

eDNA sampling - complementing to port sampling

Brofjorden port, Lysekil 2016

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Method – parallel sampling plankton and benthos

- Organisms manually sorted to identify all specimens to species or higher taxonomic level
- DNA is extracted from bulk samples
- DNA metabarcoding
- DNA was sequenced using next generation sequencing techniques – Illumina
- Matched against taxonomic reference sequences from public archives and target species databases (GenBank, BOLD).

Results

Method species identification	No. of taxa	Species level	%	No. of IAS/NIS	No. of Helcom/Ospar	IAS species
Traditional	212	131	62%	4	2	<i>Mnemiopsis leydi</i> , <i>Crassostrea gigas</i>
eDNA	153	119	77%	5	5	

Acartia tonsa, *Crassostrea gigas*, *Crepidula fornicata*, *Amphibalanus improvisus* and *Caprella mutica*. (*Mnemiopsis leydi*)

Results 2

Methods	traditional	eDNA
Settling panel	75%	56%
Benthic	82%	64%
Plankton	9%	66%

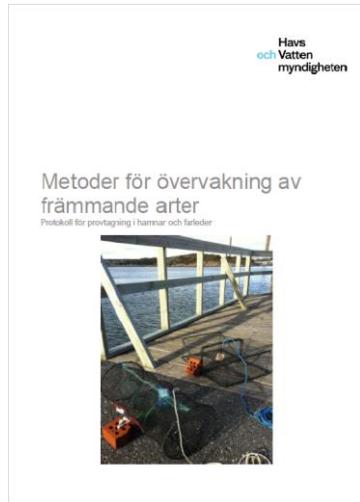


Conclusion: Traditional methods vs. eDNA

- Traditional methods
 - more species in general
- DNA based methods
 1. more IAS (higher specificity)
 2. invasive species more often (higher sensitivity)
 3. was able to detect invasive species among the plankton (early warning).

Monitoring program reports

<https://www.havochvatten.se/hav/uppdrag--kontakt/publikationer/publikationer/2016-09-21-metoder-for-overvakning-av-frammande-arter.html>



<https://www.havochvatten.se/hav/uppdrag--kontakt/publikationer/publikationer/2017-06-07-test-och-utvardering-av-ny-overvakning-av-frammande-arter-i-hamnar-och-utsatta-omraden.html>

- **Helcom/Ospar JHP**

Test and evaluation of port survey 2014 (Swe.) and 2016 (Eng. summary)

- **Report on eDNA**

Will be published in 1st quarter of 2018 (Eng. summary)

Rapid assessment – test and evaluation in Swedish waters 2017

- The Skagerrak
 - Brofjorden, Lysekil petroleum port
- The Baltic Sea
 - Bullandö, marina off Stockholm
 - Nynäshamn port
 - Nynäshamn marina

Report on eRAS

Will be published in summer 2018