



Final Report

**FEHMARNBELT FIXED LINK
Marine Biology Services (FEMA)**

Marine Fauna and Flora - Baseline

Benthic Flora of the Fehmarnbelt Area

E2TR0020 - Volume I

APPENDICES



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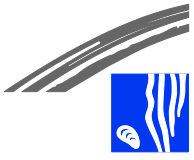


Note to the reader:

In this report the time for start of construction is artificially set to 1 October 2014 for the tunnel and 1 January 2015 for the bridge alternative. In the Danish EIA (VVM) and the German EIA (UVS/LBP) absolute year references are not used. Instead the time references are relative to start of construction works. In the VVM the same time reference is used for tunnel and bridge, i.e. year 0 corresponds to 2014/start of tunnel construction; year 1 corresponds to 2015/start of bridge construction etc. In the UVS/LBP individual time references are used for tunnel and bridge, i.e. for tunnel construction year 1 is equivalent to 2014 (construction starts 1 October in year 1) and for bridge construction year 1 is equivalent to 2015 (construction starts 1st January).



APPENDICES



A P P E N D I X 1

Video Transects (Position, Approximate Length and Depth Range) Visited in 2009 and 2010



Table App. 1.1 Video transects (position, approximate length and depth range) visited in 2009.

Transect ID	Start		End		Approximate length (km)	Depth range (m)
	Longitude*	Latitude*	Longitude*	Latitude*		
<i>Lolland coast</i>						
LoR-W-09	10° 59.00	54° 46.90	10° 54.00	54° 45.00	6.4	2.8-13.5
LoR-W-08	11° 00.20	54° 45.60	10° 58.00	54° 43.80	4.1	2.8-10.1
LoR-W-07	11° 04.00	54° 44.60	11° 02.50	54° 42.70	4.0	2.5-12.2
Lo-W-06	11° 08.00	54° 43.90	11° 06.25	54° 41.85	4.3	2.9-15.7
Lo-W-05	11° 11.20	54° 43.15	11° 08.90	54° 41.00	4.7	2.1-16.2
Lo-W-04	11° 14.10	54° 42.45	11° 12.30	54° 40.35	4.3	3.3-13.7
Lo-W-03	11° 16.70	54° 41.60	11° 14.50	54° 39.00	5.3	4.1-15.0
Lo-W-02	11° 18.80	54° 40.35	11° 16.40	54° 37.60	5.5	3.7-15.0
Lo-W-01	11° 20.25	54° 39.50	11° 18.10	54° 37.00	5.0	4.9-16.7
Lo-00-00	11° 21.75	54° 38.80	11° 19.80	54° 36.50	4.9	2.1-16.0
Lo-E-01	11° 22.70	54° 38.50	11° 20.50	54° 36.05	4.9	1.9-16.2
Lo-E-02	11° 23.50	54° 38.30	11° 21.55	54° 36.05	4.5	1.7-14.0
Lo-E-03	11° 25.10	54° 37.65	11° 22.90	54° 35.10	5.0	1.9-12.4
Lo-E-04	11° 27.35	54° 36.55	11° 25.20	54° 34.10	5.0	2.2-16.5
LoR-E-05	11° 45.00	54° 32.50	11° 45.00	54° 29.50	5.6	6.9-16.6
LoR-E-06	11° 51.00	54° 33.80	11° 51.00	54° 30.70	5.8	2.7-9.6
LoR-E-07	11° 59.75	54° 32.65	12° 04.40	54° 30.70	6.0	6.8-8.9
Total Lolland					85	
<i>Rødsand Lagoon</i>						
RO-01	11° 31.50	54° 38.20	11° 31.50	54° 35.90	4.3	1.0-2.6
RO-02	11° 35.00	54° 39.40	11° 35.00	54° 35.60	6.5	0.5-2.5
RO-03	11° 39.00	54° 39.40	11° 39.00	54° 35.70	6.5	1.0-3.5
RO-04	11° 43.00	54° 39.00	11° 43.00	54° 36.10	5.3	0.7-5.3
RO-05	11° 47.00	54° 38.80	11° 47.00	54° 35.00	6.8	1.6-7.5
RO-06	11° 51.00	54° 39.00	11° 51.00	54° 34.50	8.3	5.5-7.9
Total Rødsand					37.7	
<i>Langeland</i>						
LA-01	10° 46.10	54° 47.00	10° 48.10	54° 47.00	2.1	1.9-18.4
LA-02	10° 45.40	54° 46.00	10° 47.00	54° 46.00	2.3	1.8-19.1
LA-03	10° 44.70	54° 45.00	10° 46.50	54° 45.00	2.3	3.3-22.0
LA-04	10° 44.10	54° 44.00	10° 46.00	54° 44.00	2.3	3.5-26.0
Total Langeland					9	
<i>Eastern Kiel Bight including Orth Bight</i>						
FE-S-W02	11° 11.06	54° 31.04	11° 12.57	54° 32.56	3.7	0.7-24.5
FE-S-W04	11° 06.28	54° 31.75	11° 06.94	54° 33.78	4.0	1.2-19.0
FE-S-W05	11° 03.63	54° 32.00	11° 03.68	54° 34.63	4.9	1.5-21.2
FE-S-W06	11° 02.00	54° 30.84	10° 59.09	54° 32.15	4.2	1.9-9.8
FE-S-W08	11° 00.52	54° 28.43	10° 55.49	54° 29.46	5.9	1.2-10.0
KB-S-W01	10° 52.65	54° 28.72	10° 52.82	54° 32.03	6.4	11.0-15.8
KB-S-W02	10° 49.55	54° 32.45	10° 49.29	54° 28.75	7.0	11.4-20.4
KB-S-W03	10° 45.78	54° 28.48	10° 45.95	54° 31.50	5.8	11.5-32.5
KB-S-W04	10° 47.99	54° 19.82	10° 48.02	54° 22.56	5.5	10.2-18.5
KB-S-W05	10° 44.64	54° 19.44	10° 44.69	54° 22.62	6.2	14.7-17.5
OB-S-W01	11° 04.60	54° 26.68	11° 05.16	54° 24.43	4.6	0.7-6.4



OB-S-W02	11° 02.57	54° 26.60	11° 03.33	54° 24.86	3.7	0.5-7.0
Total Eastern Kiel Bight including Orth Bight					61.9	
<i>Fehmarnbelt</i>						
BE-S-W01	11° 01.57	54° 38.72	11° 01.66	54° 37.33	4.9	17.4-38.2
BE-S-W02	10° 58.96	54° 36.13	10° 59.35	54° 38.42	4.7	17.8-34.8
BE-S-W03	10° 56.74	54° 36.55	10° 56.32	54° 33.87	5.3	12.6-28.1
BE-S-W04	10° 52.22	54° 32.45	10° 52.64	54° 34.10	4.6	14.3-23.4
Total Fehmarnbelt					19.5	
<i>Fehmarn Coast</i>						
FE-S-W01	11° 12.75	54° 30.40	11° 13.48	54° 31.12	1.8	1.6-12.3
FE-S-E01	11° 14.63	54° 29.36	11° 17.49	54° 30.35	5.1	2.0-21.6
FE-S-E02	11° 15.68	54° 28.12	11° 19.49	54° 29.03	4.9	1.6-21.8
Total Fehmarn Coast					11.8	
<i>Großenbrode</i>						
GR-S-E02	11° 07.85	54° 22.80	11° 10.22	54° 22.88	3.3	2.2-6.8
GR-S-E04	11° 07.48	54° 22.33	11° 09.52	54° 21.25	3.5	1.5-9.4
GR-S-E06	11° 06.29	54° 21.80	11° 07.37	54° 20.81	2.7	1.4-11.9
Total Großenbrode					9.5	
<i>Sagasbank</i>						
SB-S-E02	11° 12.21	54° 18.29	11° 12.04	54° 14.98	6.8	8.1-20.9
SB-S-E04	11° 10.16	54° 18.26	11° 10.10	54° 15.18	6.1	9.3-14.3
Total Sagasbank					12.9	
<i>Staberhuk</i>						
FE-S-E03	11° 16.65	54° 27.12	11° 20.95	54° 28.11	5.1	1.6-23.1
FE-S-E04	11° 17.97	54° 25.61	11° 21.92	54° 26.67	5.4	1.8-19.5
FE-S-E06	11° 18.75	54° 24.55	11° 21.94	54° 24.43	4.2	1.6-20.3
FE-S-E07	11° 18.83	54° 24.16	11° 20.53	54° 23.68	2.1	2.1-17.3
FE-S-E09	11° 17.69	54° 24.19	11° 17.83	54° 23.47	1.5	1.5-11.7
Total Staberhuk					17.8	



Table App. 1.2 Video transects (position, approximate length and depth range) visited in 2010.

Transect ID	Start		End		Approximate length (km)	Depth range (m)
	Longitude	Latitude	Longitude	Latitude		
<i>Lolland coast</i>						
LoR-W-09	10° 59.00	54° 46.90	10° 54.00	54° 45.00	6.4	2.8-13.5
LoR-W-08	11° 00.20	54° 45.60	10° 58.00	54° 43.80	4.1	2.8-10.1
LoR-W-07	11° 04.00	54° 44.60	11° 02.50	54° 42.70	4.0	2.5-12.2
Lo-W-06	11° 08.00	54° 43.90	11° 06.25	54° 41.85	4.3	2.9-15.7
Lo-W-05	11° 11.20	54° 43.15	11° 08.90	54° 41.00	4.7	2.1-16.2
Lo-W-04	11° 14.10	54° 42.45	11° 12.30	54° 40.35	4.3	3.3-13.7
Lo-W-03	11° 16.70	54° 41.60	11° 14.50	54° 39.00	5.3	4.1-15.0
Lo-W-02	11° 18.80	54° 40.35	11° 16.40	54° 37.60	5.5	3.7-15.0
Lo-W-01	11° 20.25	54° 39.50	11° 18.10	54° 37.00	5.0	4.9-16.7
Lo-00-00	11° 21.75	54° 38.80	11° 19.80	54° 36.50	4.9	2.1-16.0
Lo-E-01	11° 22.70	54° 38.50	11° 20.50	54° 36.05	4.9	1.9-16.2
Lo-E-02	11° 23.50	54° 38.30	11° 21.55	54° 36.05	4.5	1.7-14.0
Lo-E-03	11° 25.10	54° 37.65	11° 22.90	54° 35.10	5.0	1.9-12.4
Lo-E-04	11° 27.35	54° 36.55	11° 25.20	54° 34.10	5.0	2.2-16.5
Lo-E-04b	11° 28,10	54° 35,85	11° 27,10	54° 33,30	5,0	2.5-11.6
Lo-E-04c	11° 31,00	54° 35,50	11° 31,00	54° 31,80	6,5	1.6-7.8
LoR-E-05	11° 45.00	54° 32.50	11° 45.00	54° 29.50	5.6	6.9-16.6
LoR-E-06	11° 51.00	54° 33.80	11° 51.00	54° 30.70	5.8	2.7-9.6
LoR-E-07	11° 59.75	54° 32.65	12° 04.40	54° 30.70	6.0	6.8-8.9
Total Lolland					91.9	
<i>Außenschlei</i>						
AU-S-W01	10°06.81	54°42.38	10°07.22	54°42.55	0.6	13.7-20.2
AU-S-W02	10°06.29	54°41.48	10°08.77	54°41.95	2.9	13.8-20.1
AU-S-W03	10°06.11	54°40.76	10°07.78	54°40.31	2.2	14.8-20.1
Total Außenschlei					5.7	
<i>Eastern Kiel Bight</i>						
Fe-S-W05	11°03.61	54°32.02	11°01.62	54°33.74	4.1	1.7-12.1
Fe-S-W06	11°02.00	54°30.85	10°58.97	54°32.18	4.4	3.1-10.1
Fe-S-W07	11°00.97	54°29.73	10°56.39	54°30.64	5.7	3.0-10.7
Fe-S-W08	11°00.51	54°28.44	10°55.48	54°29.47	5.9	2.0-10.4
Hb-S-W01	10°38.51	54°20.77	10°39.64	54°21.28	1.7	2.4-10.2
Hb-S-W02	10°37.97	54°21.13	10°39.12	54°21.76	1.9	2.7-10.1
Hb-S-W03	10°37.26	54°21.35	10°38.19	54°22.24	2.0	1.8-9.1
Kb-S-W01	10°52.65	54°28.73	10°52.81	54°32.03	7.0	11.0-17.3
Kb-S-W02	10°49.29	54°28.74	10°49.53	54°32.45	8.1	12.3-21.3
Kb-S-W03	10°45.94	54°31.47	10°45.77	54°28.48	6.4	12.1-17.0
Kb-S-W04	10°47.97	54°19.83	10°47.89	54°22.37	5.2	10.5-17.7
Kb-S-W05	10°44.62	54°19.45	10°44.44	54°22.44	6.7	15.0-17.3
Total Eastern Kiel Bight					59.1	
<i>Fehmarnbelt</i>						
Be-S-W01	11°01.61	54°37.42	11°01.19	54°38.87	3.4	15.9-21.6
Be-S-W02	10°59.29	54°38.41	10°58.96	54°36.13	5.1	18.7-34.9
Be-S-W03	10°56.69	54°36.50	10°56.32	54°33.86	5.4	12.6-25.2
Be-S-W04	10°52.23	54°32.45	10°52.64	54°34.11	3.4	15.3-18.0
Total Fehmarnbelt					17.3	



Fehmarn Coast

Fe-S-00	11°14.23	54°29.90	11°15.57	54°31.06	2.8	3.8-20.0
Fe-S-E01	11°14.66	54°29.37	11°16.91	54°30.24	3.6	2.8-18.7
Fe-S-E02	11°15.69	54°28.12	11°19.49	54°29.03	5.0	2.5-21.6
Fe-S-W01	11°12.77	54°30.44	11°13.42	54°31.14	1.7	2.8-12.0
Total Fehmarn Coast					13.1	

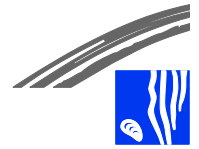
Sagasbank

Sb-S-E02	11°12.03	54°14.99	11°12.16	54°18.30	6.4	8.3-15.7
Sb-S-E04	11°10.14	54°18.26	11°10.11	54°15.18	6.1	9.4-13.9
Total Sagasbank					12.5	

Staberhuk

Fe-S-E03	11°16.67	54°27.12	11°19.01	54°27.66	3.1	2.2-16.4
Fe-S-E04	11°18.023	54°25.51	11°20.77	54°26.16	4.2	3.0-18.2
Fe-S-E06	11°18.85	54°24.54	11°21.89	54°24.45	3.7	4.3-20.5
Fe-S-E09	11°17.74	54°24.17	11°17.83	54°23.48	1.6	2.7-12.6
Total Staberhuk					12.6	

* Projection: WGS84



A P P E N D I X 2

Method Harmonization and Results of Ring Test for Benthic Vegetation in the Summer of 2009



Method Harmonization Workshop

A workshop was conducted to harmonize the sampling and analysing methods and to ensure identical data quality among the sampling teams carrying out the fieldwork. The benthic vegetation workshop programme included different tasks of fieldwork and laboratory work.

Fieldwork - frame sampling for biomass and vegetation coverage estimates

Before fieldwork started example protocols and method descriptions for frame sampling were handed out to the participants. When discussing the basic details for fieldwork it became evident that different methods to determine vegetation cover in the field exist in Denmark and Germany: In Germany all coverage estimations performed underwater refer to the base area. Substrate specific cover of vegetation is calculated afterwards upon the coverage values of the different sediment types and the vegetation cover detected in the field. In Denmark all coverage estimations carried out underwater refer to suitable substrate and not to the base area of the frame. However, as the cover of suitable substrate is also estimated, total cover is easily calculated.

All three divers exercised site description, frame sampling for vegetation and coverage estimations in circles. Unfortunately wind became stronger in the afternoon so that soft bottom sampling (*Zostera* above- and below-ground biomass) had to be cancelled. But at least the technique for one frame could be practised.

The following decisions have been made after this fieldwork day to ensure comparable data acquisition on both sides:

- Every sediment description made by divers has to follow EN ISO 14688-1. These descriptions are important especially for the mixed sediment areas ("coarse sediments" = coarse gravel, pebbles, cobbles, boulders), as it is not possible to take samples for grain size analysis within these areas. As fine sediment types cannot be distinguished by the naked eye, these classes are gathered to a "silt/mud/clay"-class. As clay reefs are common along the West coast of Fehmarn, this special class was included in the sediment classification.
- All estimations of sediment types within the whole base area or within the frame have to be made in percentages with 5 % accuracy. This means that the sum of percentages of the different sediment types has to be 100 %.
- The "example protocol for sites" was checked and modified. The categories in this protocol should be followed for coverage estimations in circles (25 m²). All cover estimations for vegetation should be substrate specific with 5 % accuracy. For every site 2–3 overview photos for documentation have to be taken.
- The "example protocol for frames" was checked and modified. The categories on this protocol should be followed for coverage estimations within the frames. All cover estimations for vegetation should be done with 5% accuracy.

Laboratory work – soft and hard benthic vegetation sample processing

Before laboratory work starts example protocols and method descriptions for species identification and biomass determination were handed out to the participants. Accuracy of biomass measurements (0.1 g), drying temperatures and



durations are listed there. It was agreed to follow the specifications made in the German SOP for biomass determination and species identification.

For species nomenclature the WoRMS list (World Register of Marine Species – www.marinepecies.org) should be used and if some names are not listed there Algaebase (Listing the worlds algae - www.algaebase.org) should be the source. Additionally, MariLim should deliver a list of algae species identified during the last national monitoring surveys.

The “example protocols” were checked and modified. If identification is not possible to species level a brief comment should be inserted in the protocol, stating why it was not possible (e. g. not fertile or holdfast lacking).

Video recording, data analysis of recordings

A short description of the methods for underwater video was handed out to the participants. It was discussed and the fundamental principles were illustrated.

In the field, the German and the Danish video systems were demonstrated in practice. Both video systems were drop-down systems towed in low speed behind a boat. The camera systems proved to be comparable with respect to the field of vision. However, low fidelity of colours from the Danish camera made it difficult to distinguish between green and red algae. Both systems show navigational data in the video stream (position, depth, time, name of transect) and also log these data into a separate log file for later processing. During the field exercise, all aspects of the practical handling were executed, such as towing speed, height above sea floor, angle of camera with respect to the sea floor.

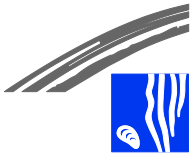
Back in the office, the recorded videos were examined. The quality of the videos was good, despite the bad visibility in the water on that day. The quality was discussed with respect to speed and it was shown from example videos that towing speeds larger than 1 kn would rapidly decrease the quality and make it very hard to estimate coverage. It was demonstrated how the height of the camera above the sea floor would influence the field of vision and the possibilities of identifying algae and estimating coverage.

The processing of the videos and the recording of coverage into the log file were shown. It was agreed to add the categories *Potamogeton* and *Ruppia* to the categories present in the German processing guideline, because these groups will also occur in the Rødsand area.

Ring Test

For the identification of taxonomic differences between the involved laboratories (DBL and MariLim) a ring test was conducted. During the baseline sampling programme, some “extra” samples were taken in different vegetation communities and depth intervals:

- *Fucus* zone within the 2–5 m interval along the west coast of Fehmarn (MariLim responsible)
- Red algae zone of deep waters within the 10–15 m interval along the east coast of Fehmarn (MariLim responsible)
- Flowering plant (angiosperm) zone within the 0–1 m interval of Orth Bight (MariLim responsible)



- Red algae zone of shallow waters within the 5–10 m depth interval along the coast of Lolland (DHI/DBL responsible)

Ring test samples were fixed in ethanol and first processed within the responsible laboratory. Taxa were sorted and determined to the lowest possible taxonomical level. Every taxon was separated in numbered vials. Each sample set consisting of different vials was then sent to the other laboratory for species determination.

A total of 44 reference specimens were checked within the ring test (Table App. 2.1). Some taxa occurred twice as they are naturally part of different vegetation communities (e. g. *Ceramium virgatum* or *Coccotylus truncatus*). In Appendix 2 the different sample sets with the included taxa of the ring test are listed. For the following taxa, determination differed between laboratories.

Coccotylus truncatus – *Phyllophora pseudoceranooides*

It is known from monitoring programmes and QA-workshops that these taxa can be difficult to distinguish as specimens exist with morphological features that refer to both taxa. Because of these difficulties these two taxa have already been combined for the coverage estimations performed by divers. But also the species determination in the laboratory was not distinct. Both species will be listed and used in the analysis under the combined category *Coccotylus/Phyllophora*.

Chaetomorpha linum – *Chaetomorpha melagonium*

Normally the determination between the two species is unproblematic. However, if only short pieces of the algae are present it can be difficult to distinguish between these two species. Both species will be listed and used in the analysis under the genus *Chaetomorpha*.

Membranoptera alata (cf. *Pantoneura*) – *Membranoptera alata*

Both laboratories listed the species under the correct species name *Membranoptera alata*. The used specimen featured a specific morphological habit that resembles another genus called *Pantoneura*. It was only checked if both laboratories would recognize such anomaly. As this specimen was classed under the correct species name, the difference has no consequence for the data analysis and a clarification between laboratories is not needed. But the advice to the taxonomic experts will be given to note such anomalies in the species identification protocol.

Ectocarpus siliculosus – *Ectocarpus/Pylaiella*

The determination between *Ectocarpus siliculosus* and *Pylaiella littoralis* is only possible if chloroplasts are visible, opposite branching is present or the algae is fertile. Therefore it was agreed for the baseline programme to use the category *Ectocarpus/Pylaiella*, if these characters were not developed/available. For the specimen used in the ring test, a determination to species level was possible, but as the term *Ectocarpus/Pylaiella* was usually used during the baseline programme, the difference has no consequence for the data analysis and a clarification between laboratories is not needed. But the advice will be given to the taxonomic experts to determine to species level whenever it is possible, and comment upon the determination in the species identification protocol.

Derbesia marina – *Vaucheria litorea*

Although these two taxa belong to different taxonomic divisions (Chlorophyta: Bryopsidophyceae and Heterokontophyta: Xanthophyceae) the determination between them is not simple as chloroplasts or reproductive structures have to be visible. As these species are not common and abundant in the field, the difference between laboratories has no significant consequence for the data analysis. But as *Vaucheria litorea* is red listed in Germany, the difference has to be cleared at a meeting before the laboratory analysis starts for the second sampling year. Until

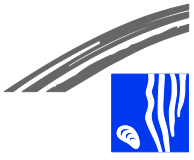


then both species will be listed and used in the analysis under the combined category *Derbesia/Vaucheria*.

In conclusion the result of the ring test showed a high level of agreement between laboratories in species identification. The found differences were taken into account during data analysis and will not influence the results of the baseline study or the Environmental Impact Assessment.

Table App. 2.1 Overview of ringtest samples and results. Red marked ones are species/taxa with discrepancies in determination between laboratories.

