Marine biology and bioinformatics

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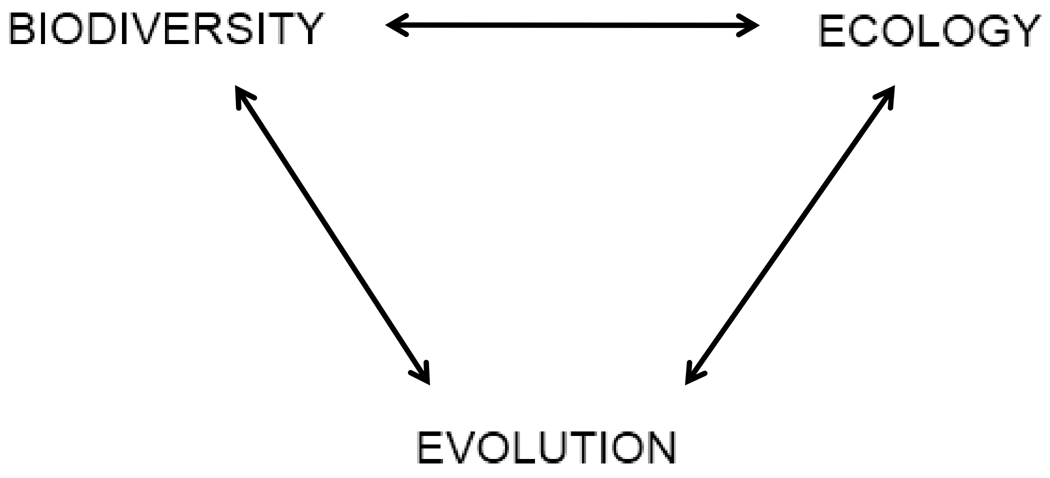
White Sea biological station

