

# A DNA metabarcoding approach to profile macrobenthos and zooplankton biodiversity

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## I. SAMPLING



## VII. CONCLUSION

We developed a standardized DNA metabarcoding pipeline. This provides a useful tool to identify species in mixed macrobenthos samples. This approach will be applied to zooplankton communities, but more research is needed. Other target barcodes (e.g. COI) or other barcoding primers may provide an alternative for the species which were not detected based on the 18S target barcode. Quantification of biomass based on obtained read counts needs more research.

## II. MORPHOLOGICAL IDENTIFICATION

53 individual species were collected



## VI. RESULTS: Effectiveness of the 18S barcoding primers

Phylum	Species	Unique	Mix equal amount	
Mollusca	<i>Abra alba</i>	✓	✓	
	<i>Macoma balthica</i>	✓	✓	
	<i>Kurtiella bidentata</i>	✓	✓	
	<i>Mya truncata</i>	✓	✓	
	<i>Spisula solida</i>	✓	✓	
	Annelida	<i>Glycera tridactyla</i>	✓	✓
		<i>Lanice conchilega</i>	✓	✓
		Cirratulidae	✓	✓
		<i>Notomastus latericeus</i>	✓	✓
		<i>Owenia fusiformis</i>	✓	✓
<i>Poecilochaetus serpens</i>		✓	✓	
<i>Scoloplos armiger</i>		✓	✓	
<i>Spiophanes bombyx</i>		✓	✓	
<i>Spio sp.</i>		✓	✓	
<i>Sthenelais boa</i>		✓	✓	
Cnidaria	Anthozoa	✓	✓	
Arthropoda	<i>Gastrosaccus spinifer</i>	✓	✓	
	Pestarella	✓	✓	
Chordata	<i>Branchiostoma lanceolatum</i>	✓	✓	
Mollusca	<i>Tellina fabula</i>	✗	✗	
	<i>Maerella pygmaea</i>	✗	✗	
Annelida	<i>Magelona johnstoni</i>	✗	✗	
	<i>Malmgreniella lunulata</i>	✗	✗	
	<i>Scolelepis bonnieri</i>	✗	✗	
	<i>Ophelia borealis</i>	✗	✗	
Echinodermata	<i>Echinocardium cordatum</i>	✗	✗	
	Arthropoda	<i>Nototropis falcatus</i>	✗	✗
Echinodermata	<i>Processa modica</i>	✗	✗	
	<i>Ophiura ophiura</i>	✗	✗	
Annelida	<i>Ophiura albida</i>	✗	✗	
	<i>Eunereis longissima</i>	✗	✗	
Annelida	<i>Nephtys assimilis</i>	✗	✗	
	<i>Nephtys caeca</i>	✗	✗	
	<i>Nephtys cirrosa</i>	✗	✗	
	<i>Nephtys hombergii</i>	✗	✗	
	<i>Nephtys longosetosa</i>	✗	✗	
Ctenophora	<i>Nephtys spp</i>	✗	✗	
	<i>Nereis juv.</i>	✗	✗	
	<i>Beroe gracilis</i>	✗	✗	
Mollusca	<i>Mnemiopsis leidy</i>	✗	✗	
	<i>Pleurobrachia pileus</i>	✗	✗	
Arthropoda	<i>Nassarius reticulatus</i>	✗	✗	
	<i>Nototropis swammerdamei</i>	✗	✗	
	<i>Pontocrates arenarius</i>	✗	✗	
	<i>Urothoe brevicornis</i>	✗	✗	
	<i>Urothoe poseidonis</i>	✗	✗	
	<i>Leucothoe incisa</i>	✗	✗	
	<i>Megaluropus agilis</i>	✗	✗	
	<i>Abudomedita obtusata</i>	✗	✗	
	<i>Bathyporeia guilliamsoniana</i>	✗	✗	
	<i>Bathyporeia elegans</i>	✗	✗	
<i>Iphinoe trispinosa</i>	✗	✗		