	Transect ID	Depth interval	No.	Taxa	AphiaID	Responsible	Taxa	Responsible
Red algae phytal (medium water depth)	Fe-S-E04	10-15	1	<i>Delesseria sanguinea</i>	144744	MariLim		
	Fe-S-E04	10-15	2	<i>Phycodrys rubens</i>	144773	MariLim		
	Fe-S-E04	10-15	3	<i>Saccharina latissima</i>	234483	MariLim		
	Fe-S-E04	10-15	4	<i>Coccotylus truncatus</i>	145654	MariLim	<i>Phyllophora pseudoceranoides</i>	DBL
	Fe-S-E04	10-15	5	<i>Brongniartella byssoides</i>	144792	MariLim		
	Fe-S-E04	10-15	6	<i>Cystoclonium purpureum</i>	145615	MariLim		
	Fe-S-E04	10-15	7	<i>Desmarestia viridis</i>	145310	MariLim		
	Fe-S-E04	10-15	8	<i>Chaetomorpha linum</i>	145027	MariLim	<i>Chaetomorpha melagonium</i>	DBL
	Fe-S-E04	10-15	9	<i>Membranoptera alata</i>	144758	MariLim		
	Fe-S-E04	10-15	10	<i>Desmarestia aculeata</i>	145307	MariLim		
	Fe-S-E04	10-15	11	<i>Furcellaria lumbicalis</i>	145620	MariLim		
	Fe-S-E04	10-15	12	<i>Rhodomela confervoides</i>	144854	MariLim		
Fucus phytal	SB-S-E02_Süd	10-15	1	<i>Membranoptera alata (cf. pantoneura)</i>	143891	MariLim	<i>Membranoptera alata</i>	DBL
	FE-S-W06	2-5	1	<i>Sphaerotrichia divaricata</i>	144931	MariLim		
	FE-S-W06	2-5	2	<i>Ectocarpus siliculosus</i>	145410	MariLim	<i>Pylaiella/Ectocarpus</i>	DBL
	FE-S-W06	2-5	3	<i>Polysiphonia fibrillosa</i>	144634	MariLim		
	FE-S-W06	2-5	4	<i>Fucus serratus</i>	145546	MariLim		
	FE-S-W06	2-5	5	<i>Dumontia contorta</i>	145228	MariLim		
	FE-S-W06	2-5	6	<i>Ceramium virgatum</i>	178915	MariLim		
	FE-S-W06	2-5	7	<i>Ceramium tenuicome</i>	144569	MariLim		
	FE-S-W06	2-5	8	<i>Aglaothamnion/Callithamnion</i>	143825/143832	MariLim		
	FE-S-W06	2-5	9	<i>Ahnfeltia plicata</i>	144422	MariLim		
	FE-S-W06	2-5	10	<i>Polysiphonia fucoides</i>	144639	MariLim		
Angiosperm phytal	OB-S-W01	0-1m	1	<i>Lamprothamnium papulosum</i>	179053	MariLim		
	OB-S-W01	0-1m	2	<i>Derbesia marina</i>	144462	MariLim	<i>Vaucheria littoralis</i>	DBL
	OB-S-W01	0-1m	3	<i>Zostera noltii</i>	145796	MariLim		
	OB-S-W01	0-1m	4	<i>Tolypella nidifica</i>	416187	MariLim		
	OB-S-W01	0-1m	5	<i>Chara canescens</i>	399468	MariLim		
	OB-S-W01	0-1m	6	<i>Chara baltica</i>	399467	MariLim		
	OB-S-W01	0-1m	7	<i>Zannichellia palustris</i>	416222	MariLim		
	OB-S-W01	0-1m	8	<i>Ruppia maritima</i>	234031	MariLim		
	OB-S-W01	0-1m	9	<i>Ruppia cirrhosa</i>	416218	MariLim		
	OB-S-W01	0-1m	10	<i>Chara aspera</i>	399466	MariLim		
Red algae phytal (shallow water)	Lo_E_04 v01	5-10	1	<i>Phyllophora pseudoceranoides</i>	145664	DBL		
	Lo_E_04 v01	5-10	2	<i>Ceramium virgatum</i>	178915	DBL		
	Lo_E_04 v01	5-10	3	<i>Ceramium tenuicome</i>	144569	DBL		
	Lo_E_04 v01	5-10	4	<i>Polysiphonia fibrillosa</i>	144634	DBL		
	Lo_E_04 v01	5-10	5	<i>Aglaothamnion/Callithamnion</i>	143825/143832	DBL		
	Lo_E_04 v01	5-10	6	<i>Polysiphonia fucoides</i>	144639	DBL		
	Lo_E_04 v01	5-10	7	<i>Coccotylus truncatus</i>	145654	DBL		
	Lo_E_04 v01	5-10	8	<i>Furcellaria lumbicalis</i>	145620	DBL		
	Lo_E_04 v01	5-10	9	<i>Rhodomela confervoides</i>	144854	DBL		
	Lo_E_04 v01	5-10	10	<i>Delesseria sanguinea</i>	144744	DBL		



A P P E N D I X 3

Description of methods used for community analysis, criteria for allocation of benthic flora communities and diversity parameters



Community analysis

Community analysis is the process of grouping biological data sets with species information by using differences or similarities. Two different methodological approaches can be used for vegetation classification: the floristic (species) composition and/or the dominance principle. In the first approach similarities in species composition are determined by species-relevé associations. Within each group characteristic species are identified, which show a high consistency in their specific association. Their abundance (= dominance) has no or only low relevance for the definition of characteristic species. The second approach uses the relative abundance and uses the dominant species to identify groups. The methods analyse different aspects of macrophyte assemblages, but supplement each other in terms of informative value (Trempe 2005). Both approaches have been used to define benthic flora communities in the baseline study:

- TWINSpan analysis for floristic composition (characteristic species) and
- Cluster and MDS analysis for the dominance principle

Floristic (species) composition

TWINSpan (Two-way INdicator SPecies ANALysis) uses as source a raw table, in which the species composition of each sampling station is listed together with the specific coverage and/or biomass information of each species. A frequency table is produced, in which species are grouped based on their relative presence (number of stations with a certain species divided through number of all stations). As neither unique occurring nor rare species are useful for community classification, species with medium frequency are of high importance in the identification of groups (differential species). Rare species are excluded (< 5 % frequency). In this table stations are grouped by using differential species. The classification or grouping is done divisive meaning that all observations start in one cluster, and splits are performed recursively as one moves down the hierarchy, by using the TWINSpan-Logarithms of Hill (1979) for ordination („Reciprocal Averaging – RA“). Stations are sorted in two groups: negative “-“ = without differential species, positive “+“ = with differential species. This two-way classification is iteratively refined and continued in a hierarchical fashion to subdivide the groups until the minimum group size initially selected by the user is obtained. In the original output a table is produced showing species-by-site (quadrant or sample) relationships (Seaby & Henderson 2007).

How many divisions that are needed or how many species that should be included in the groups at the lowest division is a crucial input of the analysis. Those parameters may influence the outcome of the analysis strongly, but are difficult to generalise. They depend on the specific size of the data set (number of stations and species). A comparison of the outcome with other community analysis methods and literature data on vegetation community classification of the investigation areas is necessary to extract clearly defined community characteristics.

Dominance principle

Multivariate methods like cluster analysis or multidimensional scaling (MDS) identify groups within the data set by using certain variables (species composition, abundance, biomass). The groups are homogenous and are differentiated from each other by the variables. The analyses were based on the Bray-Curtis dissimilarity index (Bray & Curtis 1957), which quantifies the (biological community) dissimilarity between all pairs of sites on basis of abundance and the occurrence of common or differential species. To down weight the influence of



dominant species and to stress the importance of rare species, biomass data were square root transformed before calculation of Bray-Curtis dissimilarity index:

$$BC_{ij} = \sum \frac{|n_{ik} - n_{jk}|}{(n_{ik} + n_{jk})}$$

n_i = abundance of the i^{th} species
 n_j = abundance of the j^{th} species
 k = area

Cluster analysis relies on a hierarchical grouping of samples by using the group average of their distances (dissimilarities). The results of a cluster analysis are displayed in a hierarchical tree-like structure, the dendrogram. On the dendrogram, firstly two groups are defined, and within these groups subgroups are defined. This process is called group average and is continued until all stations are grouped. Sites that are most alike will cluster (group) together, whereas those sites that are more dissimilar are unlikely to join the same cluster.

Multidimensional scaling (MDS) ordines data along a gradient of similarities or distances. The result is illustrated in a two-dimensional graph, in which each point represents one sample (station). The closer the points, the more similar the species assemblages are in those samples.

Cluster analysis or MDS are capable of identifying and graphically illustrating groups within the data set, but allow no identification of which species that are important for the grouping. SIMPER-Analysis (SIMilarity PERcentage) can be used to express the similarity (in percentage) within each group and which species (in percentage) are important for the similarity within each group. Additionally, the analysis shows the dissimilarity (in percentage) between groups and which species (in percentage) that are responsible for the dissimilarity between groups. How appropriate a species is to distinguish between groups, can be determined by the standard deviation to the similarity coefficient: the smaller the standard deviation the better an indicator for similarities or dissimilarities (Clark & Warwick 1994).

Community definition and allocation rules

In the final result the data set is divided into certain groups characterised by either group characteristic species or differential species. For the definition of benthic flora communities in the investigation area only those communities and characteristic species have been adopted, which have been identified by both approaches and already mentioned in literature for the western Baltic Sea.

Absolute biomass data were chosen as source for the community analyses as those data include the most detailed and precise species information. All stations with biomass sampling could therefore be allocated to specific flora communities. To classify also stations, for which only coverage estimations by divers have been assessed, several criteria for the allocation have been defined:

- Only stations with a vegetation cover $\geq 10\%$ are classified into benthic flora communities. Drifting mats of macrophytes are not considered for the classification. This is in accordance with the basic rule for biomass sampling (only stations with $\geq 10\%$ cover are sampled). Stations with less than 10% cover are categorised to single vegetation stands.
- Stations that comprise only one characteristic species are categorised to the corresponding flora community.
- Stations that comprise characteristic species of different communities are allocated to that community for which the characteristic species has the highest dominance (coverage). One exception are stations that inhabit characteristic species of hard and soft bottom communities with $\geq 10\%$ cover each. Those are categorised as mixed communities (eelgrass/algae),



to highlight the ecological important information of mixed sediment and community relationships.

- Stations that comprise characteristic species of different communities with identical cover degrees were allocated by expert judgement by using additional ecological information (e. g. water depth, sediment characteristics).

Diversity parameters

For diversity analysis several parameters have been assessed: species richness, Simpson's dominance index, Simpson's index of diversity, Shannon's diversity index.

Species richness is the simplest measure for diversity. It is determined as number of species per investigation unit (e. g. per station, depth interval, spatial area or flora community).

Simpson's dominance index (D) equals the probability that two individuals taken at random from the dataset of interest represent the same species. It takes into account the number of species and the relative abundance of each species:

$$D = \sum_{i=1}^S \left(\frac{n_i}{N}\right)^2$$

n_i = abundance of the i^{th} species
 N = total abundance
 S = total number of species

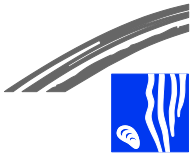
The value for D can vary between 0 and 1, with 1 representing the lowest diversity – only one species occurs. As this relation is not very intuitive usually the transformation $1-D$ is used and called Simpson's index of diversity. This index equals the probability that the two individuals represent different species and values near 1 represent a high diversity. Simpson's index of diversity is also a measure for evenness. Abundant species are weighted stronger compared to species with low abundance, as rare species with low abundances have only low influence on the index value.

Shannon's diversity index (H) quantifies the entropy within a dataset and takes into account the number of species and the relative abundance of each species:

$$H = - \sum_{i=1}^S p_i \ln p_i \quad p_i = \frac{n_i}{N}$$

p_i = proportion of individuals of the i^{th} species
 S = total number of species

Theoretically the H-value has no upper limit. In realistic biological communities Shannon's diversity index varies between 0 (only one species) and 4.5. Due to the dependency of Shannon's diversity index of the total number of species, comparisons between communities is difficult as high species numbers with a very uneven distribution of abundance result in the same H-value as low species numbers and an even distribution of abundance.



A P P E N D I X 4

Cluster and MDS Plots for Macroalgae and Flowering plant Communities in Fehmarnbelt in the Summer of 2009



MDS and Cluster plots for macroalgae community analysis

Used abbreviations:

BE: Fehmarnbelt, transects Be-S-W01 to Be-S-W04

FeE: East side of Fehmarn, transects Fe-S-E01 to Fe-S-E09

FeW: West side of Fehmarn, transects Fe-S-W01 to Fe-S-W08

GR: Großenbrode, transects Gr-S-E01 to Gr-S-E07

LA: Langeland, transects LA-01 to LA-04

LO: Lolland coast, transects Lo-W-01 to Lo-W-09, Lo-00, Lo-E-01 to Lo-E-06

SB: Sagasbank, transects Sb-S-E01 to Sb-S-E04

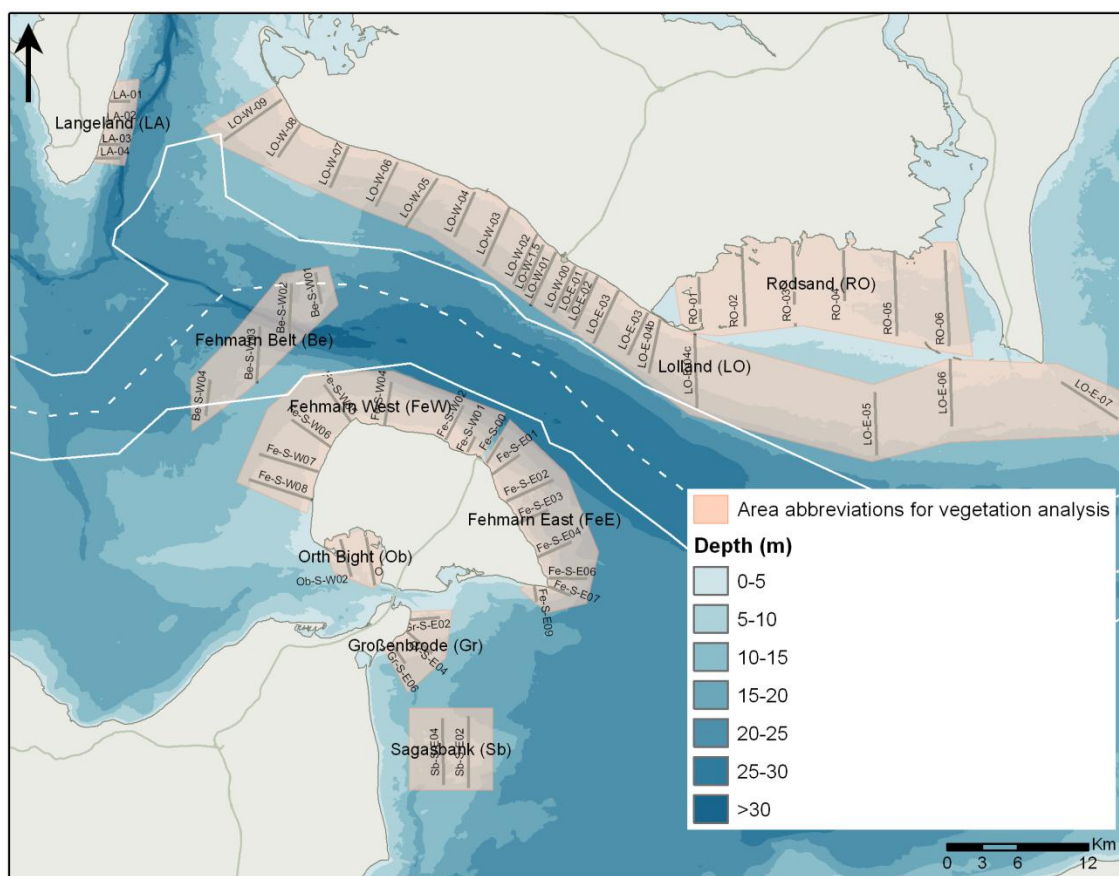
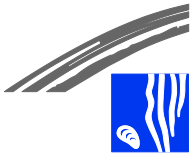
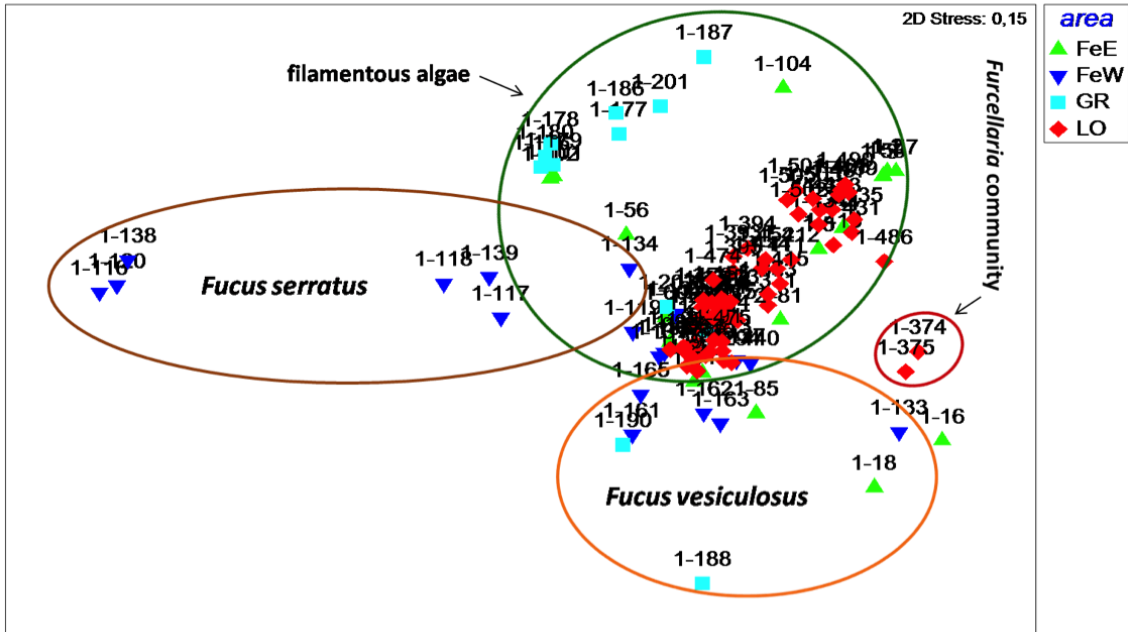


Figure App. 4.1 Names and abbreviations for geographical regions used for the community analysis.