Three whales of environmental biology



ADAPTATION and SPECIES INTERACTION

IDENTIFICATION

BIODIVERSITY

ECOLOGY

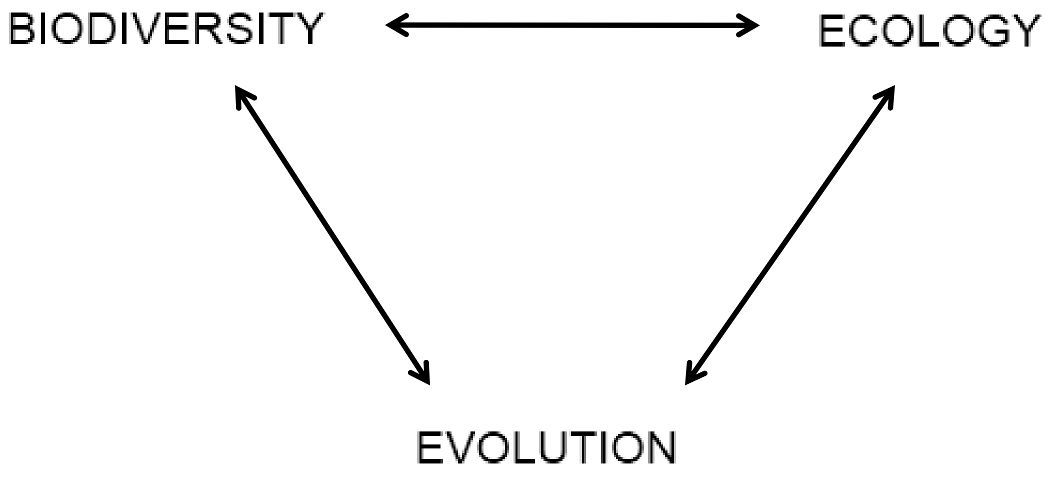
EVOLUTION

PHYLOGENY

In terms of molecular genetics and bioinformatics

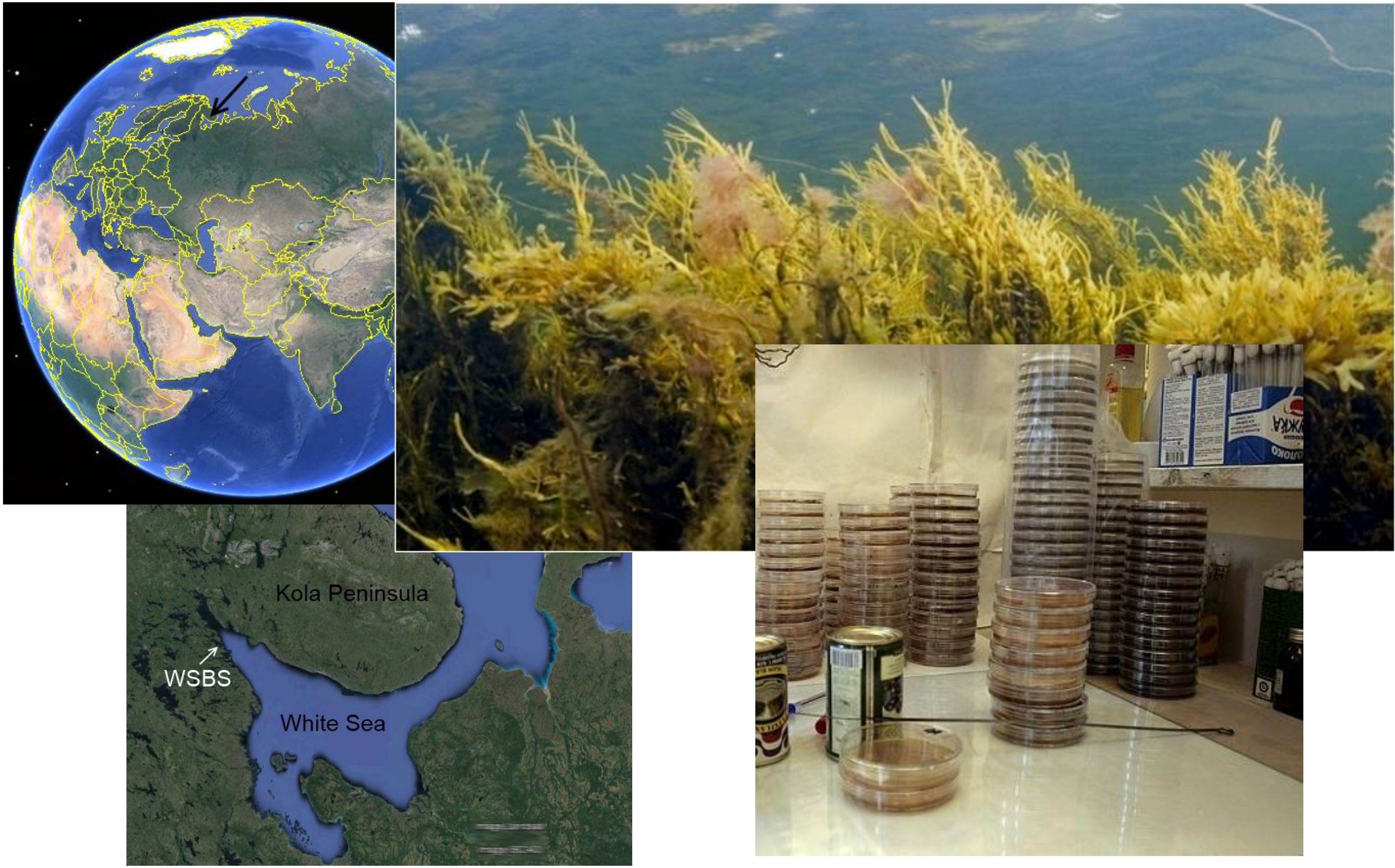
Metagenomics

Gene expression studies



Genomics

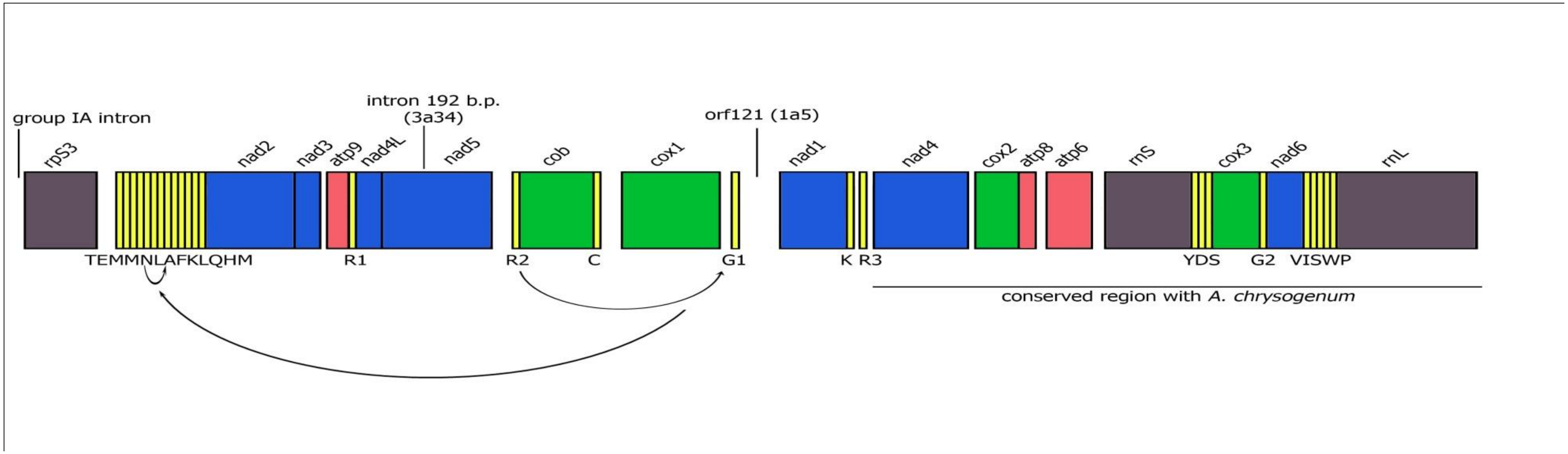
At first, biodiversity