18S sequence information available in public databases

No 18S sequence information available in public databases

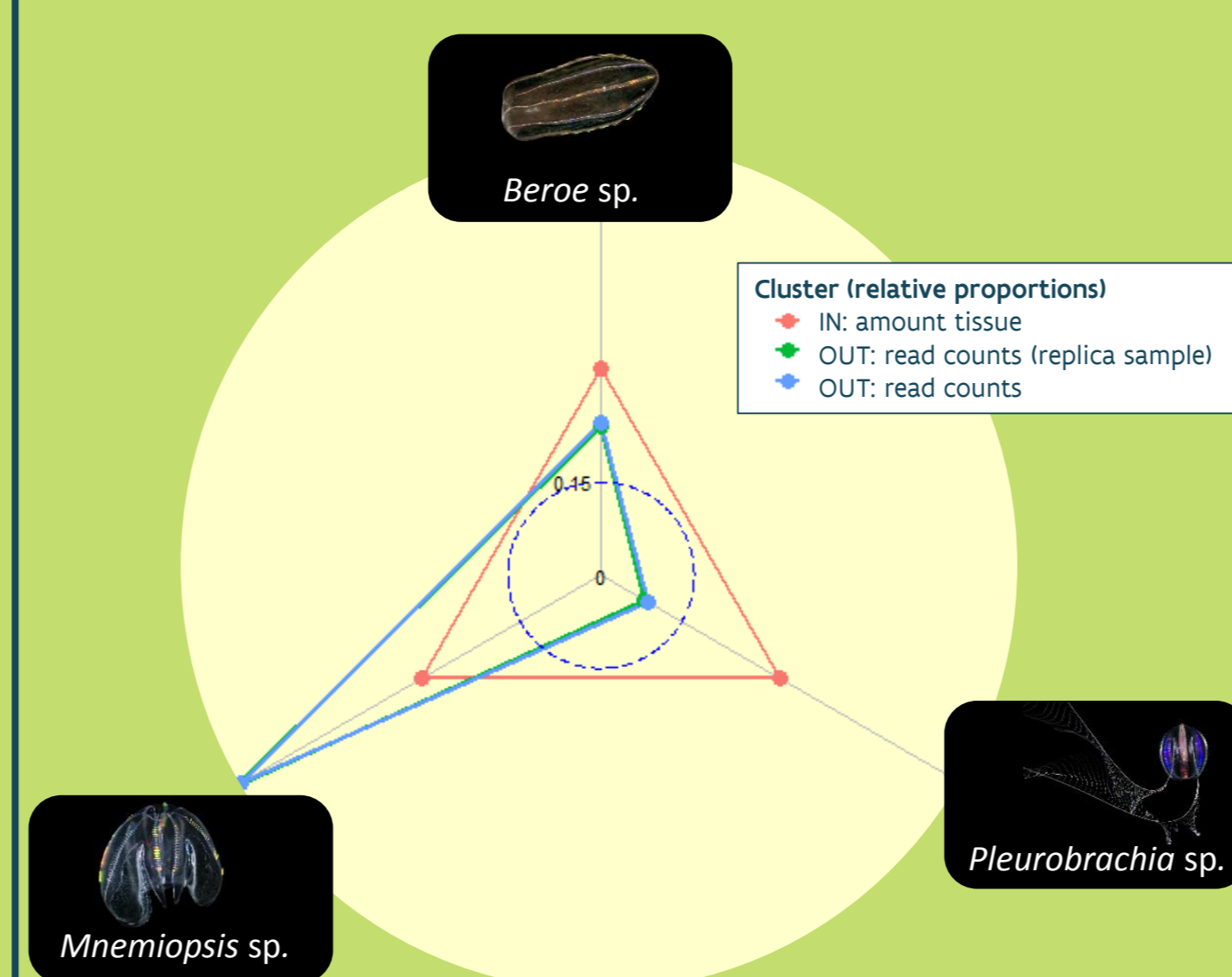
Taxonomic identification only to genus level