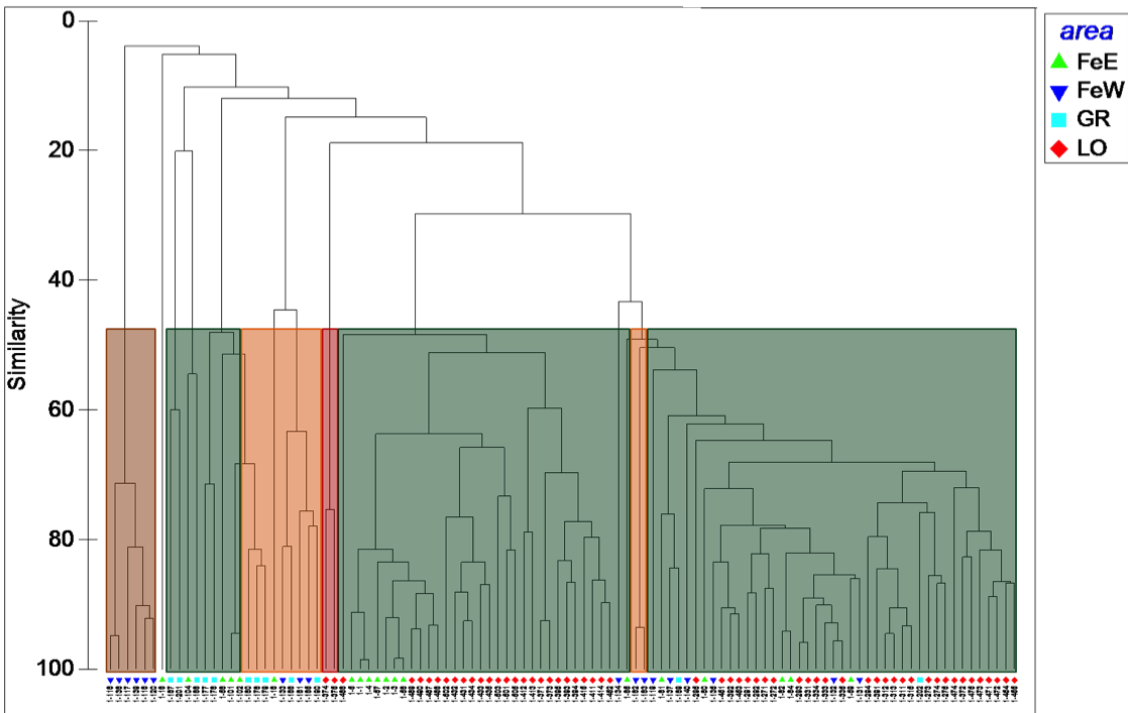


0-2m

Transform: Square root
Resemblance: S17 Bray Curtis similarity



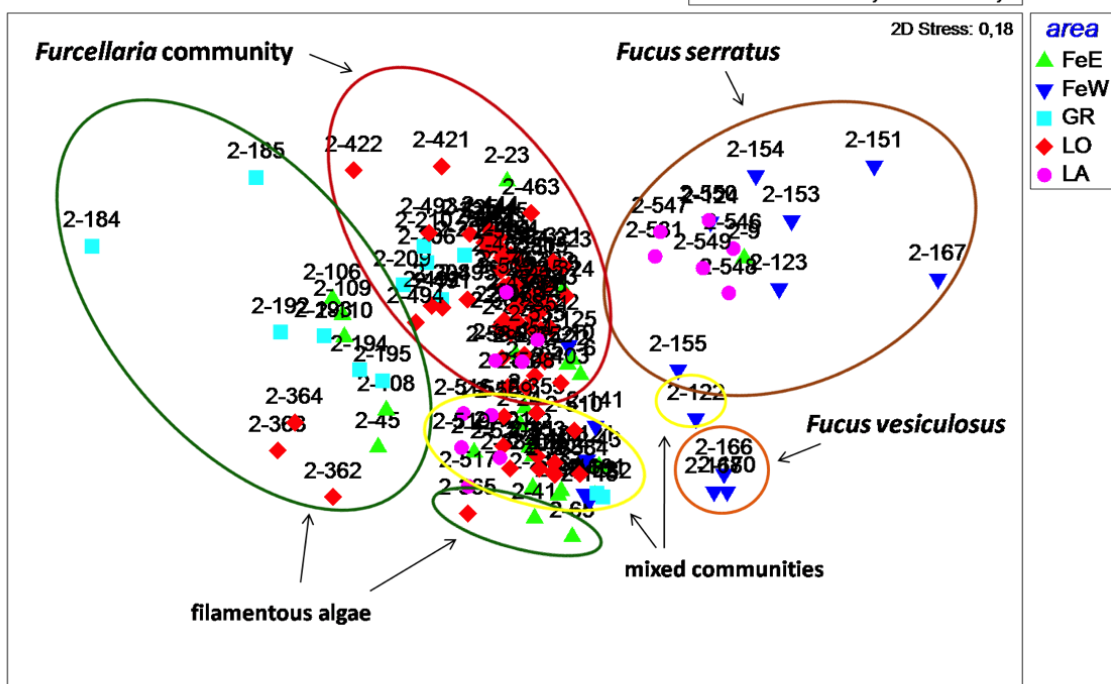
0-2m



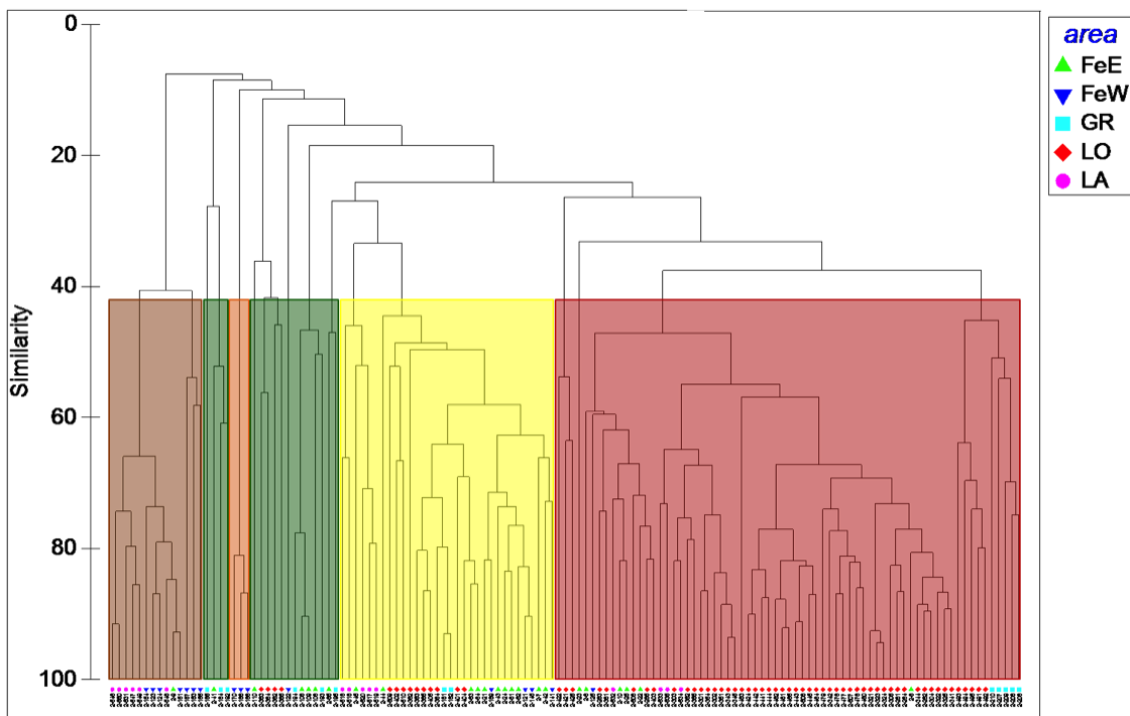


2-5m

Transform: Square root
Resemblance: S17 Bray Curtis similarity



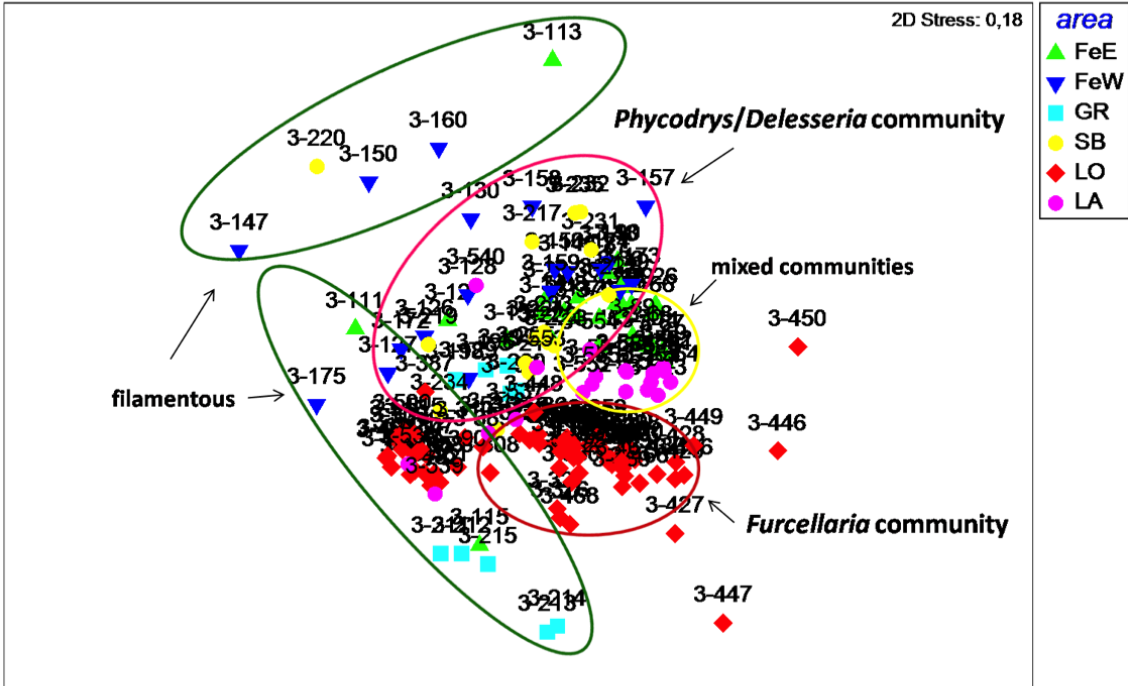
2-5m



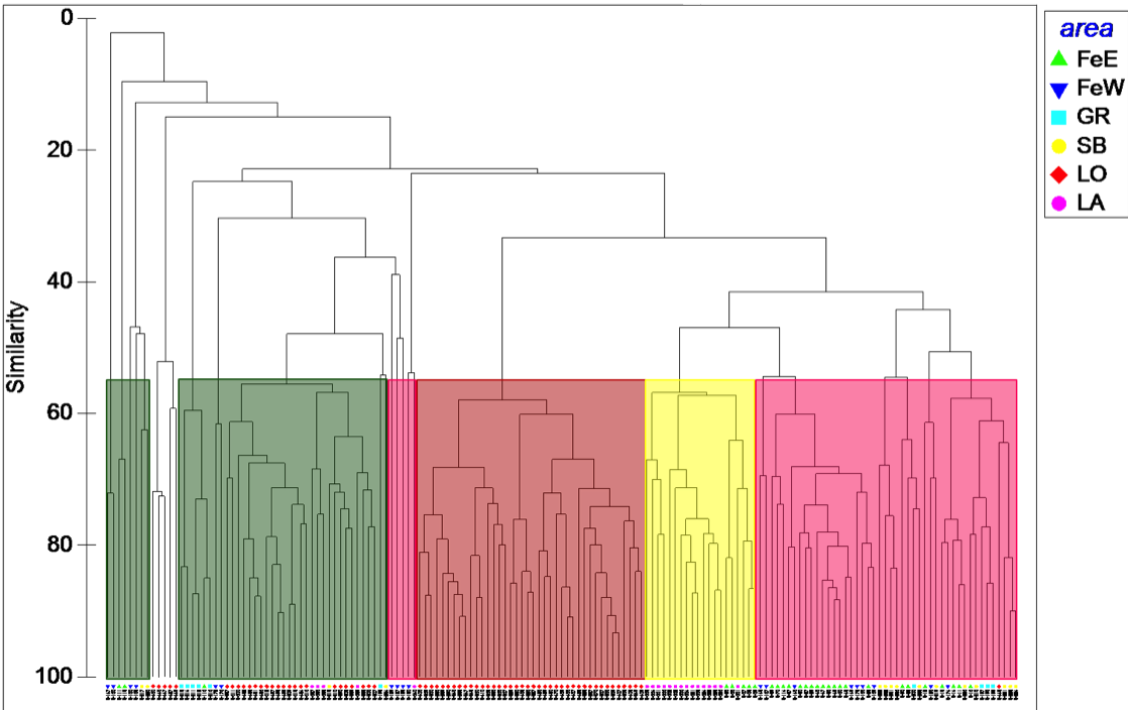


5-10m

Transform: Square root
Resemblance: S17 Bray Curtis similarity



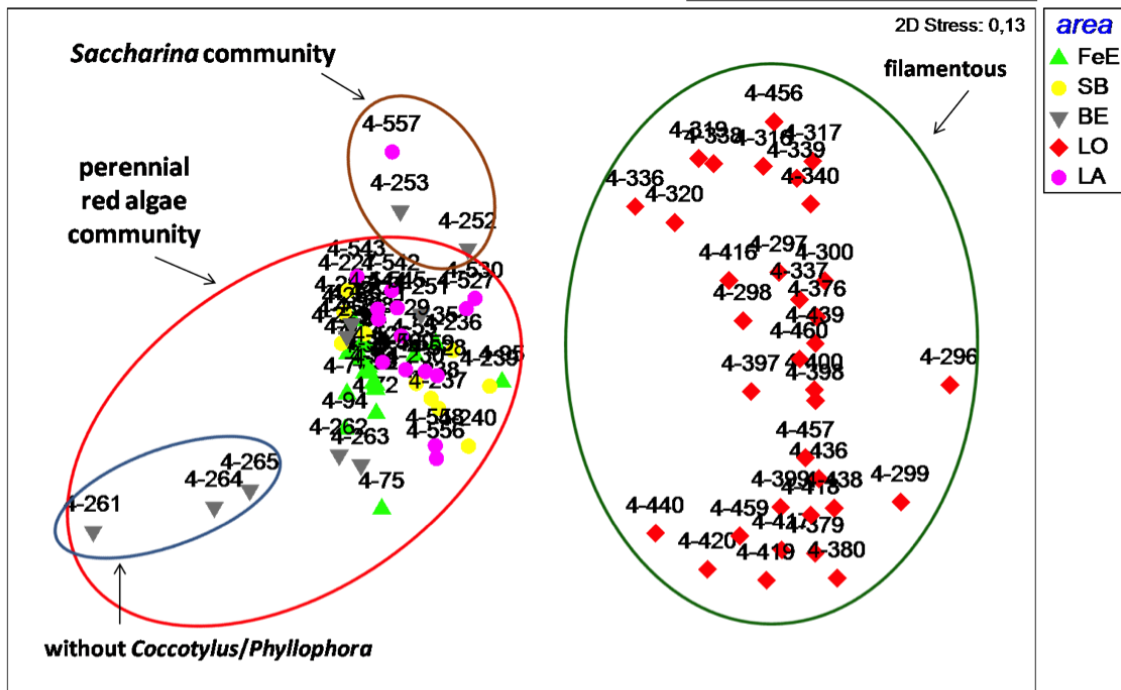
5-10m



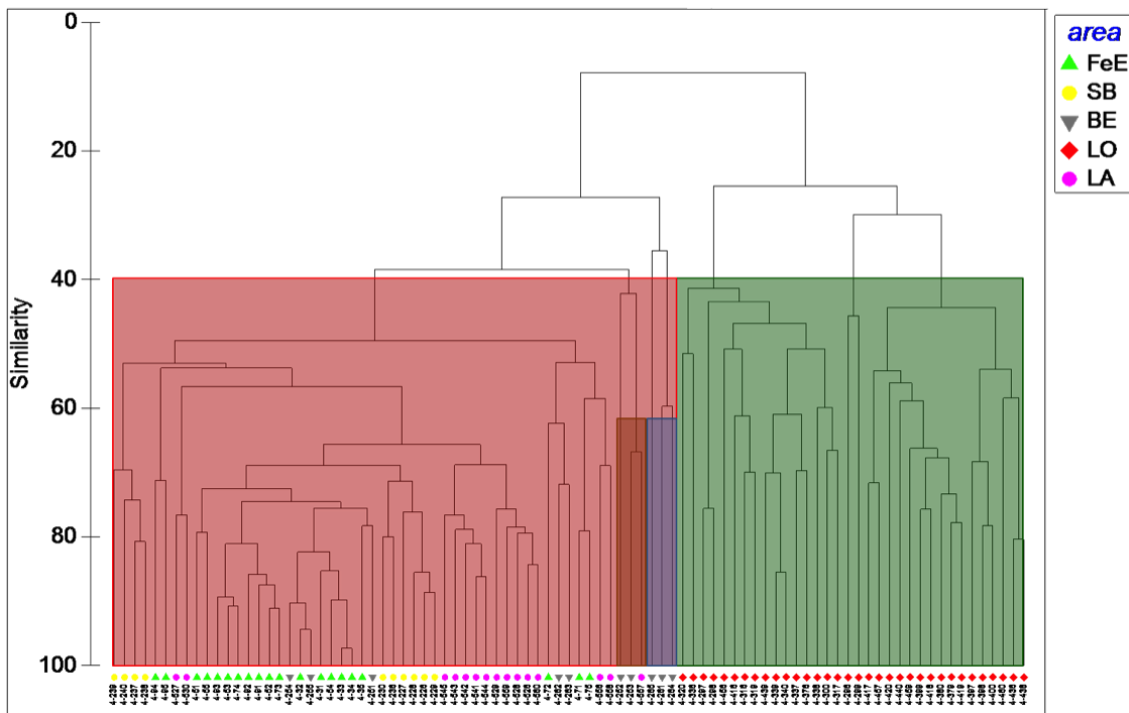


10-15m

Transform: Square root
Resemblance: S17 Bray Curtis similarity



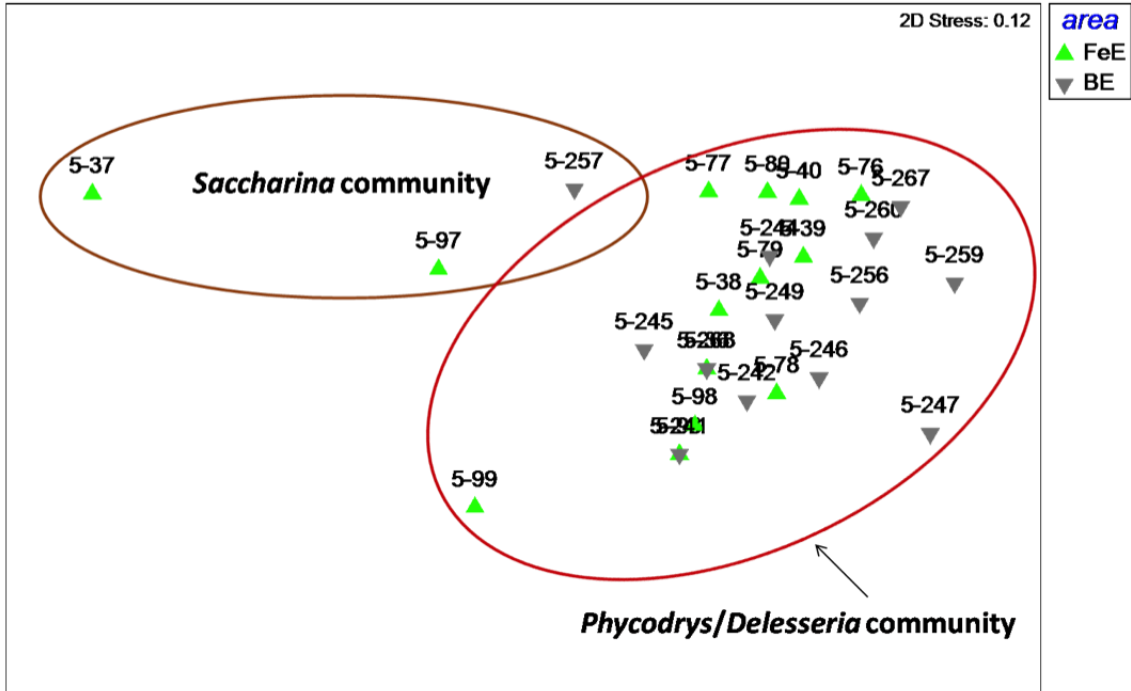
10-15m



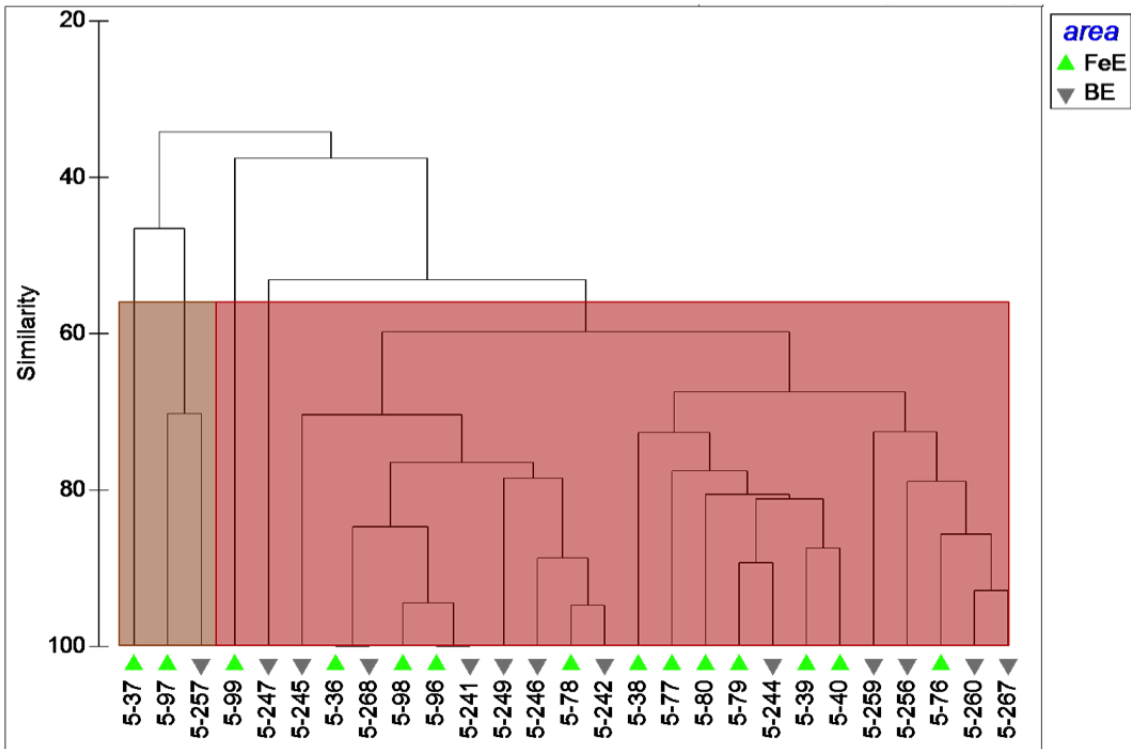


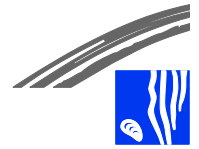
15-20m

Transform: Square root
Resemblance: S17 Bray Curtis similarity



15-20m

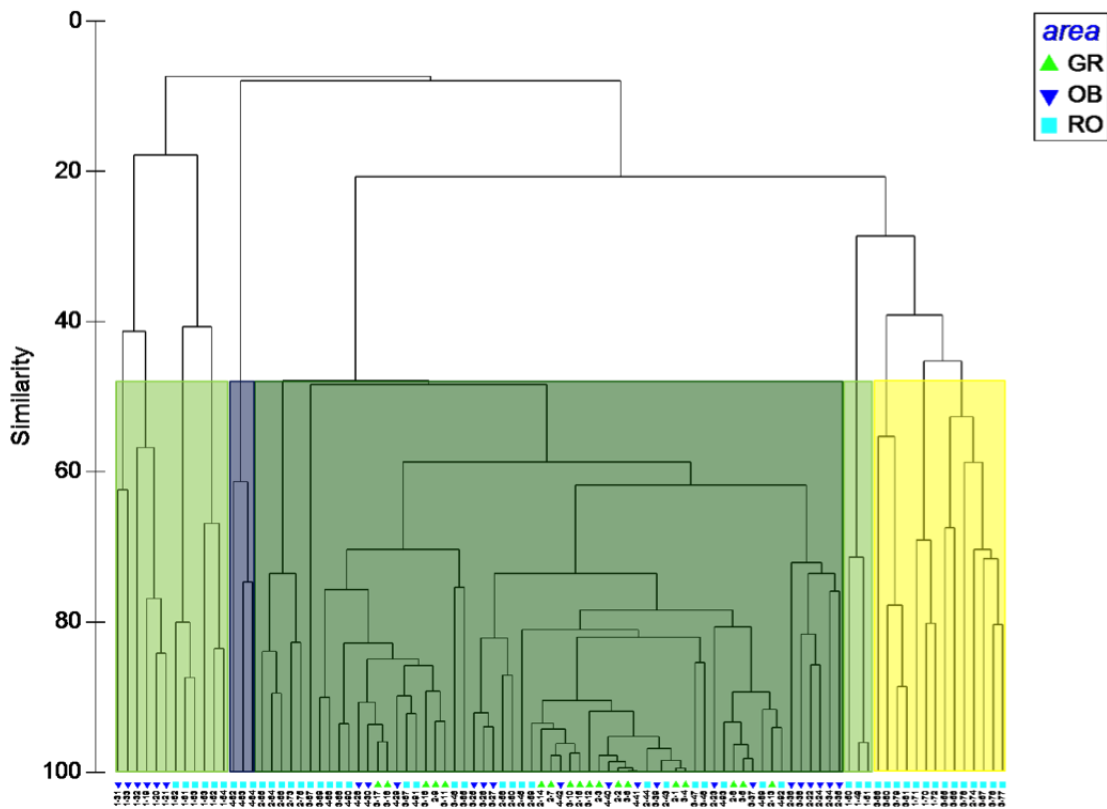
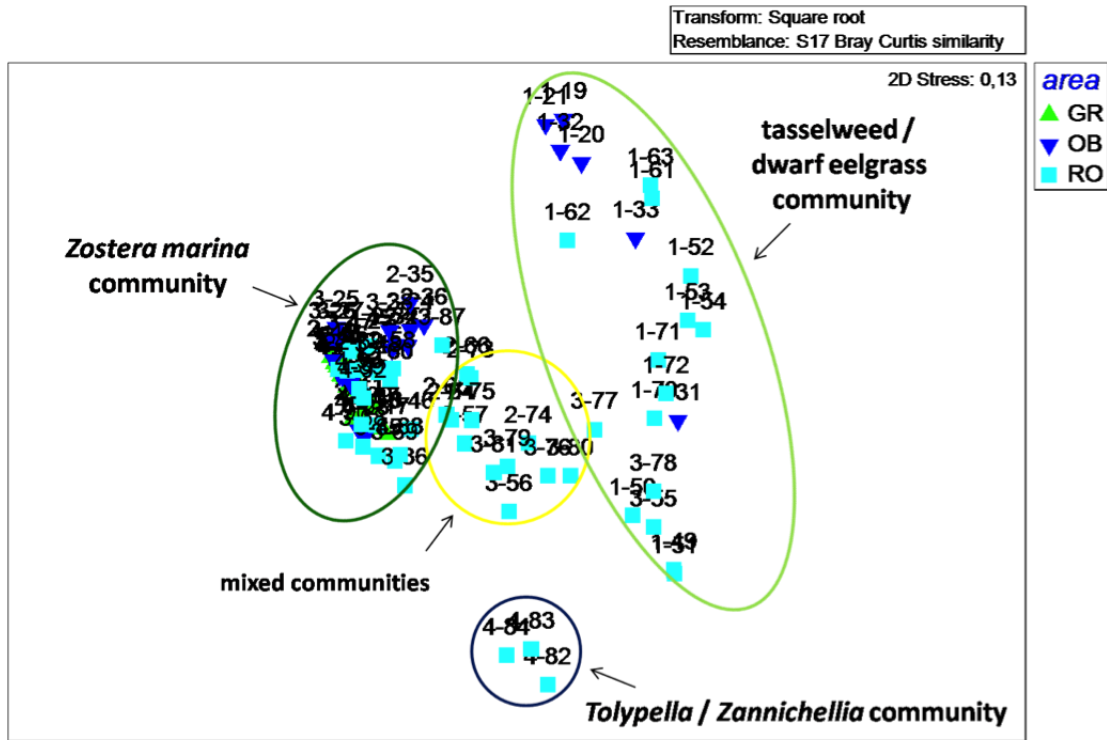