Konovalova O. 2012. Mycobiota of brown alga Ascophyllum nodosum (L.) LeJolis in White and Barents seas. PhD thesis. Lomonosov Moscow State University

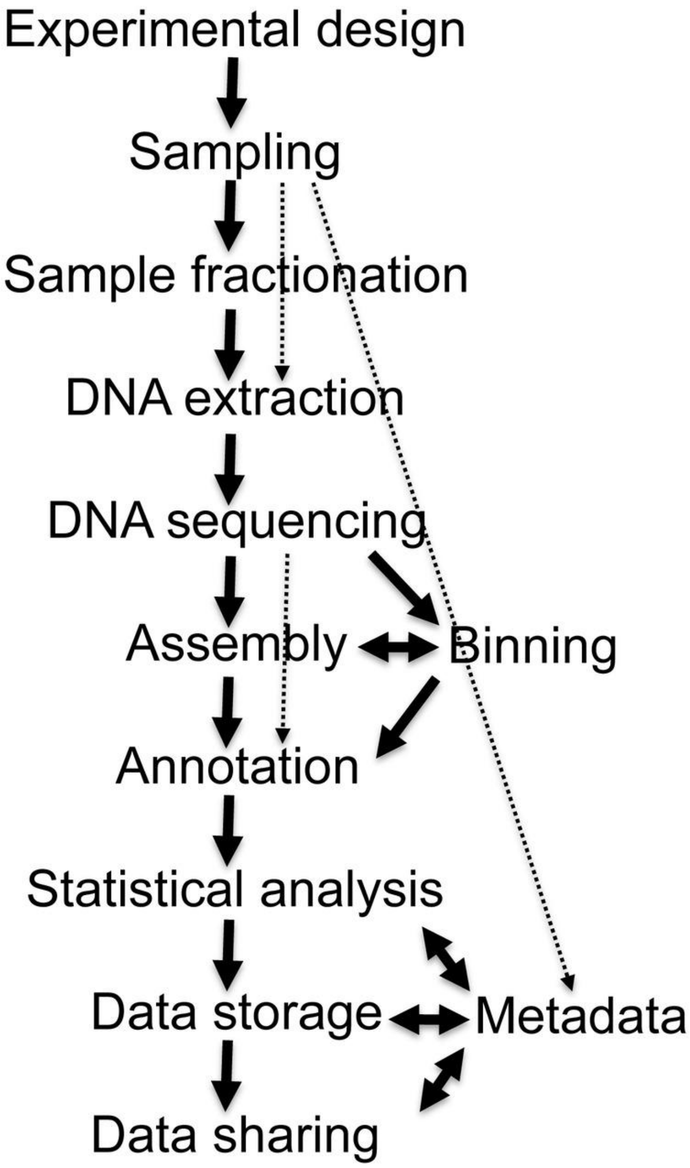
Phylogenetic studies

- Phylogenetics analysis of different group of marine fungi
- Genomic studies of marine fungus *Acremonium fuci* – comparative analysis of mitochondrial genome (almost done)



Konovalova O., Logacheva M. 2015. MITOCHONDRIAL GENOME OF MARINE FUNGUS ACREMONIUM FUCI. Mitochondrial DNA. In press.