Not detected species

42/53 species detected

Barcode sequences were added to our DNA reference library

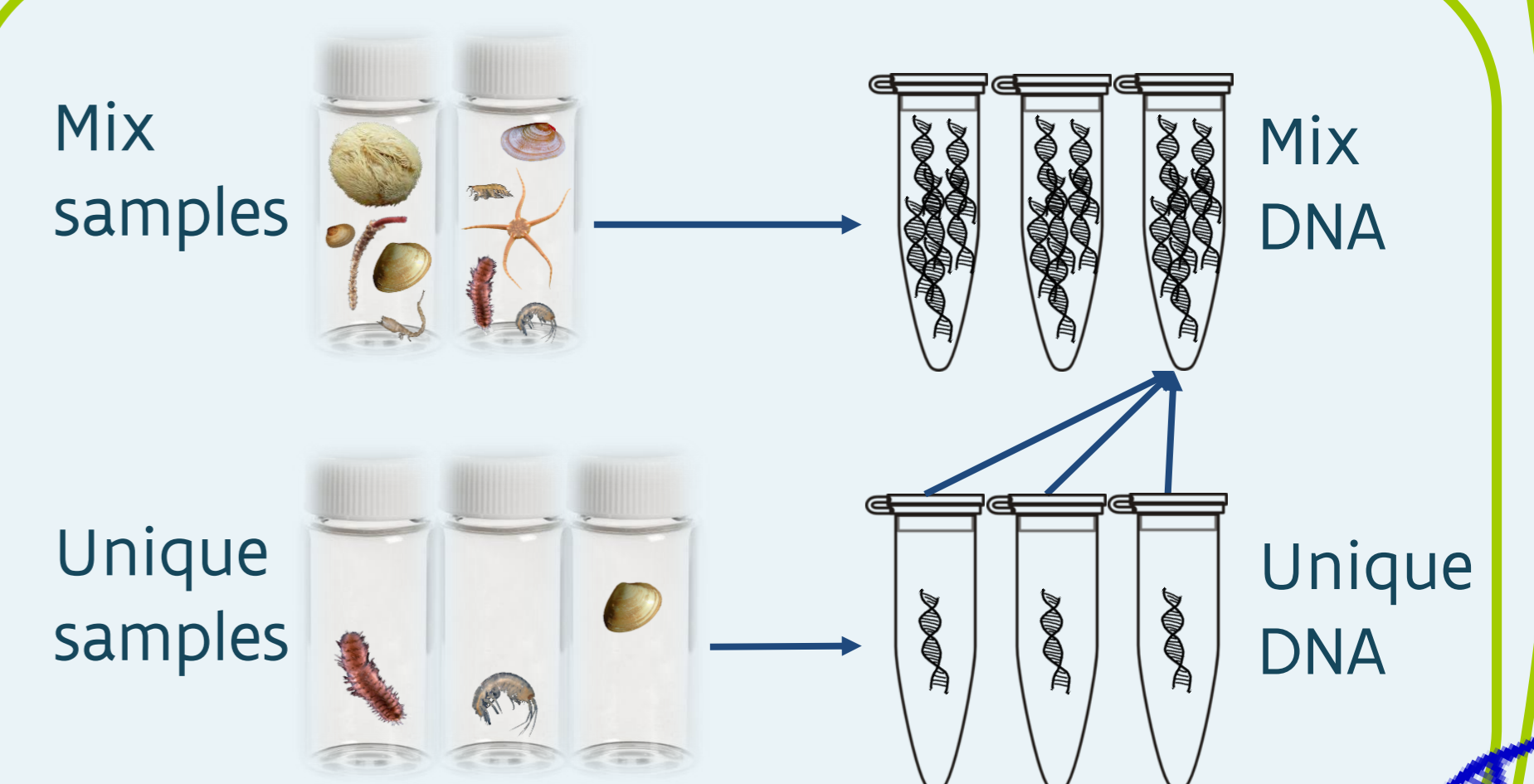
### Quantitative relationship?



