, consider adding "... and can be compared between different datasets, provided the same genetic locus has been sequenced." to the last sentence.
2	Page 3. Glossary	Organismal DNA – suggestion: "DNA derived directly from whole or part of the organism present in a sample (eg Coral fragments, fungal mycelium etc)"
3	Page 4. F. Background	Consider changing "...the current maturity of DNA metabarcoding methodology..." to "...the current maturity of DNA metabarcoding methodologies..."
4	Page 4. F. Background	Consider changing "...while it seems especially suitable..." to "...which is especially suitable..."
5	Page 4.	Consider changing "...molecular genetics, and bioinformatics." to "...molecular ecology, and bioinformatics."
6	Page 7 G.4	Consider removing "preservation and storage" from the chapter title as it is repeated in G.6

	Page/Section	Comment
7	Page 8 G.6	It should additionally be flagged that the use of preservation buffers, ethanol etc. do not allow long term storage but may be feasible for short periods of time when freezing is not an option.
8	Page 8: H.1	Repetition of the exact wording twice – consider: “...1) lysis of cells and biological material, which may include mechanical, chemical or enzymatic cell disruption, mechanical, chemical, or enzymatic disruption”
9	Page 8: H.1	Consider rephrasing to “separation of DNA from the other cell and cellular components”
10	Page 9: H.5	Consider the addition of DNA dilution for removing inhibition issues.
11	Page 10: I	“...minimum performance requirements...” of sequencing: Do the authors here refer to the choice of the sequencing kit should match the minimum length of the amplicon being sequenced. This should be clarified as non-experts won’t understand this. Additionally, a caution on using sequencing kits that are too long for the amplicon should be noted.
12	Page 10: J.1	Quality filtering: A discussion on the parameters to be considered here (e.g., primer mismatches, q-values, minimum overlap etc) could be added
13	Page 11: J3	Consider rephrasing “.. but should be applied..” to “but should also be applied and documented ...”
14	Throughout document:	There are many double spaces, make sure to check for these errors thoroughly.