Metagenomics



Experimental design

Sampling

Sample fractionation

DNA extraction

DNA sequencing

Assembly

Binning

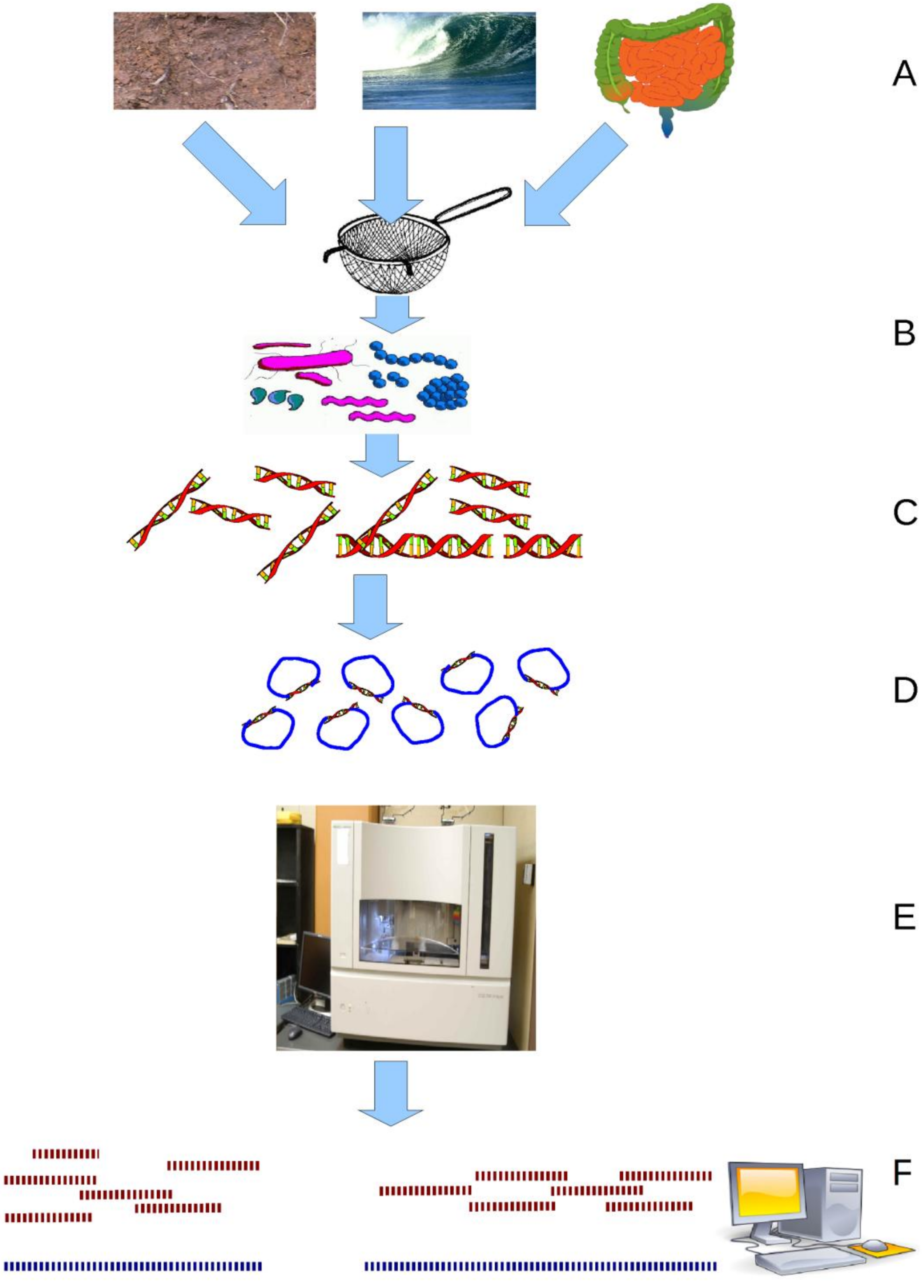
Annotation

Statistical analysis

Data storage