MDS and Cluster plots for angiosperm community analysis

Used abbreviations:

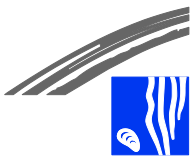
- GR: Großenbrode, transects Gr-S-E02, Gr-S-E04, Gr-S-E06
- OB: Orth Bight, transects Ob-S-W01, Ob-S-W02
- RO: Rødsand Lagoon, transects Ro-01 to Ro-06





A P P E N D I X 5

Results of Analysis of Similarities (ANOSIM) for Macroalgae and Flowering plant Communities in Feh- marnbelt in the summer of 2009



Macroalgae

0-2m biomass

Global Test

Sample statistic (Global R): 0.484

Significance level of sample statistic: 0.1%

Number of permutations: 999 (Random sample from a large number)

Number of permuted statistics greater than or equal to Global R: 0

Pairwise Tests

R	Significance	Possible	Actual	Number >=	
Groups	Statistic	Level %	Permutations	Permutations	Observed
FeE, FeW	0.148	0.5	Very large	999	4
FeE. GR	0.248	0.1	141120525	999	0
FeE. LO	0.378	0.1	Very large	999	0
FeW. GR	0.305	0.1	86493225	999	0
FeW. LO	0.493	0.1	Very large	999	0
GR. LO	0.753	0.1	Very large	999	0

	FeE	FeW	Gr	Lo
FeE				
FeW				
Gr				
Lo				

2-5m biomass

Global Test

Sample statistic (Global R): 0.43

Significance level of sample statistic: 0.1%

Number of permutations: 999 (Random sample from a large number)

Number of permuted statistics greater than or equal to Global R: 0

Pairwise Tests

R	Significance	Possible	Actual	Number >=	
Groups	Statistic	Level %	Permutations	Permutations	Observed
FeE, FeW	0.246	0.2	Very large	999	1
FeE. GR	0.215	0.1	Very large	999	0
FeE. LO	0.324	0.1	Very large	999	0
FeE. LA	0.187	0.7	Very large	999	6
FeW. GR	0.402	0.1	67863915	999	0
FeW. LO	0.669	0.1	Very large	999	0
FeW. LA	0.203	1.1	300540195	999	10
GR. LO	0.484	0.1	Very large	999	0
GR. LA	0.306	0.1	37442160	999	0
LO. LA	0.402	0.1	Very large	999	0

	FeE	FeW	Gr	Lo	La
FeE					
FeW					
Gr					
Lo					
La					



5-10m biomass

Global Test

Sample statistic (Global R): 0.398

Significance level of sample statistic: 0.1%

Number of permutations: 999 (Random sample from a large number)

Number of permuted statistics greater than or equal to Global R: 0

Pairwise Tests

R	Significance	Possible	Actual	Number >=	
Groups	Statistic	Level %	Permutations	Permutations	Observed
FeE, FeW	0.217	0.1	Very large	999	0
FeE. GR	0.495	0.1	635745396	999	0
FeE. SB	0.232	0.1	Very large	999	0
FeE. LO	0.496	0.1	Very large	999	0
FeE. LA	0.351	0.1	Very large	999	0
FeW. GR	0.332	0.1	20030010	999	0
FeW. SB	0.12	1.8	Very large	999	17
FeW. LO	0.67	0.1	Very large	999	0
FeW. LA	0.33	0.1	Very large	999	0
GR. SB	0.232	0.7	3268760	999	6
GR. LO	0.342	0.1	Very large	999	0
GR. LA	0.58	0.1	30045015	999	0
SB. LO	0.417	0.1	Very large	999	0
SB. LA	0.418	0.1	Very large	999	0
LO. LA	0.25	0.1	Very large	999	0

	FeE	FeW	Gr	Lo	La	Sb
FeE		Green	Yellow	Yellow	Yellow	Green
FeW	Green		Yellow	Red	Yellow	Green
Gr	Yellow	Yellow		Yellow	Red	Green
Lo	Yellow	Red	Yellow		Yellow	Yellow
La	Yellow	Yellow	Red	Yellow		Yellow
Sb	Green	Green	Green	Yellow	Yellow	

10-15m biomass

Global Test

Sample statistic (Global R): 0.513

Significance level of sample statistic: 0.1%

Number of permutations: 999 (Random sample from a large number)

Number of permuted statistics greater than or equal to Global R: 0

Pairwise Tests

R	Significance	Possible	Actual	Number >=	
Groups	Statistic	Level %	Permutations	Permutations	Observed
FeE. SB	0.438	0.1	30045015	999	0
FeE. BE	0.491	0.1	30045015	999	0
FeE. LO	0.877	0.1	Very large	999	0
FeE. LA	0.311	0.1	Very large	999	0
SB. BE	0.378	0.1	92378	999	0
SB. LO	0.783	0.1	Very large	999	0
SB. LA	0.398	0.1	3268760	999	0
BE. LO	0.876	0.1	Very large	999	0
BE. LA	0.336	0.4	3268760	999	3



LO. LA 0.815 0.1 Very large 999 0

	FeE	Lo	La	Sb	Be
FeE					
Lo					
La					
Sb					
Be					

15-20m biomass

Global Test

Sample statistic (Global R): -0.006

Significance level of sample statistic: 46.5%

Number of permutations: 999 (Random sample from 20058300)

Number of permuted statistics greater than or equal to Global R: 464

Flowering plant (angiosperm) communities

0-6m biomass

Global Test

Sample statistic (Global R): 0.029

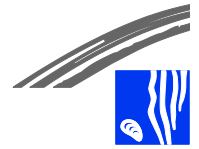
Significance level of sample statistic: 24%

Number of permutations: 999 (Random sample from a large number)

Number of permuted statistics greater than or equal to Global R: 239

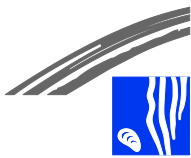
Pairwise Tests

R Groups	Significance Statistic	Possible Level %	Actual Permutations	Number >= Permutations	Observed
GR, OB	0.051	11.2	Very large	999	111
GR, RO	-0.023	59	Very large	999	589
OB, RO	0.097	3.6	Very large	999	35



A P P E N D I X 6

Results of Analysis of Similarity Percentage (SIMPER) for Macroalgae and Flowering plant Communities in Fehmarnbelt in the summer of 2009



Macroalgae

0–2m

Data worksheet

Name: Data1

Data type: Biomass

Sample selection: All

Variable selection: All

Parameters

Resemblance: S17 Bray Curtis similarity

Cut off for low contributions: 90.00%

Group FeE

Average similarity: 24.47

Species	Av.Abund	Av.Sim	Sim/SD	Contrib%	Cum.%
Clad sp	5.53	12.65	0.46	51.72	51.72
Poly fuco	3.71	9.34	0.53	38.18	89.90
Cera virg	1.12	1.92	0.19	7.84	97.74

Group FeW

Average similarity: 30.74

Species	Av.Abund	Av.Sim	Sim/SD	Contrib%	Cum.%
Poly fuco	6.28	16.15	0.75	52.54	52.54
Fucu serr	13.54	8.93	0.37	29.06	81.60
Fucu vesi	4.53	2.76	0.28	8.96	90.56

Group GR

Average similarity: 23.71

Species	Av.Abund	Av.Sim	Sim/SD	Contrib%	Cum.%
Cera virg	5.85	18.25	0.82	76.97	76.97
Poly fibr	1.38	1.58	0.19	6.67	83.64
Poly fuco	1.32	1.38	0.19	5.81	89.46
Fucu vesi	3.63	1.05	0.12	4.41	93.87

Group LO

Average similarity: 50.79

Species	Av.Abund	Av.Sim	Sim/SD	Contrib%	Cum.%
Poly fuco	5.91	25.14	1.15	49.50	49.50
Clad sp	4.12	11.05	0.70	21.75	71.25
Cera virg	1.23	4.28	1.12	8.43	79.69
Cera tenu	1.22	3.78	1.08	7.44	87.13
Poly fibr	0.76	3.34	1.11	6.58	93.71

Groups FeE & FeW

Average dissimilarity = 82.43

Species	Group FeE		Group FeW		Contrib%	Cum.%
	Av.Abund	Av.Abund	Av.Diss	Diss/SD		
Fucu serr	0.00	13.54	24.40	0.74	29.60	29.60
Poly fuco	3.71	6.28	15.99	1.06	19.40	49.00
Clad sp	5.53	0.92	13.98	0.87	16.96	65.96
Fucu vesi	3.41	4.53	13.55	0.63	16.43	82.39
Cera virg	1.12	1.64	5.46	0.85	6.63	89.02



Chor filu 1.11 0.00 2.34 0.23 2.84 91.86

Groups FeE & GR

Average dissimilarity = 87.20

Species	Group FeE	Group GR	Av.Diss	Diss/SD	Contrib%	Cum.%
	Av.Abund	Av.Abund				
Cera virg	1.12	5.85	20.00	1.13	22.94	22.94
Clad sp	5.53	0.32	19.89	0.84	22.80	45.74
Poly fuco	3.71	1.32	14.51	0.91	16.64	62.38
Fucu vesi	3.41	3.63	12.87	0.50	14.76	77.15
Poly fibr	0.20	1.38	6.40	0.51	7.34	84.49
Chor filu	1.11	0.00	3.15	0.23	3.61	88.10
Dumo cont	0.22	0.49	3.06	0.56	3.50	91.60

Groups FeW & GR

Average dissimilarity = 85.90

Species	Group FeW	Group GR	Av.Diss	Diss/SD	Contrib%	Cum.%
	Av.Abund	Av.Abund				
Fucu serr	13.54	0.00	24.94	0.75	29.04	29.04
Poly fuco	6.28	1.32	17.98	1.04	20.93	49.97
Fucu vesi	4.53	3.63	15.33	0.74	17.85	67.81
Cera virg	1.64	5.85	13.53	1.01	15.75	83.57
Poly fibr	0.10	1.38	4.26	0.49	4.95	88.52
Clad sp	0.92	0.32	2.57	0.73	2.99	91.51

Groups FeE & LO

Average dissimilarity = 68.78

Species	Group FeE	Group LO	Av.Diss	Diss/SD	Contrib%	Cum.%
	Av.Abund	Av.Abund				
Clad sp	5.53	4.12	21.16	1.18	30.77	30.77
Poly fuco	3.71	5.91	17.83	1.26	25.92	56.69
Cera virg	1.12	1.23	6.50	0.90	9.44	66.14
Cera tenu	0.65	1.22	4.70	1.13	6.83	72.97
Fucu vesi	3.41	0.18	4.55	0.26	6.61	79.58
Poly fibr	0.20	0.76	3.12	1.23	4.54	84.12
Chor filu	1.11	0.00	3.00	0.23	4.37	88.49
Agla Call	0.00	0.60	2.08	1.27	3.03	91.52

Groups FeW & LO

Average dissimilarity = 73.39

Species	Group FeW	Group LO	Av.Diss	Diss/SD	Contrib%	Cum.%
	Av.Abund	Av.Abund				
Fucu serr	13.54	0.00	24.24	0.75	33.03	33.03
Poly fuco	6.28	5.91	13.32	1.18	18.14	51.17
Fucu vesi	4.53	0.18	10.42	0.61	14.19	65.36
Clad sp	0.92	4.12	9.68	0.95	13.19	78.55
Cera virg	1.64	1.23	4.33	1.19	5.90	84.45
Cera tenu	0.19	1.22	2.90	1.13	3.95	88.40
Poly fibr	0.10	0.76	2.03	1.26	2.76	91.16



Groups GR & LO

Average dissimilarity = 83.51

Species	Group GR	Group LO	Av.Diss	Diss/SD	Contrib%	Cum.%
	Av.Abund	Av.Abund				
Poly fuco	1.32	5.91	19.51	1.33	23.36	23.36
Cera virg	5.85	1.23	17.68	1.02	21.17	44.53
Clad sp	0.32	4.12	14.04	0.94	16.81	61.34
Fucu vesi	3.63	0.18	9.35	0.46	11.19	72.53
Poly fibr	1.38	0.76	7.03	0.73	8.42	80.95
Cera tenu	0.00	1.22	4.09	1.16	4.90	85.85
Dumo cont	0.49	0.00	2.34	0.50	2.81	88.66
Agla Call	0.00	0.60	2.16	1.29	2.58	91.24

2-5m

Data worksheet

Name: Data1

Data type: Biomass

Sample selection: All

Variable selection: All

Parameters

Resemblance: S17 Bray Curtis similarity

Cut off for low contributions: 90.00%

Group FeE

Average similarity: 29.82

Species	Av.Abund	Av.Sim	Sim/SD	Contrib%	Cum.%
Poly fuco	7.14	20.73	0.93	69.52	69.52
Cera virg	2.41	3.96	0.40	13.27	82.79
Furc lumb	3.57	2.88	0.34	9.65	92.44

Group FeW

Average similarity: 25.19

Species	Av.Abund	Av.Sim	Sim/SD	Contrib%	Cum.%
Fucu serr	13.19	11.65	0.50	46.25	46.25
Poly fuco	4.43	9.53	0.56	37.84	84.08
Fucu vesi	3.01	2.94	0.22	11.66	95.75

Group GR

Average similarity: 20.77

Species	Av.Abund	Av.Sim	Sim/SD	Contrib%	Cum.%
Cera virg	3.88	8.84	0.80	42.58	42.58
Furc lumb	3.23	3.45	0.46	16.63	59.21
Poly stri	1.09	2.43	0.26	11.70	70.91
Sper repe	2.28	2.16	0.37	10.42	81.32
Poly fuco	1.08	1.44	0.14	6.96	88.28
Ecto Pyla	1.05	1.34	0.34	6.45	94.73



Group LO

Average similarity: 42.93

Species	Av.Abund	Av.Sim	Sim/SD	Contrib%	Cum.%
Furc lumb	14.47	22.41	1.03	52.21	52.21
Poly fuco	4.21	8.40	0.77	19.57	71.78
Cera virg	4.01	6.50	1.07	15.15	86.93
Cera tenu	1.26	1.73	0.58	4.02	90.95

Group LA

Average similarity: 36.70

Species	Av.Abund	Av.Sim	Sim/SD	Contrib%	Cum.%
Fucu serr	25.06	9.63	0.40	26.24	26.24
Poly fuco	5.22	6.37	1.01	17.37	43.61
Furc lumb	5.66	3.65	0.62	9.94	53.55
Poly fibr	2.92	3.08	0.69	8.39	61.94
Cera virg	2.54	2.85	1.07	7.76	69.70
Cocc Phyl	4.62	2.39	0.44	6.50	76.20
Rhod conf	2.24	1.60	0.41	4.35	80.56
Dele sang	1.82	1.33	0.60	3.62	84.18
Poly elong	1.82	1.31	0.60	3.56	87.74
Cera tenu	1.10	1.17	0.97	3.20	90.94

Groups FeE & FeW

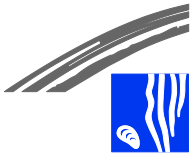
Average dissimilarity = 80.95

Species	Group FeE		Group FeW		Contrib%	Cum.%
	Av.Abund	Av.Abund	Av.Diss	Diss/SD		
Fucu serr	2.05	13.19	24.94	0.90	30.82	30.82
Poly fuco	7.14	4.43	14.36	1.23	17.74	48.56
Fucu vesi	0.00	3.01	8.25	0.54	10.19	58.75
Furc lumb	3.57	1.19	8.01	0.72	9.90	68.65
Cera virg	2.41	0.54	6.19	0.70	7.65	76.30
Dele sang	0.53	1.11	3.44	0.41	4.25	80.55
Poly stri	1.08	0.18	2.68	0.43	3.32	83.87
Rhod conf	0.58	0.72	2.27	0.46	2.80	86.67
Poly fibr	0.87	0.00	2.26	0.41	2.79	89.46
Agla Call	0.50	0.44	1.76	0.44	2.17	91.63

Groups FeE & GR

Average dissimilarity = 81.29

Species	Group FeE		Group GR		Contrib%	Cum.%
	Av.Abund	Av.Abund	Av.Diss	Diss/SD		
Poly fuco	7.14	1.08	20.48	1.30	25.20	25.20
Furc lumb	3.57	3.23	12.25	0.93	15.07	40.26
Cera virg	2.41	3.88	11.79	0.97	14.50	54.76
Poly stri	1.08	1.09	6.46	0.67	7.95	62.71
Sper repe	0.00	2.28	4.89	0.71	6.02	68.73
Poly fibr	0.87	0.70	4.63	0.58	5.70	74.43
Ecto Pyla	0.09	1.05	3.16	0.63	3.89	78.31
Cera tenu	0.50	0.83	3.15	0.53	3.88	82.19
Fucu serr	2.05	0.00	3.04	0.21	3.74	85.93



Cocc Phyl	0.40	0.65	2.37	0.60	2.92	88.85
Dele sang	0.53	0.45	2.07	0.49	2.54	91.39

Groups FeW & GR

Average dissimilarity = 91.98

Species	Group FeW	Group GR	Av.Diss	Diss/SD	Contrib%	Cum.%
	Av.Abund	Av.Abund				
Fucu serr	13.19	0.00	26.09	0.87	28.36	28.36
Poly fuco	4.43	1.08	14.50	0.84	15.76	44.13
Fucu vesi	3.01	0.00	9.75	0.54	10.60	54.73
Cera virg	0.54	3.88	8.68	1.04	9.44	64.16
Furc lumb	1.19	3.23	7.50	0.92	8.15	72.31
Sper repe	0.00	2.28	4.43	0.71	4.81	77.13
Poly stri	0.18	1.09	3.88	0.56	4.21	81.34
Dele sang	1.11	0.45	3.48	0.35	3.78	85.12
Ecto Pyla	0.18	1.05	2.84	0.66	3.09	88.22
Poly fibr	0.00	0.70	2.02	0.45	2.20	90.42

Groups FeE & LO

Average dissimilarity = 72.26

Species	Group FeE	Group LO	Av.Diss	Diss/SD	Contrib%	Cum.%
	Av.Abund	Av.Abund				
Furc lumb	3.57	14.47	24.64	1.42	34.10	34.10
Poly fuco	7.14	4.21	12.72	1.16	17.61	51.71
Cera virg	2.41	4.01	8.40	1.02	11.63	63.34
Cocc Phyl	0.40	2.48	4.54	0.65	6.29	69.62
Poly fibr	0.87	0.97	3.45	0.71	4.78	74.40
Cera tenu	0.50	1.26	3.07	0.77	4.25	78.65
Fucu serr	2.05	0.00	2.54	0.20	3.52	82.17
Poly stri	1.08	0.00	2.34	0.38	3.24	85.41
Dele sang	0.53	0.21	1.55	0.39	2.14	87.55
Ahnf plic	0.16	0.55	1.49	0.53	2.06	89.61
Agla Call	0.50	0.34	1.44	0.68	1.99	91.60

Groups FeW & LO

Average dissimilarity = 86.52

Species	Group FeW	Group LO	Av.Diss	Diss/SD	Contrib%	Cum.%
	Av.Abund	Av.Abund				
Furc lumb	1.19	14.47	22.97	1.41	26.55	26.55
Fucu serr	13.19	0.00	20.66	0.84	23.88	50.43
Poly fuco	4.43	4.21	10.05	0.93	11.62	62.05
Fucu vesi	3.01	0.00	6.97	0.52	8.05	70.10
Cera virg	0.54	4.01	6.76	1.20	7.81	77.91
Cocc Phyl	0.00	2.48	3.85	0.58	4.45	82.36
Dele sang	1.11	0.21	2.60	0.33	3.01	85.37
Cera tenu	0.00	1.26	2.42	0.69	2.80	88.17
Poly fibr	0.00	0.97	1.81	0.87	2.09	90.26



Groups GR & LO

Average dissimilarity = 78.42

Species	Group GR	Group LO	Av.Diss	Diss/SD	Contrib%	Cum.%
	Av.Abund	Av.Abund				
Furc lumb	3.23	14.47	26.96	1.42	34.37	34.37
Poly fuco	1.08	4.21	10.60	0.95	13.52	47.89
Cera virg	3.88	4.01	9.57	1.17	12.20	60.09
Cocc Phyl	0.65	2.48	5.26	0.70	6.70	66.79
Sper repe	2.28	0.00	4.22	0.69	5.39	72.18
Cera tenu	0.83	1.26	4.09	0.73	5.22	77.40
Poly stri	1.09	0.00	3.67	0.47	4.68	82.08
Poly fibr	0.70	0.97	3.30	0.76	4.21	86.29
Ecto Pyla	1.05	0.10	2.65	0.61	3.38	89.67
Poly sp	0.00	0.61	1.64	0.27	2.10	91.76

Groups FeE & LA

Average dissimilarity = 77.16

Species	Group FeE	Group LA	Av.Diss	Diss/SD	Contrib%	Cum.%
	Av.Abund	Av.Abund				
Fucu serr	2.05	25.06	25.04	0.83	32.45	32.45
Furc lumb	3.57	5.66	7.98	1.03	10.34	42.79
Poly fuco	7.14	5.22	7.22	1.42	9.35	52.14
Cocc Phyl	0.40	4.62	6.28	0.79	8.13	60.28
Poly fibr	0.87	2.92	4.44	1.07	5.75	66.03
Rhod conf	0.58	2.24	4.23	0.69	5.48	71.51
Cera virg	2.41	2.54	4.06	1.18	5.26	76.78
Poly elong	0.27	1.82	2.88	0.68	3.73	80.51
Dele sang	0.53	1.82	2.60	0.96	3.37	83.88
Ecto Pyla	0.09	1.90	2.06	0.76	2.67	86.54
Agla Call	0.50	1.37	1.93	0.93	2.50	89.04
Cera tenu	0.50	1.10	1.71	1.18	2.21	91.25