Quantitative relationships between read counts and biomass need to be verified for all species separately

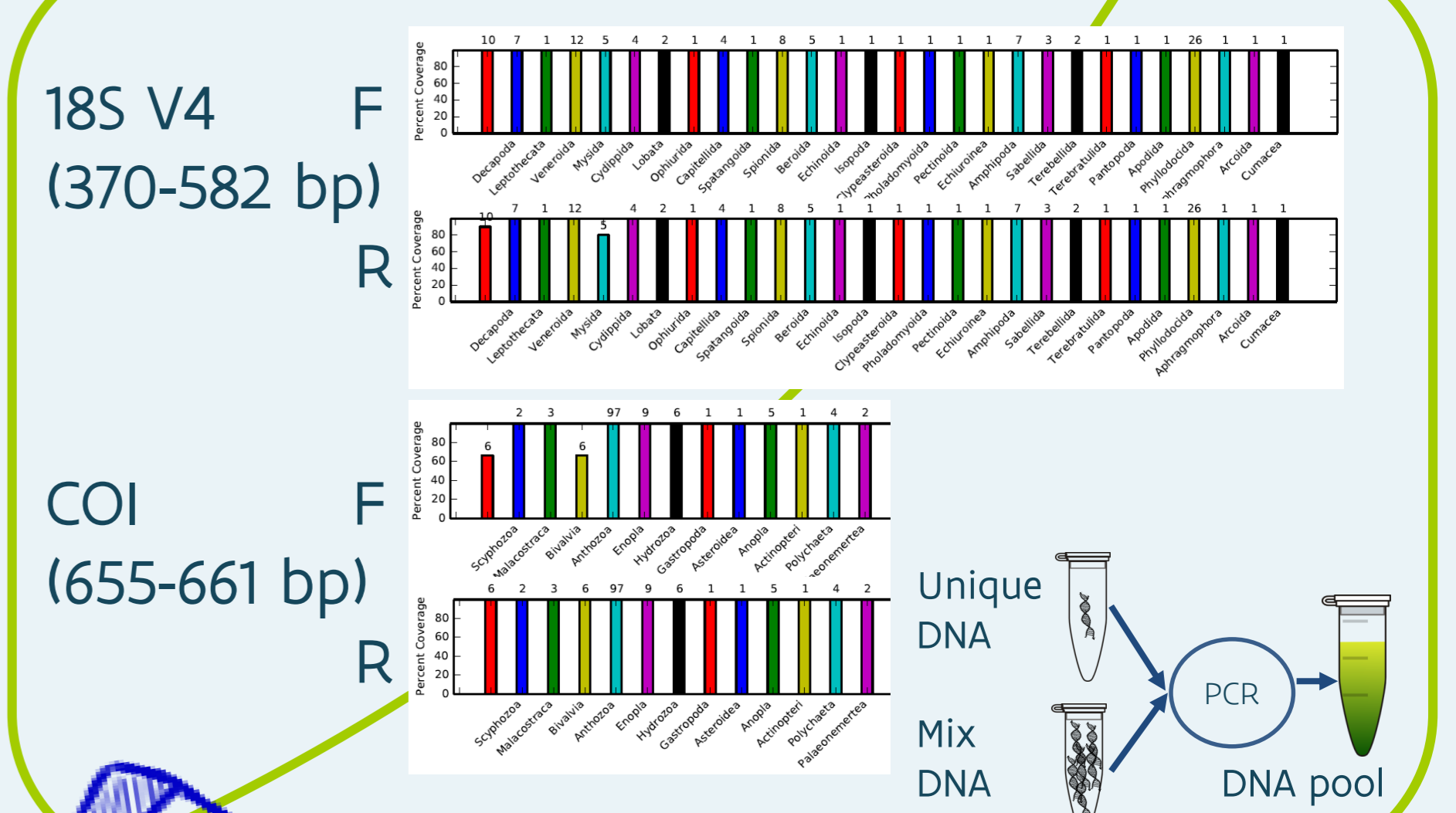
## III. SAMPLE PREPARATION

### DNA extraction



## IV. BARCODING PRIMERS

### Amplicon + Index PCR



## V. AMPLICON SEQUENCING

### Data analysis

MiSeq platform  
2 x 300 bp  
96 samples

1. Reference DNA database
2. Read preprocessing
3. OBITools analysis

We thank the aggregate extraction industry through the Sand Fund for financing this research. Shiptime on RV Belgica was provided by Belspo and RBINS OD Nature.

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