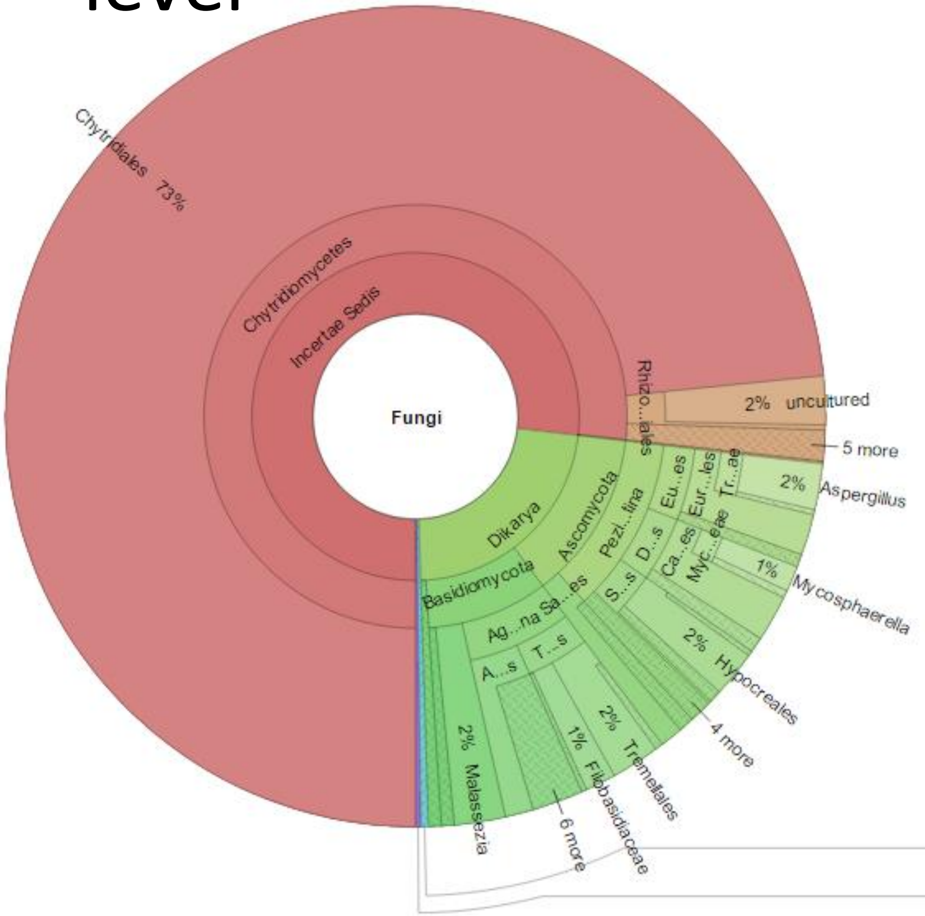
Metadata

Data sharing



Metagenomics. White Sea

- 993 OTUs, 44 identified to genus level



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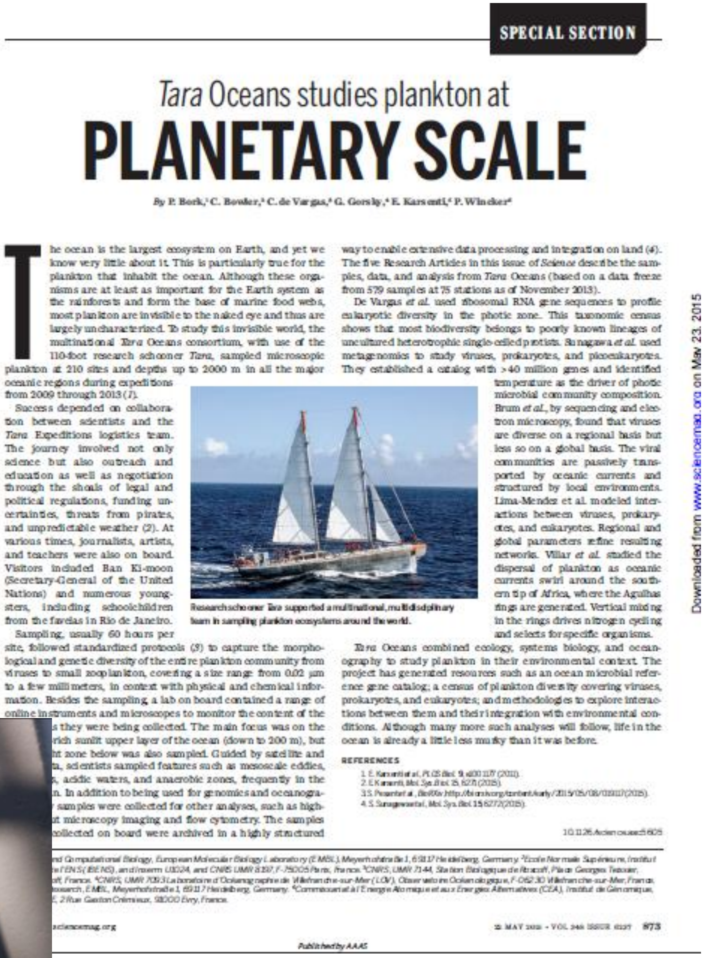
Problems