Groups FeW & LA

Average dissimilarity = 79.39

Species	Group FeW	Group LA	Av.Diss	Diss/SD	Contrib%	Cum.%
	Av.Abund	Av.Abund				
Fucu serr	13.19	25.06	28.58	1.17	36.00	36.00
Furc lumb	1.19	5.66	6.62	0.99	8.34	44.34
Poly fuco	4.43	5.22	6.37	1.27	8.02	52.36
Cocc Phyl	0.00	4.62	5.84	0.75	7.36	59.72
Poly fibr	0.00	2.92	4.31	1.04	5.43	65.15
Fucu vesi	3.01	0.00	4.14	0.54	5.22	70.37
Rhod conf	0.72	2.24	3.64	0.70	4.58	74.95
Dele sang	1.11	1.82	3.24	0.75	4.08	79.03
Cera virg	0.54	2.54	3.19	1.24	4.01	83.04
Poly elong	0.29	1.82	2.77	0.71	3.48	86.53
Ecto Pyla	0.18	1.90	1.98	0.77	2.50	89.02
Agla Call	0.44	1.37	1.96	0.83	2.47	91.50



Groups GR & LA

Average dissimilarity = 85.18

Species	Group GR Av.Abund	Group LA Av.Abund	Av.Diss	Diss/SD	Contrib%	Cum. %
Fucu serr	0.00	25.06	25.68	0.80	30.14	30.14
Poly fuco	1.08	5.22	7.95	1.10	9.33	39.48
Furc lumb	3.23	5.66	7.92	1.09	9.30	48.78
Cocc Phyl	0.65	4.62	6.78	0.80	7.96	56.74
Poly fibr	0.70	2.92	4.69	1.02	5.50	62.24
Cera virg	3.88	2.54	4.61	1.23	5.42	67.66
Rhod conf	0.00	2.24	4.33	0.64	5.08	72.74
Poly elong	0.00	1.82	3.18	0.65	3.73	76.47
Dele sang	0.45	1.82	2.91	0.95	3.42	79.88
Sper repe	2.28	0.11	2.79	0.74	3.28	83.16
Ecto Pyla	1.05	1.90	2.69	0.95	3.16	86.32
Cera tenu	0.83	1.10	2.36	0.90	2.77	89.09
Agla Call	0.00	1.37	1.87	0.84	2.19	91.28

Groups LO & LA

Average dissimilarity = 74.26

Species	Group LO Av.Abund	Group LA Av.Abund	Av.Diss	Diss/SD	Contrib%	Cum. %
Fucu serr	0.00	25.06	22.54	0.80	30.35	30.35
Furc lumb	14.47	5.66	13.75	1.35	18.51	48.86
Cocc Phyl	2.48	4.62	6.26	0.88	8.43	57.29
Poly fuco	4.21	5.22	5.15	1.06	6.94	64.23
Poly fibr	0.97	2.92	3.68	1.06	4.95	69.18
Cera virg	4.01	2.54	3.67	1.21	4.94	74.12
Rhod conf	0.06	2.24	3.43	0.64	4.62	78.74
Poly elong	0.01	1.82	2.55	0.66	3.44	82.17
Dele sang	0.21	1.82	2.41	0.89	3.25	85.42
Ecto Pyla	0.10	1.90	1.88	0.76	2.53	87.95
Cera tenu	1.26	1.10	1.58	0.85	2.12	90.07

5-10m

Data worksheet

Name: Data1

Data type: Biomass

Sample selection: All

Variable selection: All

Parameters

Resemblance: S17 Bray Curtis similarity

Cut off for low contributions: 90.00%

Group FeE

Average similarity: 47.90

Species	Av.Abund	Av.Sim	Sim/SD	Contrib%	Cum. %
Phyc rube	8.62	15.94	1.33	33.28	33.28
Cocc Phyl	7.75	14.68	1.52	30.65	63.93
Dele sang	5.77	9.14	1.21	19.08	83.01
Cera virg	1.89	2.37	0.65	4.95	87.96
Poly fuco	1.90	2.06	0.43	4.31	92.27



Group FeW

Average similarity: 29.38

Species	Av.Abund	Av.Sim	Sim/SD	Contrib%	Cum.%
Dele sang	5.76	9.39	0.79	31.98	31.98
Phyc rube	5.02	8.64	0.79	29.41	61.39
Poly fuco	2.60	3.81	0.52	12.95	74.34
Cocc Phyl	2.50	2.78	0.51	9.48	83.82
Clad sp	0.87	1.20	0.31	4.09	87.91
Cyst purp	1.14	1.08	0.33	3.68	91.59

Group GR

Average similarity: 43.20

Species	Av.Abund	Av.Sim	Sim/SD	Contrib%	Cum.%
Poly fuco	6.89	15.85	1.07	36.69	36.69
Cera virg	2.98	10.85	0.94	25.12	61.81
Ecto Pyla	2.62	9.42	0.76	21.81	83.63
Cocc Phyl	3.17	4.61	0.52	10.67	94.30

Group SB

Average similarity: 41.46

Species	Av.Abund	Av.Sim	Sim/SD	Contrib%	Cum.%
Cocc Phyl	6.36	13.30	1.52	32.09	32.09
Dele sang	5.07	9.36	1.12	22.58	54.68
Poly fuco	5.23	8.78	0.67	21.18	75.86
Phyc rube	2.80	3.52	0.84	8.48	84.34
Desm viri	3.19	3.13	0.45	7.55	91.89

Group LO

Average similarity: 43.40

Species	Av.Abund	Av.Sim	Sim/SD	Contrib%	Cum.%
Poly fuco	6.01	13.81	0.93	31.82	31.82
Cocc Phyl	8.77	12.56	0.84	28.94	60.75
Furc lumb	6.53	5.32	0.54	12.25	73.00
Cera virg	3.22	4.26	0.82	9.82	82.82
Poly fibr	1.60	3.13	1.00	7.21	90.03

Group LA

Average similarity: 49.91

Species	Av.Abund	Av.Sim	Sim/SD	Contrib%	Cum.%
Cocc Phyl	14.10	15.03	1.19	30.12	30.12
Dele sang	7.50	8.94	1.31	17.92	48.04
Cera virg	4.39	4.34	1.32	8.69	56.73
Poly fuco	3.25	3.65	0.62	7.31	64.04
Cyst purp	4.46	3.57	0.97	7.15	71.19
Poly fibr	2.80	3.28	0.86	6.58	77.77
Memb alat	3.74	2.77	0.94	5.55	83.32
Phyc rube	3.43	2.58	0.80	5.17	88.49
Cera tenu	1.04	1.57	1.33	3.15	91.64



Groups FeE & FeW

Average dissimilarity = 66.86

Species	Group FeE	Group FeW	Av.Diss	Diss/SD	Contrib%	Cum.%
	Av.Abund	Av.Abund				
Phyc rube	8.62	5.02	11.66	1.32	17.43	17.43
Cocc Phyl	7.75	2.50	11.05	1.56	16.53	33.96
Dele sang	5.77	5.76	10.19	1.20	15.24	49.20
Poly fuco	1.90	2.60	5.68	0.98	8.50	57.69
Desm viri	1.52	0.54	4.32	0.55	6.46	64.15
Cera virg	1.89	0.34	3.71	0.77	5.55	69.70
Cyst purp	1.50	1.14	3.43	0.85	5.13	74.84
Bryo hypn	0.00	1.27	2.80	0.41	4.19	79.03
Furc lumb	1.85	0.09	2.57	0.45	3.84	82.87
Rhod conf	1.16	0.65	2.31	0.89	3.45	86.32
Poly elong	0.11	0.87	1.90	0.48	2.84	89.16
Clad sp	0.00	0.87	1.83	0.61	2.74	91.89

Groups FeE & GR

Average dissimilarity = 73.15

Species	Group FeE	Group GR	Av.Diss	Diss/SD	Contrib%	Cum.%
	Av.Abund	Av.Abund				
Phyc rube	8.62	0.98	14.83	1.60	20.27	20.27
Poly fuco	1.90	6.89	11.44	1.27	15.63	35.91
Cocc Phyl	7.75	3.17	11.16	1.38	15.26	51.17
Dele sang	5.77	1.35	9.73	1.20	13.31	64.48
Ecto Pyla	0.19	2.62	5.76	1.12	7.87	72.35
Cera virg	1.89	2.98	5.52	1.05	7.55	79.90
Desm viri	1.52	0.33	4.52	0.52	6.18	86.08
Furc lumb	1.85	0.00	2.62	0.43	3.58	89.66
Cyst purp	1.50	0.13	2.47	0.72	3.37	93.03

Groups FeW & GR

Average dissimilarity = 81.22

Species	Group FeW	Group GR	Av.Diss	Diss/SD	Contrib%	Cum.%
	Av.Abund	Av.Abund				
Poly fuco	2.60	6.89	13.81	1.29	17.00	17.00
Dele sang	5.76	1.35	12.24	1.11	15.07	32.07
Phyc rube	5.02	0.98	10.42	1.22	12.83	44.90
Cera virg	0.34	2.98	8.17	1.17	10.06	54.97
Cocc Phyl	2.50	3.17	7.99	1.15	9.83	64.80
Ecto Pyla	0.00	2.62	7.64	1.08	9.41	74.20
Bryo hypn	1.27	0.00	3.94	0.41	4.85	79.05
Cyst purp	1.14	0.13	3.01	0.59	3.70	82.75
Clad sp	0.87	0.00	2.54	0.60	3.13	85.88
Poly elong	0.87	0.00	2.46	0.45	3.03	88.91
Poly stri	0.09	0.63	1.90	0.58	2.33	91.25

Groups FeE & SB

Average dissimilarity = 61.12

Species	Group FeE	Group SB	Av.Diss	Diss/SD	Contrib%	Cum.%
	Av.Abund	Av.Abund				



Phyc rube	8.62	2.80	11.56	1.45	18.92	18.92
Poly fuco	1.90	5.23	8.31	1.26	13.59	32.51
Cocc Phyl	7.75	6.36	8.31	1.31	13.59	46.10
Dele sang	5.77	5.07	7.86	1.14	12.86	58.96
Desm viri	1.52	3.19	6.29	0.87	10.28	69.24
Cera virg	1.89	1.05	3.33	0.84	5.45	74.70
Poly stri	0.51	1.66	3.08	0.79	5.05	79.74
Poly elong	0.11	1.25	2.99	0.39	4.89	84.63
Furc lumb	1.85	0.00	2.34	0.43	3.82	88.46
Cyst purp	1.50	0.08	2.17	0.71	3.55	92.00

Groups FeW & SB

Average dissimilarity = 71.24

Species	Group FeW	Group SB	Av.Diss	Diss/SD	Contrib%	Cum.%
	Av.Abund	Av.Abund				
Dele sang	5.76	5.07	10.66	1.24	14.97	14.97
Cocc Phyl	2.50	6.36	10.09	1.52	14.16	29.13
Poly fuco	2.60	5.23	10.07	1.28	14.14	43.27
Phyc rube	5.02	2.80	8.84	1.29	12.41	55.68
Desm viri	0.54	3.19	6.42	0.82	9.01	64.69
Poly elong	0.87	1.25	4.93	0.52	6.92	71.61
Poly stri	0.09	1.66	3.45	0.70	4.84	76.45
Bryo hypn	1.27	0.00	3.14	0.41	4.41	80.86
Cyst purp	1.14	0.08	2.49	0.59	3.50	84.36
Cera virg	0.34	1.05	2.48	0.78	3.48	87.83
Clad sp	0.87	0.00	2.04	0.61	2.87	90.70

Groups GR & SB

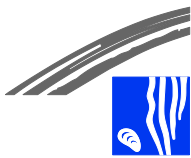
Average dissimilarity = 68.08

Species	Group GR	Group SB	Av.Diss	Diss/SD	Contrib%	Cum.%
	Av.Abund	Av.Abund				
Poly fuco	6.89	5.23	13.03	1.29	19.14	19.14
Cocc Phyl	3.17	6.36	10.54	1.41	15.49	34.63
Dele sang	1.35	5.07	9.76	1.29	14.34	48.97
Ecto Pyla	2.62	0.50	7.06	1.14	10.36	59.34
Desm viri	0.33	3.19	6.72	0.79	9.88	69.21
Cera virg	2.98	1.05	6.24	1.11	9.17	78.38
Phyc rube	0.98	2.80	5.05	1.11	7.42	85.80
Poly stri	0.63	1.66	4.18	0.87	6.14	91.94

Groups FeE & LO

Average dissimilarity = 75.79

Species	Group FeE	Group LO	Av.Diss	Diss/SD	Contrib%	Cum.%
	Av.Abund	Av.Abund				
Phyc rube	8.62	0.00	13.26	1.68	17.50	17.50
Cocc Phyl	7.75	8.77	11.82	1.44	15.60	33.10
Furc lumb	1.85	6.53	9.39	0.92	12.38	45.48
Poly fuco	1.90	6.01	9.02	1.12	11.90	57.39
Dele sang	5.77	0.06	8.72	1.28	11.51	68.90
Cera virg	1.89	3.22	4.75	1.10	6.27	75.16
Desm viri	1.52	0.27	3.47	0.54	4.58	79.75



Poly fibr	0.04	1.60	2.59	1.24	3.42	83.16
Cyst purp	1.50	0.58	2.38	0.83	3.14	86.30
Cera tenu	0.00	1.35	2.07	1.06	2.73	89.03
Poly sp	0.00	0.90	1.70	0.30	2.24	91.27

Groups FeW & LO

Average dissimilarity = 85.09

Species	Group FeW	Group LO	Av.Diss	Diss/SD	Contrib%	Cum.%
	Av.Abund	Av.Abund				
Cocc Phyl	2.50	8.77	14.24	1.26	16.73	16.73
Poly fuco	2.60	6.01	10.83	1.10	12.73	29.45
Dele sang	5.76	0.06	10.12	1.06	11.90	41.35
Furc lumb	0.09	6.53	9.97	0.85	11.71	53.07
Phyc rube	5.02	0.00	8.81	1.14	10.35	63.42
Cera virg	0.34	3.22	5.54	1.12	6.51	69.93
Poly fibr	0.66	1.60	3.80	1.07	4.46	74.39
Bryo hypn	1.27	0.00	2.96	0.41	3.48	77.87
Cyst purp	1.14	0.58	2.69	0.69	3.16	81.03
Cera tenu	0.00	1.35	2.43	1.09	2.86	83.89
Poly elong	0.87	0.30	2.29	0.56	2.69	86.58
Poly sp	0.00	0.90	2.07	0.30	2.43	89.01
Clad sp	0.87	0.00	1.93	0.61	2.26	91.28

Groups GR & LO

Average dissimilarity = 70.10

Species	Group GR	Group LO	Av.Diss	Diss/SD	Contrib%	Cum.%
	Av.Abund	Av.Abund				
Cocc Phyl	3.17	8.77	15.22	1.30	21.71	21.71
Poly fuco	6.89	6.01	12.46	1.22	17.77	39.49
Furc lumb	0.00	6.53	10.59	0.85	15.11	54.60
Cera virg	2.98	3.22	6.44	1.27	9.19	63.79
Ecto Pyla	2.62	0.35	5.94	1.11	8.47	72.27
Poly fibr	0.00	1.60	3.38	1.26	4.82	77.09
Cera tenu	0.00	1.35	2.62	1.10	3.73	80.82
Dele sang	1.35	0.06	2.57	0.59	3.67	84.49
Poly sp	0.00	0.90	2.26	0.30	3.23	87.71
Phyc rube	0.98	0.00	1.77	0.75	2.53	90.24

Groups SB & LO

Average dissimilarity = 73.44

Species	Group SB	Group LO	Av.Diss	Diss/SD	Contrib%	Cum.%
	Av.Abund	Av.Abund				
Cocc Phyl	6.36	8.77	12.65	1.48	17.23	17.23
Poly fuco	5.23	6.01	9.62	1.12	13.10	30.32
Furc lumb	0.00	6.53	9.35	0.84	12.72	43.05
Dele sang	5.07	0.06	8.46	1.33	11.52	54.56
Desm viri	3.19	0.27	5.51	0.80	7.50	62.06
Cera virg	1.05	3.22	4.89	1.18	6.65	68.72
Phyc rube	2.80	0.00	4.32	1.03	5.89	74.60
Poly elong	1.25	0.30	3.44	0.44	4.68	79.28
Poly stri	1.66	0.06	3.00	0.70	4.09	83.38
Poly fibr	0.00	1.60	2.86	1.26	3.90	87.28
Cera tenu	0.08	1.35	2.22	1.07	3.02	90.30



Groups FeE & LA
Average dissimilarity = 63.49

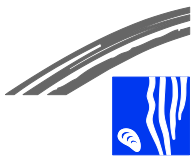
Species	Group FeE		Group LA		Diss/SD	Contrib%	Cum.%
	Av.Abund	Av.Abund	Av.Diss	Av.Diss			
Cocc Phyl	7.75	14.10	12.00	1.53	18.91	18.91	
Phyc rube	8.62	3.43	8.37	1.27	13.18	32.08	
Dele sang	5.77	7.50	6.67	1.23	10.50	42.58	
Poly fuco	1.90	3.25	4.60	0.92	7.25	49.83	
Cyst purp	1.50	4.46	4.47	1.30	7.04	56.86	
Cera virg	1.89	4.39	4.16	1.20	6.56	63.42	
Memb alat	0.65	3.74	3.83	1.16	6.04	69.46	
Poly fibr	0.04	2.80	3.74	1.02	5.89	75.35	
Furc lumb	1.85	2.39	3.71	0.77	5.84	81.19	
Desm viri	1.52	0.02	2.41	0.49	3.80	84.98	
Agla Call	0.06	1.17	1.76	0.83	2.78	87.76	
Cera tenu	0.00	1.04	1.42	1.20	2.24	90.00	
Ahnf plic	0.00	1.22	1.40	0.64	2.21	92.21	

Groups FeW & LA
Average dissimilarity = 73.82

Species	Group FeW		Group LA		Diss/SD	Contrib%	Cum.%
	Av.Abund	Av.Abund	Av.Diss	Av.Diss			
Cocc Phyl	2.50	14.10	15.84	1.58	21.46	21.46	
Dele sang	5.76	7.50	8.36	1.21	11.32	32.78	
Phyc rube	5.02	3.43	6.37	1.15	8.62	41.41	
Poly fuco	2.60	3.25	5.60	0.94	7.59	49.00	
Cera virg	0.34	4.39	5.33	1.47	7.22	56.22	
Cyst purp	1.14	4.46	5.05	1.29	6.84	63.06	
Poly fibr	0.66	2.80	4.50	1.02	6.09	69.15	
Memb alat	0.00	3.74	4.24	1.17	5.74	74.89	
Furc lumb	0.09	2.39	2.86	0.68	3.88	78.77	
Poly elong	0.87	0.92	2.18	0.82	2.95	81.72	
Bryo hypn	1.27	0.00	2.11	0.39	2.86	84.58	
Agla Call	0.00	1.17	2.10	0.80	2.85	87.43	
Cera tenu	0.00	1.04	1.66	1.15	2.24	89.68	
Ahnf plic	0.00	1.22	1.58	0.64	2.15	91.82	

Groups GR & LA
Average dissimilarity = 74.91

Species	Group GR		Group LA		Diss/SD	Contrib%	Cum.%
	Av.Abund	Av.Abund	Av.Diss	Av.Diss			
Cocc Phyl	3.17	14.10	16.32	1.57	21.78	21.78	
Dele sang	1.35	7.50	9.25	1.53	12.35	34.13	
Poly fuco	6.89	3.25	8.62	1.23	11.51	45.64	
Cyst purp	0.13	4.46	5.32	1.32	7.10	52.74	
Cera virg	2.98	4.39	4.84	1.19	6.46	59.20	
Poly fibr	0.00	2.80	4.67	1.00	6.23	65.43	
Memb alat	0.00	3.74	4.44	1.18	5.92	71.35	
Ecto Pyla	2.62	0.53	4.26	0.96	5.69	77.04	
Phyc rube	0.98	3.43	4.16	1.20	5.55	82.59	



Furc lumb	0.00	2.39	3.00	0.68	4.00	86.59
Agla Call	0.00	1.17	2.27	0.80	3.03	89.62
Cera tenu	0.00	1.04	1.78	1.13	2.37	91.99

Groups SB & LA

Average dissimilarity = 68.52

Species	Group SB Av.Abund	Group LA Av.Abund	Av.Diss	Diss/SD	Contrib%	Cum.%
Cocc Phyl	6.36	14.10	13.18	1.59	19.23	19.23
Dele sang	5.07	7.50	6.88	1.26	10.04	29.26
Poly fuco	5.23	3.25	6.64	1.25	9.69	38.95
Cyst purp	0.08	4.46	4.85	1.31	7.07	46.02
Cera virg	1.05	4.39	4.54	1.38	6.62	52.64
Phyc rube	2.80	3.43	4.29	1.25	6.26	58.90
Desm viri	3.19	0.02	4.14	0.74	6.04	64.94
Poly fibr	0.00	2.80	4.07	1.02	5.94	70.88
Memb alat	0.00	3.74	4.04	1.16	5.89	76.77
Poly elong	1.25	0.92	3.02	0.57	4.41	81.18
Furc lumb	0.00	2.39	2.71	0.67	3.95	85.13
Poly stri	1.66	0.04	2.26	0.66	3.29	88.43
Agla Call	0.00	1.17	1.94	0.82	2.82	91.25

Groups LO & LA

Average dissimilarity = 65.76

Species	Group LO Av.Abund	Group LA Av.Abund	Av.Diss	Diss/SD	Contrib%	Cum.%
Cocc Phyl	8.77	14.10	13.31	1.36	20.24	20.24
Dele sang	0.06	7.50	8.68	1.70	13.20	33.44
Furc lumb	6.53	2.39	7.61	0.93	11.57	45.01
Poly fuco	6.01	3.25	6.38	1.18	9.70	54.71
Cyst purp	0.58	4.46	4.57	1.30	6.95	61.67
Cera virg	3.22	4.39	4.54	1.30	6.90	68.56
Memb alat	0.01	3.74	3.91	1.15	5.95	74.51
Phyc rube	0.00	3.43	3.74	1.11	5.68	80.20
Poly fibr	1.60	2.80	3.05	0.99	4.63	84.83
Agla Call	0.69	1.17	1.51	0.80	2.29	87.12
Ahnf plic	0.05	1.22	1.45	0.65	2.21	89.33
Cera tenu	1.35	1.04	1.37	0.98	2.09	91.42

10-15m

Data worksheet

Name: Data1

Data type: Biomass

Sample selection: All

Variable selection: All

Parameters

Resemblance: S17 Bray Curtis similarity

Cut off for low contributions: 90.00%

Group FeE

Average similarity: 69.90

Species	Av.Abund	Av.Sim	Sim/SD	Contrib%	Cum.%
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Phyc rube	8.78	33.58	3.68	48.04	48.04
Dele sang	5.69	16.11	1.69	23.05	71.09
Cocc Phyl	4.37	15.86	3.47	22.68	93.78

