D1.2. Establishment of a complete Baltic Sea sample set (**Month 24**)

IOW, Germany, 11 December 2015

Project: BLUEPRINT

Deliverable: 1.2

Workpackage : 1

Responsable contact person:

Klaus Jürgens, Institute for Baltic Sea Research Warnemünde, Germany,

Overview

Sustainable management practice of the Baltic Sea depends on a fundamental knowledge and definition of this ecosystem, enabling a prediction of its ecological status and balance for decades to come. Current descriptors in Baltic Sea monitoring to assess biologically driven processes are largely focusing on structural components and cannot cover this demand adequately anymore. A general understanding exists that new indicators representing distinct biogeochemical processes are needed, but these remain undeveloped. The complex aquatic nutrient biogeochemistry is practically driven by bacterioplankton and it seems obvious that microbial indicators could improve the Baltic Sea environmental descriptors applied by HELCOM (http://helcom.fi/) and also biogeochemical models. In consequence, through combined experimentation and in situ analyses in different environments of the Baltic Sea, the BLUEPRINT project will advance accordant knowledge based on the identification of key functional genes, key organisms or general genetic metagenomic/-transcriptomic fingerprints determining distinct pelagic nutrient fluxes.

In order to reach this aim, partners of the BLUEPRINT project have within the last two years, since the project started, intensively and comprehensively sampled the Baltic Sea ecosystem and its different subsystems, both during several cruises, and in the frame of experimental studies with Baltic Sea plankton communities. This deliverable contains a list including roughly 1400 samples, together with different environmental parameters, that were taken so far within the framework of the BLUEPRINT project (Table 1, see explanations for each entry explained in Table 2). The list contains surface samples across the whole Baltic Sea (Baltic Sea survey, WP6), depth profiles of central and coastal oxic-anoxic interfaces (redoxclines) (WP1) and samples from a 3-year seasonal sample campaign at one specific station (LMO station, WP3). Table 1 contains furthermore samples from a transplant experiment where bacterioplankton communities from Baltic Sea with different salinities were incubated under each other's environment (transplant experiment, WP1), samples from a mixing experiment were bacterioplankton communities from suboxic and anoxic zones of the central Baltic were mixed (mixing experiment, WP1) and samples from two microcosm experiments which were incubated with different DOC sources (Microcosm, WP2). All these samples have been taken to allow genomic analyses of the (planktonic) microbial communities at different levels.

For networking and the planning of possible metastudies it is essential to keep an overview on the sampling activities of the different work packages within the BLUEPRINT project. Table 1, created for this deliverable, will therefore be available for all blueprint members in

excel format on the internal page of the BLUEPRINT website (http://blueprint-project.org/) and will regularly be updated to include the most recent samplings.

Table 2: Units and explanation of fields in Table 1.

Nr	Field	Unit	Explanations
1	Institution		
2	Study		
3	Responsible researcher		
4	Sample title		
5	Size fraction	nm	
6	Fixative		Choose from option: YES/NO; indicates if fixative for preservation of RNA was added before filtering
7	Latitude	Decimal degrees	
8	Longitude	Decimal degrees	
9	Geolocation		Chose from option: Baltic Sea (www.environmentontology.org)
10	Sampling basin		
11	Sampling station		Free text
12	Environmental material		Choose from option: Water (www.environmentontology.org)
13	Environmental biome		Choose from options: Brackish water/Marine Water/Freshwater (www.environmentontology.org)
14	Environmental feature		Choose from option: Pelagic/Chemocline/Coastal/Estuarine (www.environmentontology.org)
15	Organism		choose from option: Environmental sample/Mesocosm/Enrichment culture (www.environmentontology.org)
16	Sampling depth	m	
17	Collection date		yymmdd
18	Collection time		UTC time; hhmm
19	Sequencing Facility (Library prep)		
20	Library type		Choose from optios: Total shotgun/rRNA depleted/16S/18S/ITS/Other amplicon
21	Internal standard		Choose from option: YES/NO
22	Molecule		Choose from DNA/RNA
23	Salinity		PSU
24	Temperature	°C	
25	Turbidity	ntu	Formazine calibrated ntu
26	pH		
27	NO3-	µM	
28	NO2-	µM	
29	PO42-	µM	
30	O2	µM	
31	H2S	µM	
32	NH4+	µM	
33	SiO2-	µM	
34	Chlorophyl a	µgL-1	
35	DON	µM	
36	DOC	µM	
37	Leucin incorporation	pmol Leucin L^{-1}	

38	Thymidin incorporation	pmol Thymidin h^{-1}	
39	Bacterial count	cells L^{-1}	
40	Comment		Free text