- Biological contamination – sequencing of all living cells in the sample
- Genetic contamination – it’s hard to find universal and specific barcode for eukariots or fungi etc.
- Data contamination – chimeric sequences

Metagenomics.
Atlantic Ocean, deep-sea sampling



SPECIAL SECTION

Tara Oceans studies plankton at
PLANETARY SCALE

By P. Bork,[1] C. Bowler,[2] C. de Vargas,[3] G. Gorsky,[4] E. Karsenti,[5] P. Wincker[6]

The ocean is the largest ecosystem on Earth, and yet we know very little about it. This is particularly true for the plankton that inhabit the ocean. Although these organisms are at least as important for the Earth system as the rainforests and form the base of marine food webs, most plankton are invisible to the naked eye and thus are largely uncharacterized. To study this invisible world, the multinational *Tara* Oceans consortium, with use of the 110-foot research schooner *Tara*, sampled microscopic plankton at 210 sites and depths up to 2000 m in all the major oceanic regions during expeditions from 2009 through 2013 (*1*).

Success depended on collaboration between scientists and the *Tara* Expeditions logistics team. The journey involved not only science but also outreach and education as well as negotiation through the shoals of legal and political regulations, funding uncertainties, threats from pirates, and unpredictable weather (*2*). At various times, journalists, artists, and teachers were also on board. Visitors included Ban Ki-moon (Secretary-General of the United Nations) and numerous youngsters, including schoolchildren from the favelas in Rio de Janeiro.

Research schooner *Tara* supported a multinational, multidisciplinary team in sampling plankton ecosystems around the world.

Sampling, usually 60 hours per site, followed standardized protocols (*3*) to capture the morphological and genetic diversity of the entire plankton community from viruses to small zooplankton, covering a size range from 0.02 μm to a few millimeters, in context with physical and chemical information. Besides the sampling, a lab on board contained a range of online instruments and microscopes to monitor the content of the
s they were being collected. The main focus was on the
rich sunlit upper layer of the ocean (down to 200 m), but
ht zone below was also sampled. Guided by satellite and
ta, scientists sampled features such as mesoscale eddies,
s, acidic waters, and anaerobic zones, frequently in the
n. In addition to being used for genomics and oceanogra-
samples were collected for other analyses, such as high-
t microscopy imaging and flow cytometry. The samples
ollected on board were archived in a highly structured way to enable extensive data processing and integration on land (*4*). The five Research Articles in this issue of *Science* describe the samples, data, and analysis from *Tara* Oceans (based on a data freeze from 579 samples at 75 stations as of November 2013).

De Vargas *et al.* used ribosomal RNA gene sequences to profile eukaryotic diversity in the photic zone. This taxonomic census shows that most biodiversity belongs to poorly known lineages of uncultured heterotrophic single-celled protists. Sunagawa *et al.* used metagenomics to study viruses, prokaryotes, and picoeukaryotes. They established a catalog with >40 million genes and identified temperature as the driver of photic microbial community composition. Brum *et al.*, by sequencing and electron microscopy, found that viruses are diverse on a regional basis but less so on a global basis. The viral communities are passively transported by oceanic currents and structured by local environments. Lima-Mendez et al. modeled interactions between viruses, prokaryotes, and eukaryotes. Regional and global parameters refine resulting networks. Villar *et al.* studied the dispersal of plankton as oceanic currents swirl around the southern tip of Africa, where the Agulhas rings are generated. Vertical mixing in the rings drives nitrogen cycling and selects for specific organisms.

Tara Oceans combined ecology, systems biology, and oceanography to study plankton in their environmental context. The project has generated resources such as an ocean microbial reference gene catalog; a census of plankton diversity covering viruses, prokaryotes, and eukaryotes; and methodologies to explore interactions between them and their integration with environmental conditions. Although many more such analyses will follow, life in the ocean is already a little less murky than it was before.

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Thank you!

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