

METATRANSCRIPTOMICS OF NORTH SEA MICROEUKARYOTIC PLANKTON

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From giant whales to minute algae and bacteria, our planets' oceans and seas host a magnitude of life. Unfortunately, not all species found in these marine realms are well known. An example of these enigmatic species are eukaryotic marine protists. At the moment, a lot of the intricate genetics of the smaller eukaryotic members still is biological dark matter. This knowledge gap poses a challenge for a detailed assessment of marine ecosystem properties and functioning. Given that these microeukaryotes are the basis of marine food webs and play important roles in biogeochemical cycles, shedding light on these plankton ecosystems plays a vital role in the future of our oceans and seas.

In this project we set out to chart molecular traits of microeukaryotic plankton ecosystems from the Southern North Sea, one of the busiest marine regions of the world. High-throughput RNA sequencing data is generated from a spatial and temporal (diurnal, monthly, seasonal) sampling effort. The resulting metatranscriptomic data allows to identify key genes, species, and pathways in the present ecosystems and will be used in future ecosystem modelling efforts.

GOALS

Explore **state-of-the art RNA-Seq methods** to generate metatranscriptomic data

Create accurate descriptions of **temporal** (seasonal, diurnal) and **spatial patterns of microeukaryotic gene expression**

Identify **key genes, species, and metabolic pathways** in microeukaryotic ecosystems sampled from the Belgian Part of the North Sea

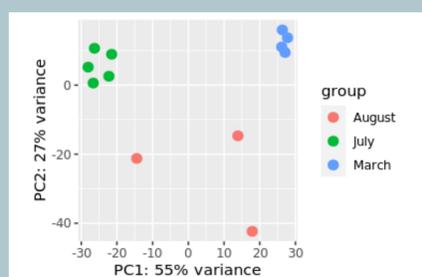
FIRST RESULTS

Several monthly sampling expeditions + 24H sampling campaign completed

From 12 samples' RNA extractions, 12 TruSeq stranded mRNA libraries generated & sequenced on Illumina NextSeq 500 up to 250M reads as a pilot study

From all the 12 samples, 818,009 unique scaffolds were assembled and identified

Of these, 70% could be taxonomically or functionally annotated



METHODS