Group SB

Average similarity: 67.75

Species	Av.Abund	Av.Sim	Sim/SD	Contrib%	Cum.%
Cocc Phyl	8.58	25.49	5.30	37.63	37.63
Phyc rube	7.26	20.74	4.00	30.61	68.23
Dele sang	6.08	14.38	2.57	21.22	89.45
Cyst purp	2.49	5.08	1.19	7.50	96.95

Group BE

Average similarity: 43.04

Species	Av.Abund	Av.Sim	Sim/SD	Contrib%	Cum.%
Phyc rube	5.63	16.18	1.64	37.59	37.59
Bron byss	3.88	8.30	1.50	19.28	56.86
Cocc Phyl	4.50	6.55	0.84	15.22	72.09
Desm acul	2.88	6.07	0.57	14.11	86.20
Dele sang	5.70	5.11	0.57	11.87	98.07

Group LO

Average similarity: 36.39

Species	Av.Abund	Av.Sim	Sim/SD	Contrib%	Cum.%
Poly fuco	2.05	12.82	0.87	35.23	35.23
Desm viri	1.64	8.92	0.64	24.51	59.73
Poly stri	1.19	8.13	0.80	22.34	82.07
Poly fibr	0.92	3.00	0.47	8.24	90.31

Group LA

Average similarity: 58.34

Species	Av.Abund	Av.Sim	Sim/SD	Contrib%	Cum.%
Phyc rube	11.39	25.05	2.05	42.94	42.94
Dele sang	8.39	15.50	2.14	26.56	69.50
Cocc Phyl	3.45	7.08	2.84	12.14	81.64
Bron byss	2.68	4.79	1.93	8.22	89.86
Poly fuco	1.13	1.21	0.85	2.07	91.93

Groups FeE & SB

Average dissimilarity = 40.07

Species	Group FeE		Group SB		Contrib%	Cum.%
	Av.Abund	Av.Sim	Av.Abund	Av.Sim		
Cocc Phyl	4.37	8.58	8.50	1.83	21.20	21.20
Dele sang	5.69	6.08	7.19	1.30	17.94	39.15
Phyc rube	8.78	7.26	5.73	1.26	14.30	53.45
Cyst purp	0.13	2.49	4.73	1.47	11.82	65.26
Poly stri	0.00	1.43	3.17	0.72	7.91	73.18
Bron byss	1.71	0.13	3.15	1.24	7.86	81.04
Sacc lati	1.57	0.00	2.94	0.45	7.34	88.38
Poly fuco	0.37	0.41	1.37	0.62	3.42	91.80



Groups FeE & BE

Average dissimilarity = 52.17

Species	Group FeE Av.Abund	Group BE Av.Abund	Av.Diss	Diss/SD	Contrib%	Cum.%
Dele sang	5.69	5.70	12.05	1.62	23.11	23.11
Phyc rube	8.78	5.63	8.77	1.32	16.80	39.91
Cocc Phyl	4.37	4.50	7.22	1.43	13.85	53.75
Desm acul	0.06	2.88	7.19	0.86	13.78	67.54
Sacc lati	1.57	2.55	5.57	0.58	10.67	78.21
Bron byss	1.71	3.88	5.43	1.65	10.40	88.61
Poly fuco	0.37	1.31	2.38	0.76	4.57	93.18

Groups SB & BE

Average dissimilarity = 57.31

Species	Group SB Av.Abund	Group BE Av.Abund	Av.Diss	Diss/SD	Contrib%	Cum.%
Dele sang	6.08	5.70	11.01	1.62	19.21	19.21
Cocc Phyl	8.58	4.50	10.55	1.28	18.40	37.61
Desm acul	0.00	2.88	6.34	0.88	11.07	48.68
Bron byss	0.13	3.88	6.31	2.11	11.01	59.68
Phyc rube	7.26	5.63	6.18	1.30	10.78	70.46
Cyst purp	2.49	0.54	4.50	1.34	7.85	78.32
Poly stri	1.43	0.00	3.10	0.68	5.41	83.72
Sacc lati	0.00	2.55	2.66	0.37	4.64	88.36
Poly fuco	0.41	1.31	2.25	0.81	3.93	92.29

Groups FeE & LO

Average dissimilarity = 93.32

Species	Group FeE Av.Abund	Group LO Av.Abund	Av.Diss	Diss/SD	Contrib%	Cum.%
Phyc rube	8.78	0.00	30.00	3.83	32.15	32.15
Dele sang	5.69	0.27	17.59	1.96	18.84	51.00
Cocc Phyl	4.37	0.52	13.48	2.52	14.45	65.44
Poly fuco	0.37	2.05	6.62	1.15	7.10	72.54
Desm viri	0.13	1.64	5.48	0.98	5.87	78.41
Bron byss	1.71	0.01	5.31	1.25	5.69	84.10
Sacc lati	1.57	0.00	4.77	0.44	5.12	89.22
Poly stri	0.00	1.19	4.04	1.07	4.33	93.55

Groups SB & LO

Average dissimilarity = 89.98

Species	Group SB Av.Abund	Group LO Av.Abund	Av.Diss	Diss/SD	Contrib%	Cum.%
Cocc Phyl	8.58	0.52	22.90	4.14	25.45	25.45
Phyc rube	7.26	0.00	20.51	4.11	22.79	48.24
Dele sang	6.08	0.27	16.03	2.09	17.81	66.05
Cyst purp	2.49	0.00	7.06	1.57	7.84	73.90
Poly fuco	0.41	2.05	5.53	1.18	6.14	80.04
Poly stri	1.43	1.19	5.30	1.07	5.89	85.93
Desm viri	0.35	1.64	4.57	1.02	5.08	91.01



Groups BE & LO

Average dissimilarity = 94.84

Species	Group BE	Group LO	Av.Diss	Diss/SD	Contrib%	Cum.%
	Av.Abund	Av.Abund				
Phyc rube	5.63	0.00	18.55	1.98	19.56	19.56
Dele sang	5.70	0.27	12.42	1.04	13.09	32.66
Desm acul	2.88	0.01	12.24	0.81	12.90	45.56
Cocc Phyl	4.50	0.52	11.23	1.36	11.84	57.40
Bron byss	3.88	0.01	10.68	2.19	11.26	68.67
Poly fuco	1.31	2.05	7.20	1.09	7.59	76.25
Desm viri	0.13	1.64	5.48	0.87	5.78	82.03
Poly stri	0.00	1.19	4.10	0.95	4.32	86.35
Sacc lati	2.55	0.00	3.39	0.37	3.57	89.92
Poly fibr	0.00	0.92	2.92	0.69	3.08	93.00

Groups FeE & LA

Average dissimilarity = 41.77

Species	Group FeE	Group LA	Av.Diss	Diss/SD	Contrib%	Cum.%
	Av.Abund	Av.Abund				
Phyc rube	8.78	11.39	8.70	1.66	20.82	20.82
Dele sang	5.69	8.39	8.56	1.40	20.49	41.31
Sacc lati	1.57	1.66	5.01	0.59	11.99	53.30
Cocc Phyl	4.37	3.45	3.47	1.36	8.31	61.61
Bron byss	1.71	2.68	3.35	1.33	8.01	69.62
Poly fuco	0.37	1.13	2.15	0.93	5.14	74.76
Poly fibr	0.00	1.06	1.77	0.52	4.23	78.99
Cyst purp	0.13	0.94	1.56	0.87	3.72	82.72
Poly elong	0.00	0.81	1.47	0.94	3.51	86.22
Cera virg	0.00	0.83	1.33	1.05	3.19	89.41
Memb alat	0.00	0.79	1.27	0.87	3.05	92.46

Groups SB & LA

Average dissimilarity = 48.72

Species	Group SB	Group LA	Av.Diss	Diss/SD	Contrib%	Cum.%
	Av.Abund	Av.Abund				
Phyc rube	7.26	11.39	9.18	1.60	18.83	18.83
Cocc Phyl	8.58	3.45	8.58	1.88	17.60	36.44
Dele sang	6.08	8.39	7.63	1.38	15.67	52.10
Bron byss	0.13	2.68	4.01	1.63	8.23	60.34
Cyst purp	2.49	0.94	3.44	1.32	7.05	67.39
Sacc lati	0.00	1.66	2.79	0.39	5.73	73.12
Poly stri	1.43	0.64	2.75	0.93	5.65	78.77
Poly fuco	0.41	1.13	1.94	0.93	3.99	82.75
Poly elong	0.36	0.81	1.69	0.93	3.47	86.22
Poly fibr	0.00	1.06	1.63	0.52	3.34	89.56
Cera virg	0.38	0.83	1.30	1.22	2.67	92.23

Groups BE & LA

Average dissimilarity = 57.27

Group BE Group LA



Species	Av.Abund	Av.Abund	Av.Diss	Diss/SD	Contrib%	Cum.%
Phyc rube	5.63	11.39	11.64	1.47	20.32	20.32
Dele sang	5.70	8.39	11.58	1.48	20.22	40.53
Cocc Phyl	4.50	3.45	5.71	1.63	9.98	50.51
Desm acul	2.88	0.25	5.38	0.90	9.40	59.91
Sacc lati	2.55	1.66	5.06	0.54	8.84	68.75
Bron byss	3.88	2.68	4.05	1.61	7.07	75.82
Poly fuco	1.31	1.13	2.73	1.06	4.76	80.58
Cyst purp	0.54	0.94	1.97	0.80	3.44	84.02
Poly fibr	0.00	1.06	1.72	0.51	2.99	87.02
Poly elong	0.28	0.81	1.58	0.97	2.76	89.78
Cera virg	0.00	0.83	1.29	1.00	2.26	92.03

Groups LO & LA

Average dissimilarity = 90.12

Species	Group LO Av.Abund	Group LA Av.Abund	Av.Diss	Diss/SD	Contrib%	Cum.%
Phyc rube	0.00	11.39	27.87	2.50	30.93	30.93
Dele sang	0.27	8.39	18.34	2.21	20.35	51.28
Cocc Phyl	0.52	3.45	7.22	2.12	8.01	59.29
Bron byss	0.01	2.68	6.26	1.81	6.95	66.24
Poly fuco	2.05	1.13	4.67	1.19	5.18	71.42
Sacc lati	0.00	1.66	4.33	0.41	4.80	76.22
Desm viri	1.64	0.00	3.99	0.93	4.43	80.65
Poly fibr	0.92	1.06	3.53	0.83	3.91	84.57
Poly stri	1.19	0.64	3.01	1.15	3.34	87.91
Poly elong	0.21	0.81	2.11	1.00	2.35	90.26

15-20m

Data worksheet

Name: Data1

Data type: Biomass

Sample selection: All

Variable selection: All

Parameters

Resemblance: S17 Bray Curtis similarity

Cut off for low contributions: 90.00%

Group FeE

Average similarity: 54.03

Species	Av.Abund	Av.Sim	Sim/SD	Contrib%	Cum.%
Phyc rube	6.00	44.66	2.21	82.65	82.65
Cocc Phyl	1.26	5.46	0.77	10.10	92.75

Group BE

Average similarity: 61.63

Species	Av.Abund	Av.Sim	Sim/SD	Contrib%	Cum.%
Phyc rube	5.88	50.14	3.48	81.35	81.35
Dele sang	2.82	10.02	0.76	16.26	97.62



Groups FeE & BE

Average dissimilarity = 42.46

Species	Group FeE	Group BE	Av.Diss	Diss/SD	Contrib%	Cum.%
	Av.Abund	Av.Abund				
Dele sang	1.43	2.82	12.61	1.23	29.69	29.69
Phyc rube	6.00	5.88	12.46	1.32	29.35	59.04
Sacc lati	1.54	0.42	7.47	0.45	17.58	76.62
Cocc Phyl	1.26	1.07	7.44	1.21	17.52	94.14

**Flowering plants (angiosperms)
0-6m**

Data worksheet

Name: Data1

Data type: Biomass

Sample selection: All

Variable selection: All

Parameters

Resemblance: S17 Bray Curtis similarity

Cut off for low contributions: 90.00%

Group GR

Average similarity: 80.57

Species	Av.Abund	Av.Sim	Sim/SD	Contrib%	Cum.%
<i>Zostera (Zostera) marina</i>	11.05	79.82	6.28	99.06	99.06

Group OB

Average similarity: 42.94

Species	Av.Abund	Av.Sim	Sim/SD	Contrib%	Cum.%
<i>Zostera (Zostera) marina</i>	8.73	34.53	1.08	80.42	80.42
<i>Potamogeton pectinatus</i>	1.44	6.81	0.49	15.85	96.27

Group RO

Average similarity: 31.04

Species	Av.Abund	Av.Sim	Sim/SD	Contrib%	Cum.%
<i>Zostera (Zostera) marina</i>	5.50	18.49	0.79	59.57	59.57
<i>Pylaiella/Ectocarpus</i>	2.74	5.59	0.65	18.01	77.59
<i>Ceramium virgatum</i>	1.05	1.94	0.53	6.25	83.84
<i>Zannichellia palustris</i>	1.47	1.70	0.35	5.48	89.32
<i>Tolypella nidifica</i>	0.71	1.09	0.29	3.52	92.85

Groups GR & OB

Average dissimilarity = 46.21

Species	Group GR	Group OB	Av.Diss	Diss/SD	Contrib%	Cum.%
	Av.Abund	Av.Abund				
<i>Zostera (Zostera) marina</i>	11.05	8.73	30.76	1.14	66.57	66.57
<i>Potamogeton pectinatus</i>	0.00	1.44	6.88	0.96	14.90	81.47
<i>Chara aspera</i>	0.00	0.43	1.66	0.42	3.59	85.06



Ceramium virgatum	0.09	0.33	1.41	0.77	3.05	88.11
Pylaiella/Ectocarpus	0.16	0.11	1.34	0.48	2.91	91.03

Groups GR & RO

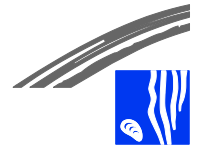
Average dissimilarity = 61.24

Species	Group GR Av.Abund	Group RO Av.Abund	Av.Diss	Diss/SD	Contrib%	Cum.%
Zostera (Zostera) marina	11.05	5.50	27.45	1.48	44.82	44.82
Pylaiella/Ectocarpus	0.16	2.74	8.80	0.93	14.37	59.20
Zannichellia palustris	0.00	1.47	4.65	0.62	7.60	66.80
Potamogeton pectinatus	0.00	1.15	3.60	0.44	5.87	72.67
Ceramium virgatum	0.09	1.05	3.58	0.82	5.85	78.52
Chaetomorpha linum	0.06	1.00	3.09	0.49	5.04	83.56
Tolypella nidifica	0.00	0.71	2.79	0.55	4.55	88.11
Zostera noltii	0.00	0.58	2.22	0.30	3.63	91.74

Groups OB & RO

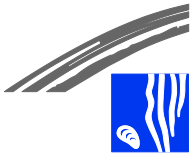
Average dissimilarity = 70.49

Species	Group OB Av.Abund	Group RO Av.Abund	Av.Diss	Diss/SD	Contrib%	Cum.%
Zostera (Zostera) marina	8.73	5.50	27.38	1.31	38.84	38.84
Pylaiella/Ectocarpus	0.11	2.74	9.30	0.92	13.20	52.04
Potamogeton pectinatus	1.44	1.15	8.00	0.88	11.36	63.39
Zannichellia palustris	0.14	1.47	5.18	0.66	7.35	70.74
Ceramium virgatum	0.33	1.05	3.83	0.85	5.43	76.18
Chaetomorpha linum	0.05	1.00	3.11	0.47	4.41	80.59
Tolypella nidifica	0.01	0.71	3.00	0.51	4.26	84.85
Zostera noltii	0.05	0.58	2.44	0.31	3.46	88.31
Chara baltica	0.00	0.77	2.05	0.36	2.91	91.22



A P P E N D I X 7

Depth dependent changes in species number, cover and biomass



Depth dependent changes in species number, cover and biomass are illustrated as box-whisker plots. The boxes represent the medium range of 50 % of the data points, also named as 25–75 % percentile.. The location of the average = arithmetic medium is illustrated with a point, the location of the median by a vertical line within the box. The more uneven the data are distributed, the more dislocated is the median line from the centre of the box. The whiskers on both sides of the box are representing the values outside the medium 50 % data range. In the following graphs the whiskers represent the minima and maxima values.

Diversity – Hard bottom vegetation (macroalgae)

The mean number per station was 11.7 species in 2009 und 13.5 species in 2010. Species number per station varied between 5 und 23 species in 2009 and between 5 und 21 species in 2010. Changes in species numbers with depth showed a bell-shaped distribution pattern (Figure App. 7-1). In both years mean species number is increasing down to the 5–10 m depth interval and shows clearly decreasing species numbers below 15 m. In 2010 the mean species number is higher compared to 2009 down to 10 m depth. Below 10 m species number are comparable in both years. In general shallow depth intervals as well as depths below 15 m have the lowest mean species number. In shallow water several stressors (wave exposure, high radiation and temperature, exsiccation), allow only few species a (temporarily limited) growth. In greater depths growth is only possible for a few species adopted to low light conditions.

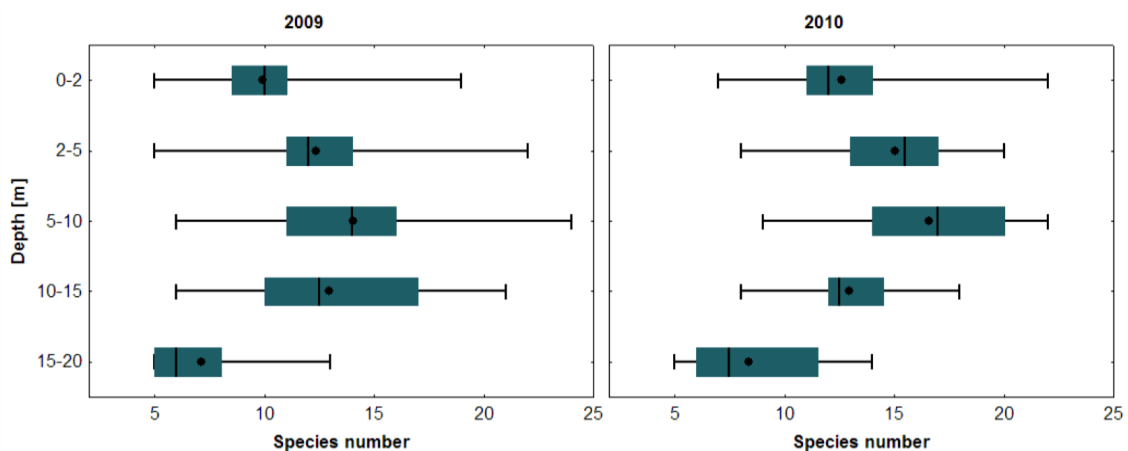


Figure App. 7.1 Variations in species number of hard bottom vegetation with depth.

Diversity – Soft bottom vegetation (higher plants and charophytes)

Soft bottom vegetation shows naturally lower species numbers compared to hard bottom vegetation. If only rooted plants like angiosperms or charophytes are taken into account *Zostera marina* is the only occurring species at most of the sites. The calculation of several diversity parameters or the creating of graphs have been set aside due to the low species numbers. The mean species number per station is 3.1 species. Species number varied between 1 und 7 species per station. *Zostera marina* occurs at nearly all soft bottom stations and inhabit clearly rank 1 in the species-ranking. *Ruppia cirrhosa* and *Potamogeton pectinatus* follow at rank 2 und 3. The charophyte *Lamprothamnium papulosum* is the most rare soft bottom species and occurs only at two sites. Species richest community is the tasselweed/dwarf eelgrass community with 4.6 species on average. The eelgrass community and the eelgrass/algae community consist usually only of one rooted



plant: *Zostera marina*. Species numbers show therefore a clear reduction with depth, as the tasselweed/dwarf eelgrass community is restricted to very shallow waters (max. 1.5 m depth).

Within all three soft bottom communities also macroalgae can occur, which grow epiphytic or drifting around the rooted plants in the tasselweed/dwarf eelgrass and eelgrass community. The species number of these epiphytic/drifting algae is low (4.2 species on average). For the eelgrass/algae community additionally also epilithic growing algae occur. Therefore the mean species number with 10.2 species is high compared to the other two soft bottom communities.

Cover – Soft bottom vegetation (higher plants and charophytes)

Mean soft bottom vegetation cover was 59.0 % and ranged from 0 to 100% per site. As soft bottom is not as scattered distributed like hard bottom, the total mean cover is higher compared to hard bottom vegetation (31 %). Cover changes with depth (Figure App. 7.1) showed highest mean total cover in shallow depths (depth interval 0–1 m and 1–2 m) and decreasing numbers in deeper areas. In the 4–6 m depth interval only 20 % (on average) of the bottom is covered by vegetation. Different to hard bottom vegetation the coverage is highest in shallow waters. The wave energy in the surf zone is lowered due to the more sheltered location of soft bottom stations and is further reduced by the soft bottom vegetation itself, which serve as a kind of biological breakwater. Due to the high light intensity in shallow waters high coverage degrees are therefore possible.

The mean substrate specific total cover was 66.9 %. Substrate specific cover was high down to 4 m depth (at least 69 % cover). Lower cover in depth > 4 m is due to the lower light availability. Higher plants and charophytes have higher light requirements compared to macroalgae and therefore the effect of light limitation is recognisable in much shallower areas compared to hard bottom vegetation. The differences between total cover and substrate specific cover are lower in all depth intervals compared to hard bottom vegetation as soft bottom is less scattered distributed and the dominant kind of substrate within the investigation area.

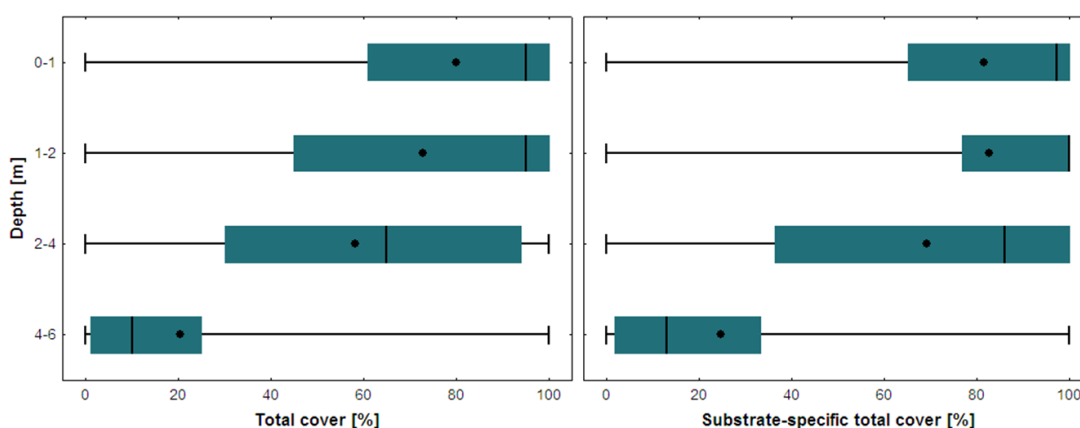


Figure App. 7.1 Variations of total cover (left) and substrate-specific cover (right) of soft bottom vegetation with depth.

Biomass – Hard bottom vegetation (macroalgae)

Mean total biomass was 308.3 g DW (dry weight) m⁻² in 2009 und 346.9 g DW m⁻² in 2010 and varied between 1.4 g DW m⁻² and 4426.9 g DW m⁻² per station.



Biomass variations with depth (Figure App. 7.2) showed highest biomass values within the 2–5 m depth interval in both years. This is the characteristic vertical distribution range of the large fucoid species, which produce high amounts of biomass per individual plant. Below this depth interval biomass is steadily decreasing with lowest amounts in the 15–20 m depth interval. Biomass variability is highest in the shallow zone (0–5 m) either due to unstable conditions but also due to the occurrence of communities with high variable biomass of characteristic species (large solid fucoids versus small fine filamentous algae). Biomass variability is decreasing with depth and lowest in the 15–20 m depth range.

Mean cover-corrected biomass was 131.0 g DW m⁻² in 2009 and 208.6 g DW m⁻² in 2010 and varied between 0.1 g DW m⁻² and 2200.1 g DW m⁻² per station. Biomass variations with depth are in both years comparable to changes in total biomass (Figure App. 7.2). Values for cover-corrected biomass are lower than total biomass values.

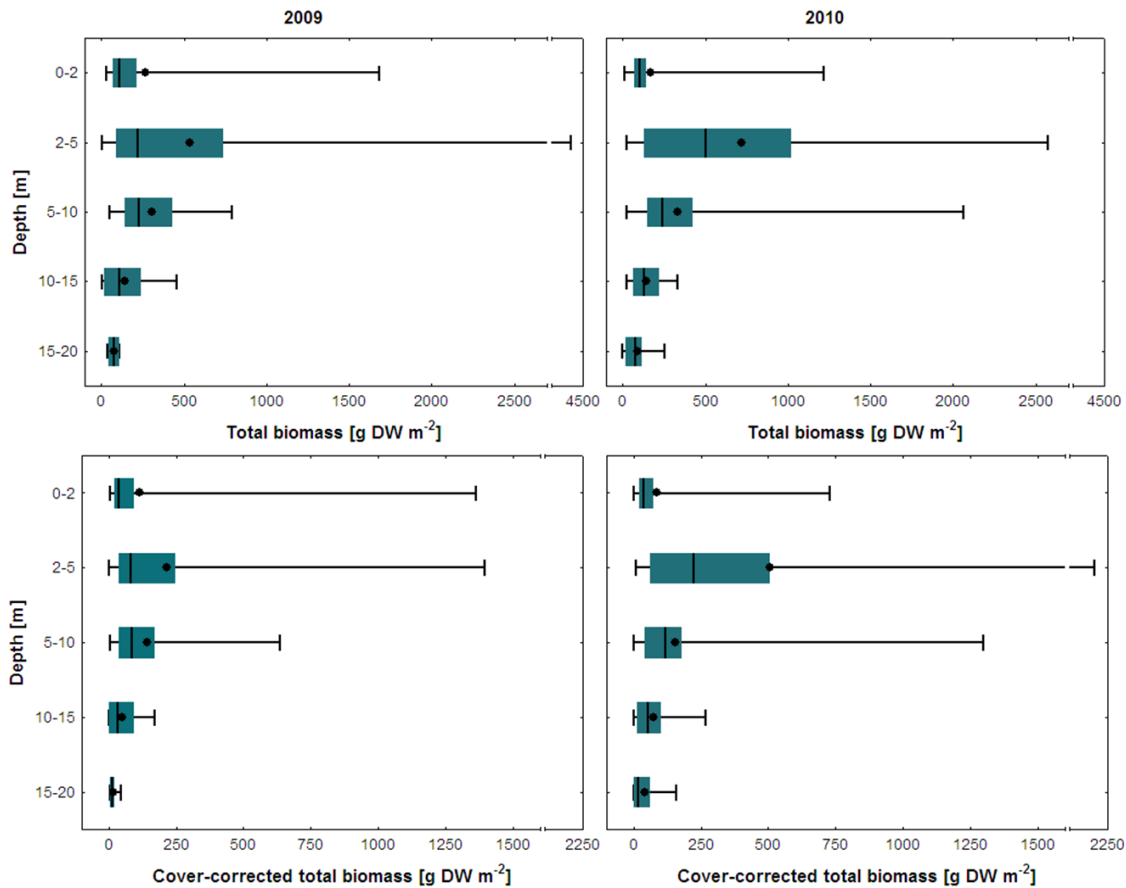
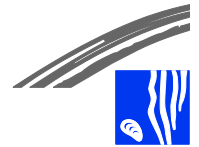


Figure App. 7.2 Variations of total biomass (above) and cover-corrected biomass (below) of hard bottom vegetation with depth.

Biomass – Soft bottom vegetation (higher plants and charophytes)

Mean total biomass was 104.4 g DW (dry weight) m⁻² and varied between 2.8 g DW m⁻² and 407.1 g DW m⁻² per station. Biomass variations with depth (Figure App. 7.3) showed highest biomass values within the 1–2 m depth interval. Within the more shallow areas small, narrow leaf species are dominant, which are not able to build up a high biomass despite high coverage degrees. In the 1–2 m



depth also *Zostera marina* occurs and produces higher biomasses compared to those smaller species. With increasing depth light is limited resulting in lower cover and biomass.

Mean cover-corrected biomass was 82.7 g DW m⁻² and varied between 0.8 g DW m⁻² and 366.4 g DW m⁻² per station. Depth dependent variations in cover-corrected biomass are again comparable to the patterns of total biomass (Figure App. 7.3). In general total and cover-corrected biomass is lower compared to hard bottom vegetation. Mean total biomass of the tasselweed/dwarf eelgrass community is 85 g DW m⁻² and 100.1 g DW m⁻² in the eelgrass community.

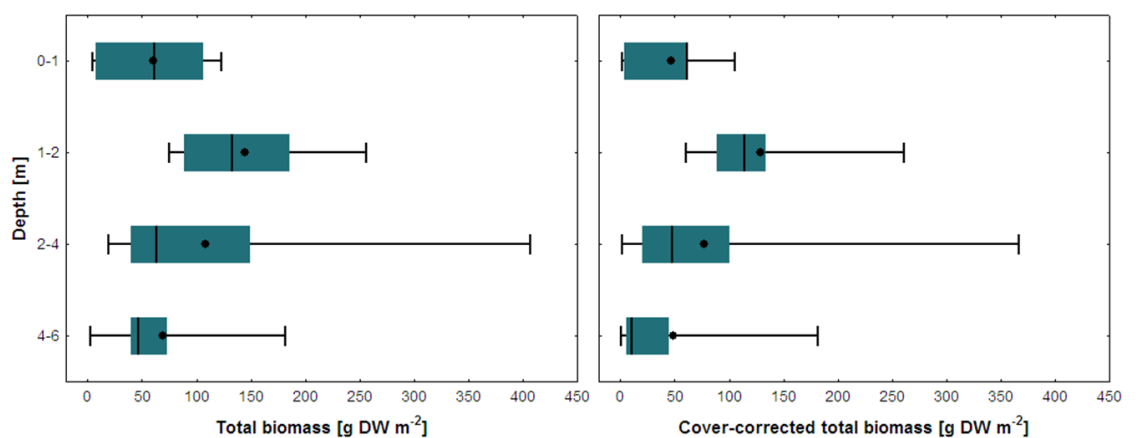
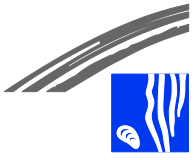


Figure App. 7.3 Variations of total biomass (left) and cover-corrected biomass (right) of soft bottom vegetation with depth.



A P P E N D I X 8

Maps of cover and cover-corrected biomass



Cover distribution of key communities

Macroalgae were widely distributed in the shallow waters along the south coast of Lolland as well as along the eastern and the western coast of Fehmarn. Furthermore, the Natura 2000 sites of Langeland, Sagasbank, Fehmarn and Großenbrode include areas with dense algae cover. The distribution in terms of diver estimated coverage estimates are shown in Figure App. 8.1.

In the alignment area and further along the coast of Lolland macroalgae were growing to a maximum depth of 10–14 m. In this area the depth distribution was limited by the availability of hard substrate. The availability of suitable hard substrate decreased significantly deeper than 8 m, resulting in an average cover of hard substrate (boulders, cobbles and pebbles) of < 10% in the depth interval between 10 and 15 m at these transects.

South of Rødsand an area with small stones and mussels provides substrate for a very sparse cover of macroalgae. Two areas with hard substrate in shallow water are known in this area: Gedser Reef and Schönheiders Pulle. Only few spots of vegetation could be seen on the video recording from Gedser Reef, no further sampling was therefore carried out here. At Schönheiders Pulle the percentages of suitable substrate ranged between 0 and 25%, and the vegetation (only filamentous species) covered on average 10% of the substrate (3.2–6.3 m depth).

Around the alignment area at Fehmarn a small, but dense vegetated area occurs just west to Puttgarden harbour. Further west only small, scattered areas of vegetation are distributed.

East of the alignment, along the east coast of Fehmarn macroalgae are distributed to a depth of about 20 m. Within this area plenty of hard substrate is available (average of all depths at all transects = 60%).

North-west of the Natura 2000 area Eastern Kiel Bight benthic vegetation was sparsely distributed to a depth of 8–11 m. Along the west coast of Fehmarn macroalgae were found to a depth of 14–17 m. Suitable substrate was very scattered in this area. Average percentage cover of hard substrate was 35 % (ranged between 0 and 90 %).

In the Natura 2000 area Fehmarnbelt hard bottom areas with bottom vegetation cover > 10% were found to a maximum depth of about 18–19 m. However, single plants occurred to depths of 32 m. Where hard substrate was available below 19 m, it was more or less completely covered by hydrozoans and sponges. The average cover of hard substrate at the sampling sites was 27%.

In the Natura 2000 area Langeland the reef area had an average cover of 33% hard substrate (range 10–80%). Macroalgae cover > 10% was found to a depth of 10 to 17 m, but the maximum depth with vegetation was 26 m in the southern part of the reef.

In the Natura 2000 area Sagasbank hard bottom areas with > 10% cover were found to a maximum depth of about 10–16 m, depending on the respective transect. The area had an average cover of 31 % hard substrate (range 5–90 %).



In the Natura 2000 area Großenbrode macroalgae cover > 10% was found to a depth of 6.5 to 10 m. The area had an average cover of 49% hard substrate (range 5–100%).

In the Natura 2000 area Staberhuk hard bottom areas with vegetation cover > 10 % were found to a maximum depth between 8 and 19 m, depending on the respective transect. The area had an average cover of 57% hard substrate (range 0–100%).

The Natura 2000 area Eastern Kiel Bight had an average cover of 39% hard substrate (range 0-100%). Macroalgae cover > 10 % was found to a depth of 8-19 m, depending on the respective transect.

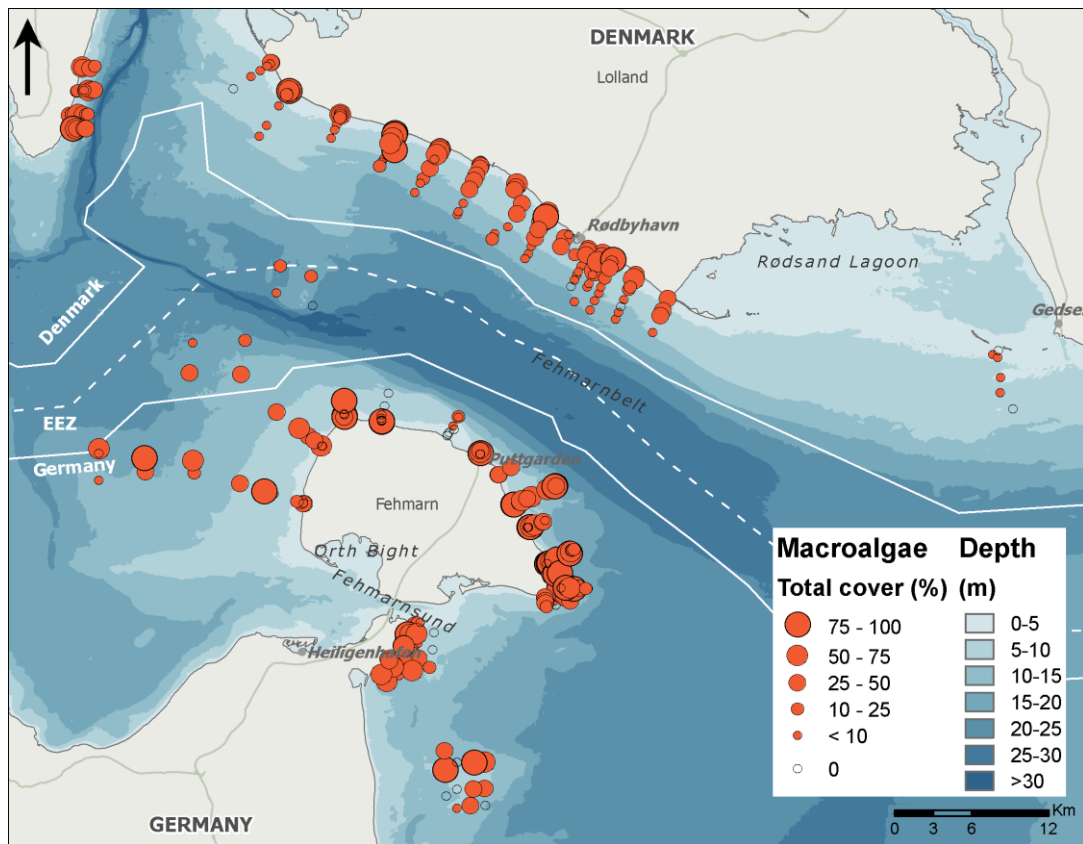


Figure App.8.1 Diver estimated total cover of macroalgae at 370 macroalgae sites along transects in the summer of 2009.

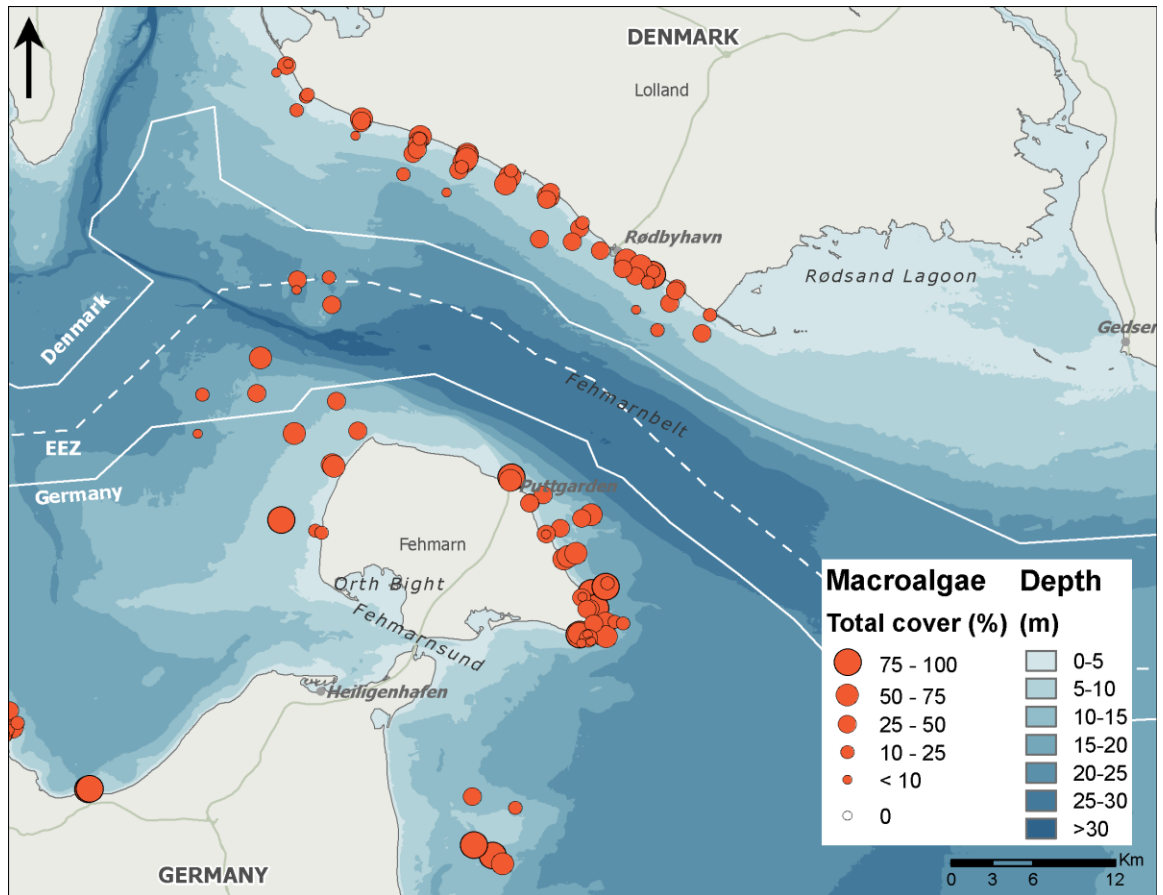


Figure App.8.2. Diver estimated total cover of macroalgae at 135 macroalgae sites along transects in the summer of 2010.

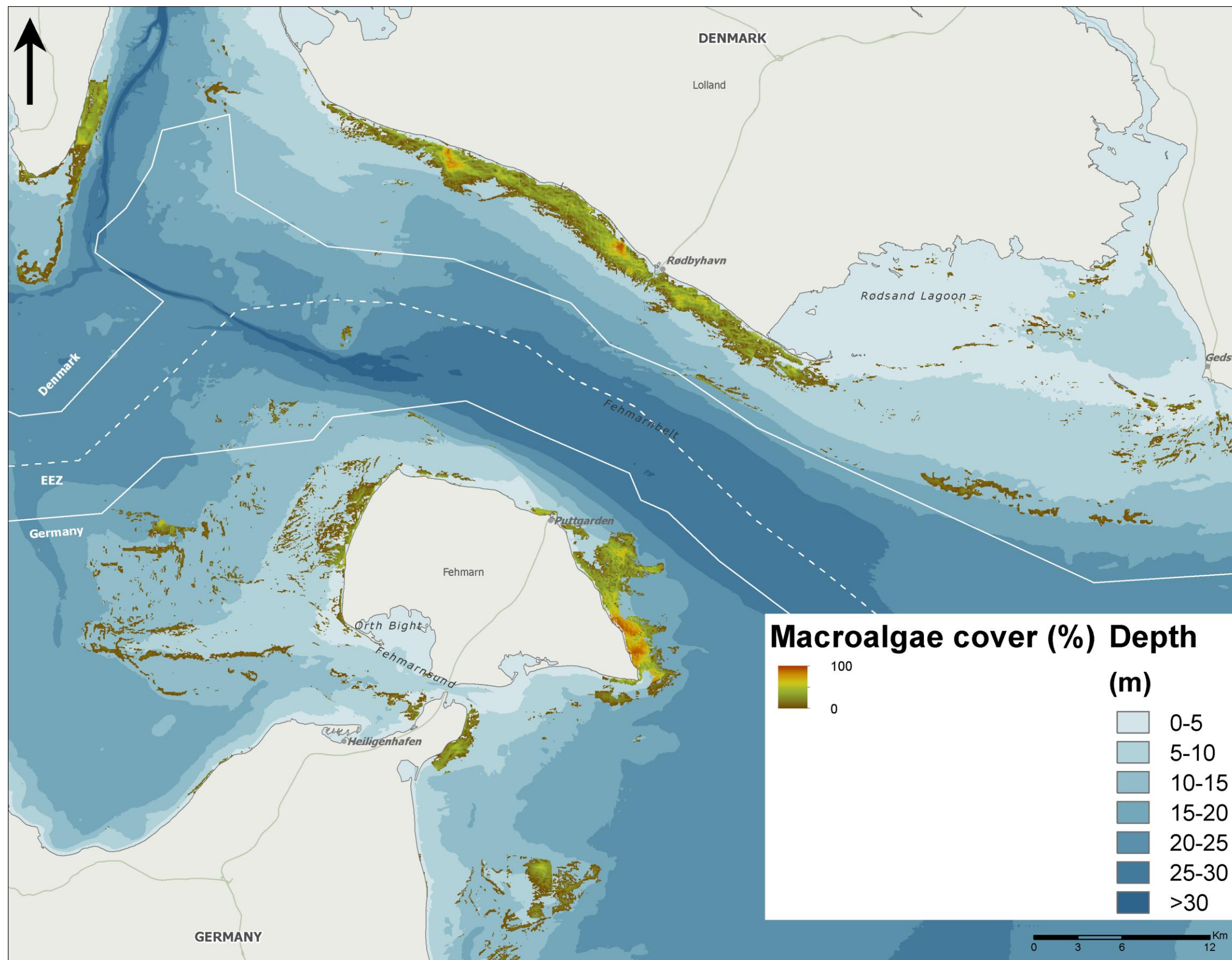


Figure App 8.3 Predicted distribution and cover of macroalgae within the investigation area in the summer of 2009. Prediction prepared using the GAM model.

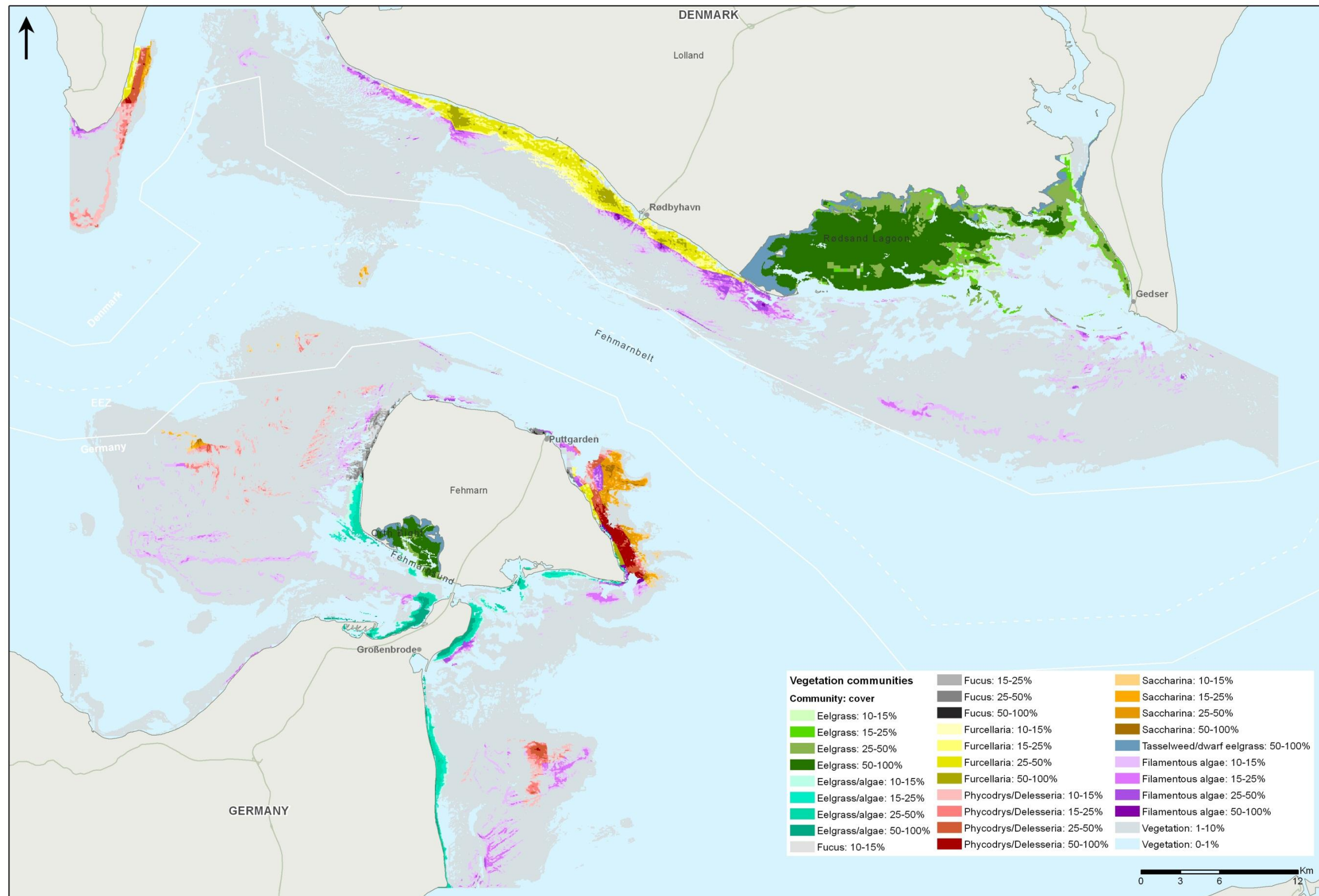


Figure App. 8.4 Distribution and coverage of the different vegetation communities within the investigation area. Based on predicted mapping of macroalgae and eelgrass and the distribution of key-communities in the area.

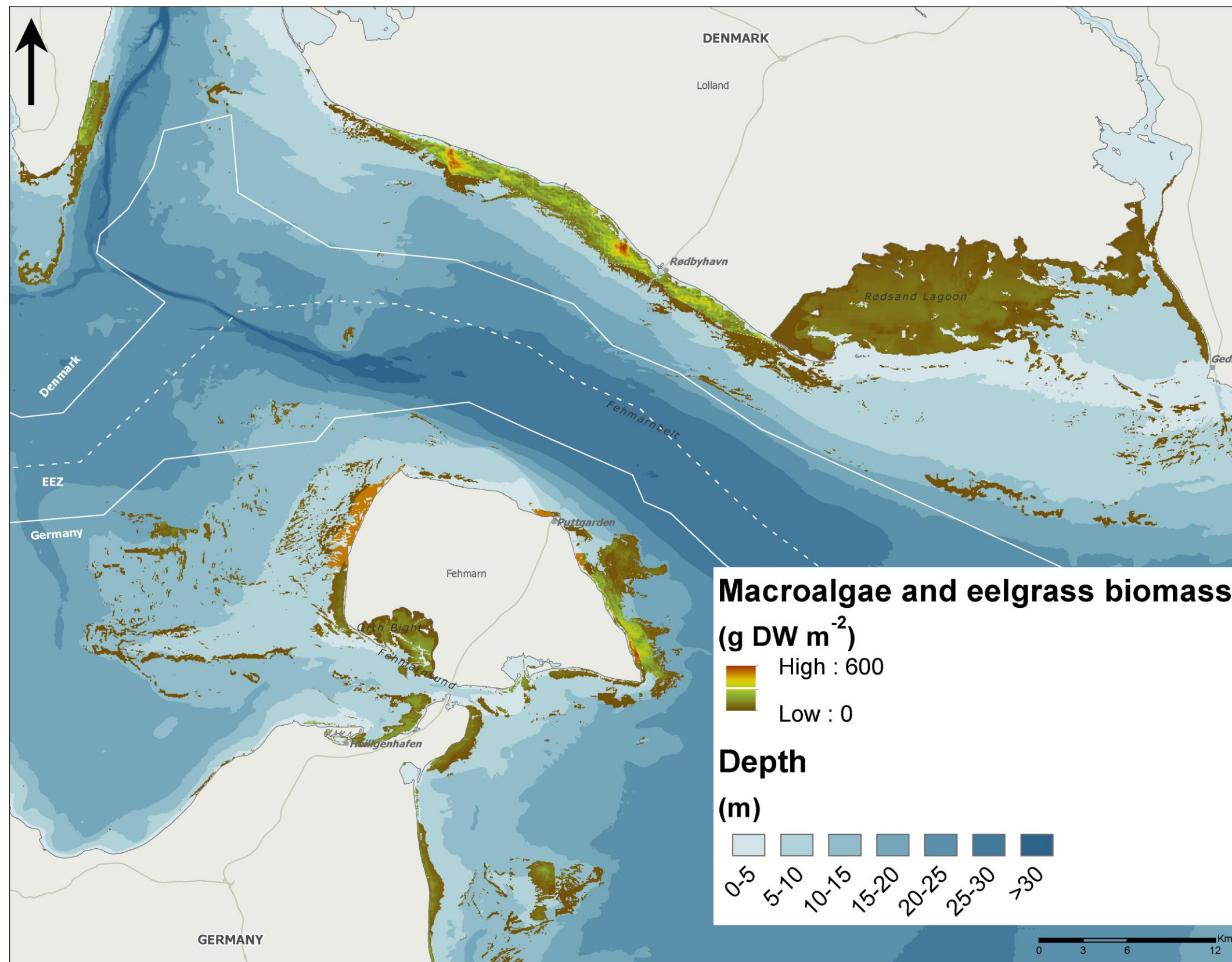


Figure App. 8.5 Cover-corrected biomass (g DW m⁻²) of macroalgae and eelgrass in Fehmarnbelt area in the summer of 2009. Based on the data of predicted cover (Figure and converted to cover-corrected biomass using the relationships from Table 4.13 (2009 data) and Figure 5.11



A P P E N D I X 9

Mapping of hard substrate



Availability of hard substrate is a key factor for predicting and mapping the abundance and distribution of macroalgae.

A map of hard substrate was constructed that summarized our knowledge of existence of hard substrate based on several data sources of varying origin and scale. The procedure was as follows:

1. Background values, where no other information is available.
 - a. The FEMA substrate map was used as background in the Fehmarnbelt area. Data on hard substrate from video analysis were used to give an average value of hard substrate in each of the substrate categories. The percentage cover we obtained from the videos will however be too high because we have deliberately sampled in areas where we expected hard substrate for macroalgae sampling. However, in Rødsand and Orth Bight the focus of the investigation was not hard substrate and the observed % of hard substrate therefore lower (68 %) than the value obtained for all areas with sand. We used the 68 % as a factor to reduce the average % hard substrate in all substrate categories where video data was used.

Table App. 9 - 1

Sediment	% cover of hard substrate used in map of hard substrate
<i>Bedrock crystalline</i>	<i>100</i>
<i>Residual deposits on prequaternary sediments</i>	<i>80</i>
<i>Residual deposits on till</i>	<i>16.8</i>
<i>Sand, partly gravel/stones</i>	<i>14.7</i>
<i>Sandy mud</i>	<i>4.6</i>
<i>Residual deposits on quaternary clay/peat</i>	<i>2.3</i>
<i>Mud</i>	<i>1.2</i>

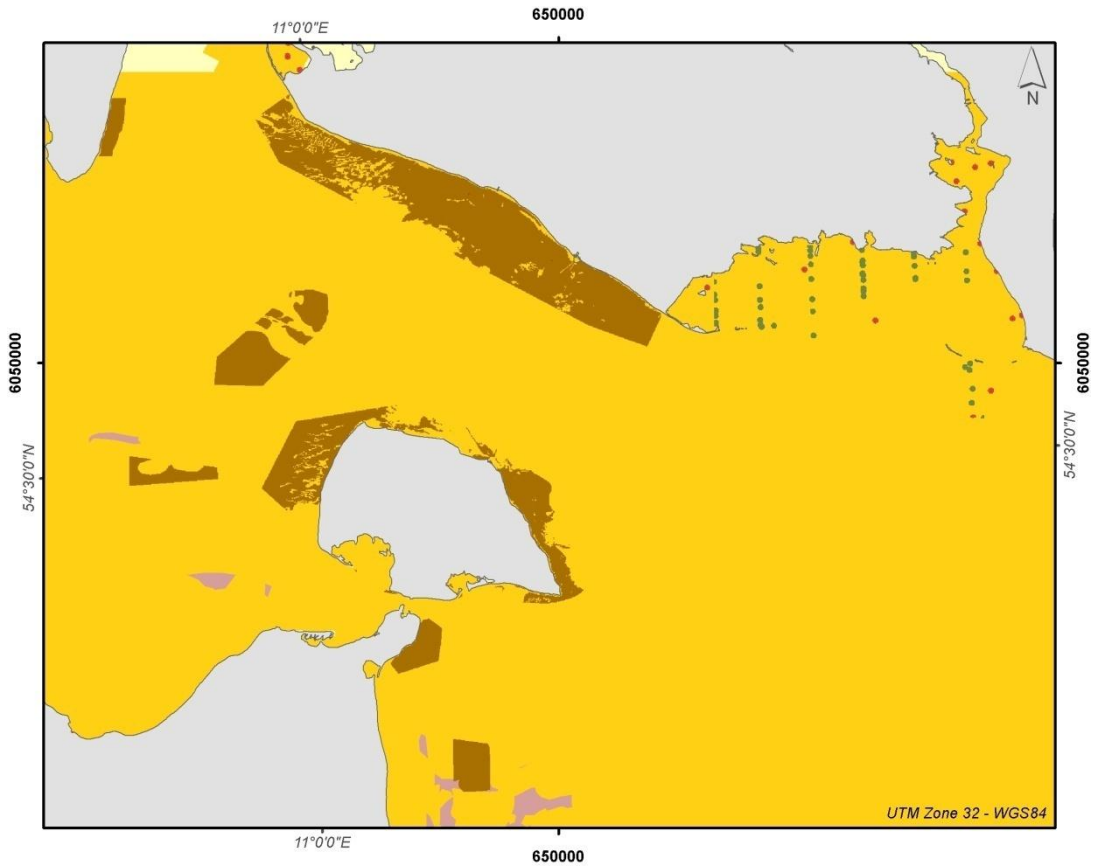
- b. Outside the area of the FEMA substrate map the GEUS map of the seabed was used. Data on hard substrate from video analysis were used to give an average value of hard substrate in each of the substrate categories. The same procedure as described in a) was used here. No data was available for % cover of hard substrate on thin sandy sediment and it was estimated to be ½ of the sandy mud value.



Table App. 9 - 2

Sediment	% cover of hard substrate used in map of hard substrate
<i>Mixed sediment/Boulders</i>	28.7
<i>Coarse sediment/Boulders</i>	18.2
<i>Sand</i>	12.6
<i>Muddy sand</i>	5.4
<i>Sandy mud</i>	4.6
<i>Thin sand</i>	2.3

2. Additional knowledge of hard substrate area:
 - a. The FEMA substrate map show large areas defined as coarse sediment/boulders. These are areas where hard sediment is potentially occurring. In areas where we have FEMA divers' estimates of hard substrata these data were interpolated on the coarse sediment/boulders (in Großenbode also on sand). This was done by Nearest Neighbour Interpolation on the point data from the divers within the boundaries of the convex hull and the relevant classes in the FEMA substrate map. The datapoints in Rødsand were interpolated by the Inverse Distance Weight (IDW) method with a maximum search radius of 250 m.
 - b. On top of the two maps (but not in the area of the aerial photo) the areas of gravel, stones, residual deposits, and/or crystalline rock from Reimers' map were added. Source: (Reimers 2010): Sea Bottom Sediment Map of the Western Baltic, State Agency for Agriculture, Environment and Rural Areas Schleswig-Holstein; based on (Hermansen & Jensen 2000): Digital Sea Bottom Sediment Map around Denmark and data of the Federal Maritime and Hydrographic Agency, Germany (BSH) and the Christian-Albrechts-University of Kiel; compiled by (A. Sekinger 2002).
 - c. The habitat mapping group provided a shape file with reefs in the Natura 2000 area 'Fehmarnbelt'. Within these areas the diver estimated coverages were interpolated by applying the Nearest Neighbor method as described above.
3. From the Danish National Environmental Research Institute (NERI) all data on hard substrate (estimated in connection with vegetation sampling) from the monitoring programme was obtained as points. This information was applied by interpolating the points with a maximum search radius of 250 m with IDW.



FEMA hard substrate map - datasources

- FEMA diver estimates interpolated (NN)
- FEMA diver estimates interpolated (IDW)
- NERI monitoring points interpolated
- FEMA substrate map
- Reimers Sea Bottom Sediment Map
- GEUS Seabed Map

0 5 10 20 Km

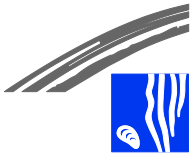


Figure App. 9-1 The datasources of the hard substrate map. NN = Natural Neighbor, IDW = Inverse distance weight



A P P E N D I X 1 0

Statistics for predictive mapping of macroalgae and eelgrass cover



Macroalgae

Predictive modelling of distribution and cover of macroalgae was done using the statistical analysis Generalised Additive Models (GAMs). The models were fitted with a binomial error distribution, which is suitable as the values are restricted between 0 and 1 (Zuur et al. 2009). The models were fitted using the "mgcv" R package (Wood 2006).

Total cover of macroalgae, obtained by divers' estimates in 2009 were used as dependent variable. Data on physical and chemical factors - potentially important for the distribution and abundance of macroalgae - were obtained from FEHY models and FEMA mapping of hard substrate.

The predictor variables that together significantly explained most of the variability in the data set, were used in the final model. The final predictor variables used were: hard substrate, depth, shear stress, current speed and slope (Table App. 10 - 1 and Figure App. 10 - 1). For significance an approximate F-test was used: the higher the f-value the stronger the correlation between predictor and test variable.

Spatial autocorrelation was found in model residuals when tested using Moran's I over 10 lags by defining the nearest neighbourhood as the 4 nearest samples (= one lag). Significant autocorrelation was found in the first two lags (Moran's I 0.12 and 0.07). The Morans's I values are relatively low (possible range -1 to 1) and not expected to have a significant impact on our results.

*Table App. 10 - 1 F-values and significance for the environmental predictor variables used in the final predictive model of macroalgae cover. *** = $p < 0.001$, ** = $p < 0.01$*

Predictor variabel	F value	P-value
Hard substrate	84.9	***
Depth	26.3	***
Shear stress	18.0	***
Current speed	18.5	***
Secchi depth	6.0	**
Slope	25.0	***

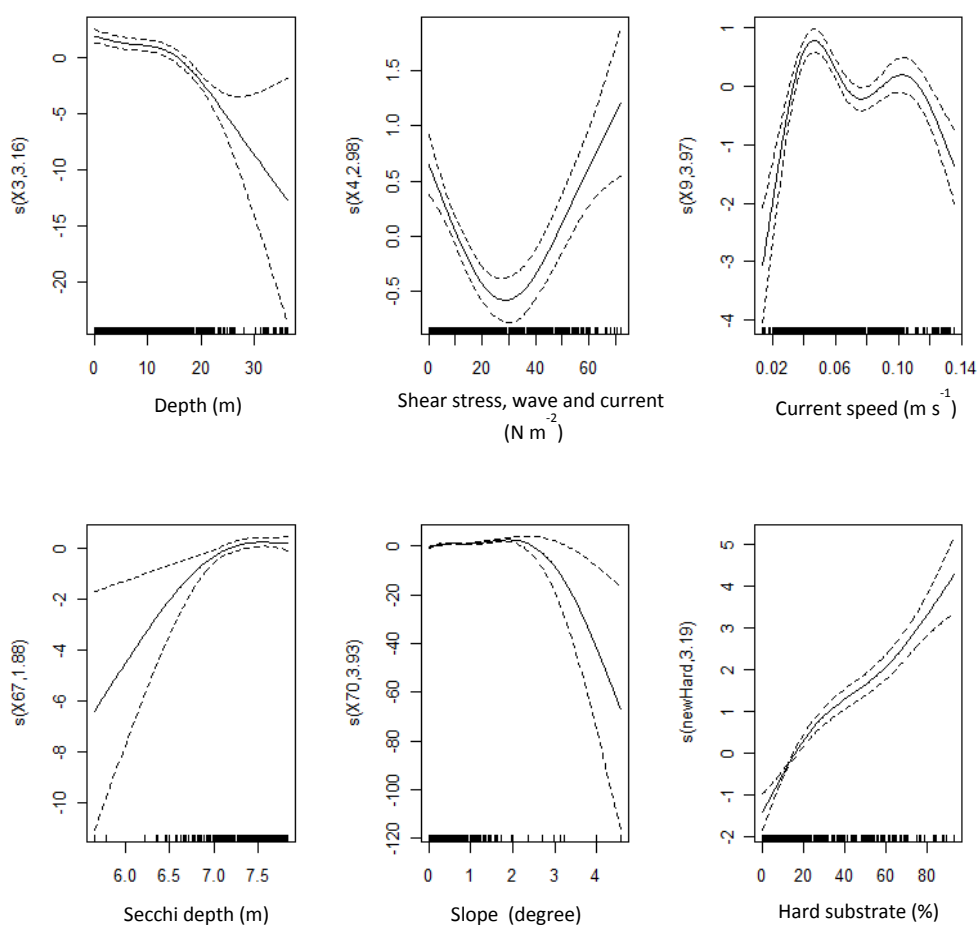


Figure App. 10 - 1 Graphs showing the response of macroalgal cover to variations in the environmental response variables. Partial GAM plots for the macroalgae model. The values of the environmental variables are shown on the X-axis and the probability on the Y-axis in logit scale. The degree of smoothing is indicated in the legend of the Y-axis. The dotted lines indicates the 95 % confidence bands.

The GAM model explained 54.7% of the variability in macroalgae cover (deviance explained). The agreement between predicted and observed values (the fit of the model) was assessed using Pearson's correlation; a correlation coefficient of 0.71 was obtained. Plotting the observed against the predictive values also assessed the agreement.

There was a good agreement between observed and predicted data. The agreement was assessed using Pearson's correlation, Spearman rank correlation and linear regressions. Using 2/3 of the data for modelling and 1/3 of the data for validation a good agreement between observed and predicted values were found using all three analysis (Pearson's correlation = 0.69, Spearman rank correlation = 0.54). A 'perfect model' would result in a linear regression with a slope near 1 and an intercept near 0.0. The relationship between observed and predicted data from Fehmarnbelt was highly significant and had a slope of 0.89 and an intercept of 0.0055 ($R^2 = 0.45$).

There was a relatively good relationship (Pearson's correlation = 0.37, Spearman rank correlation = 0.42) between total cover observed in 2010 and predicted cover,



suggesting that the pattern of macroalgal cover is consistent between years although the actual values show some year to year variability.

Figure App. 10-2 show observed and predicted values. Observed cover of macroalgae are shown as circles, the larger the circle the higher the observed cover. The model predicted cover of macroalgae is shown as color, the darker the color the higher the predicted cover. Thus large circles with dark color or small circles with light color show good agreement. The areas where the model has most difficulties in the predicting macroalgae cover was in areas with mixed substrate, where eelgrass and macroalgae occur together. These are for example areas south-west and south-east of Fehmarn.

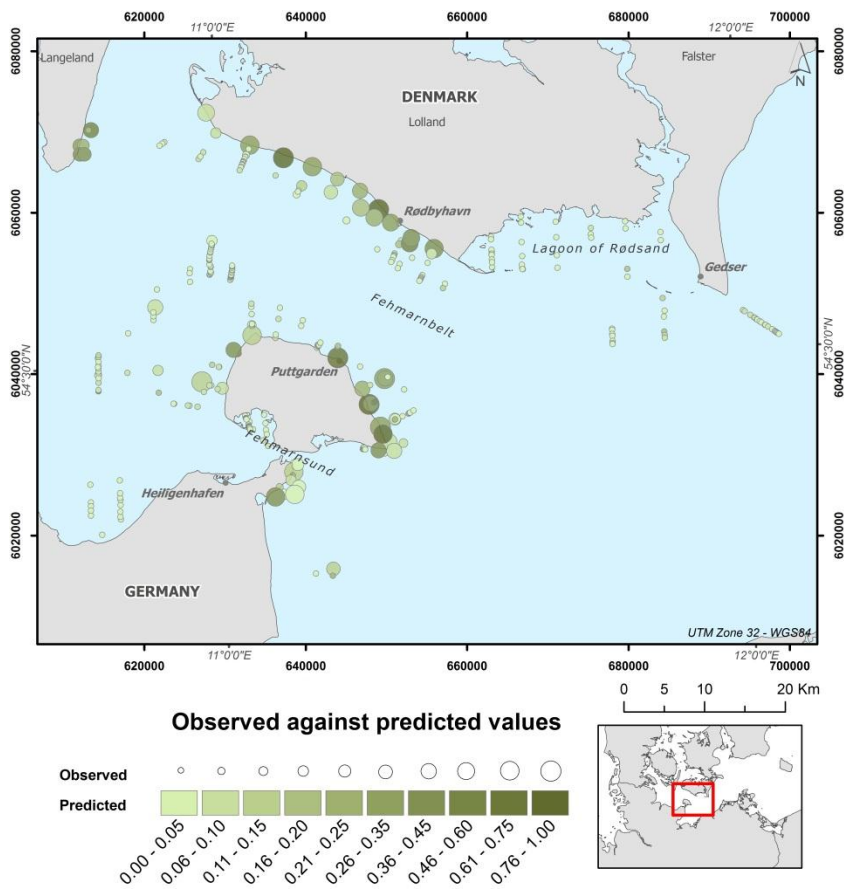


Figure App. 10-2 Observed cover of macroalgae (circles, the larger the circle the higher the observed cover) against predicted cover of macroalgae (the darker the color the higher the predicted cover).



Eelgrass (Zostera marina)

Predictive modelling of distribution and cover of eelgrass was done using Generalised Additive Models (GAMs). The models were fitted with a binomial error distribution, which is suitable as the values are restricted between 0 and 1 (Zuur et al. 2009). The models were fitted using the “mgcv” R package (Wood 2006).

Cover of *Zostera marina* obtained by video transects and divers’ estimates in 2009 (all FEMA video transects) were used as dependent variable. Data on physical and chemical factors potentially important for the distribution and abundance of *Zostera* were obtained from FEHY models.

The predictor variables that significantly explained most of the variability in the data set were used in the model. The final predictor variables used were: depth, shear stress, current speed and slope (Table App 10-2 and Figure App. 10-3). To account for some of the spatial variation that could not be explained by the environmental variables (especially within the Rødsand Lagoon), variables x and y (longitude and latitude) were included, and both were significant.

Table App.10-2 F-values and significance for the environmental predictor variables used in the final predictive model of eelgrass cover. *** = $p < 0.001$

Predictor variable	F value	P-value
Depth	177.7	***
Shear stress	12.1	***
Current speed	29.6	***
Slope	20.0	***
Longitude	12.5	***
Latitude	44.1	***

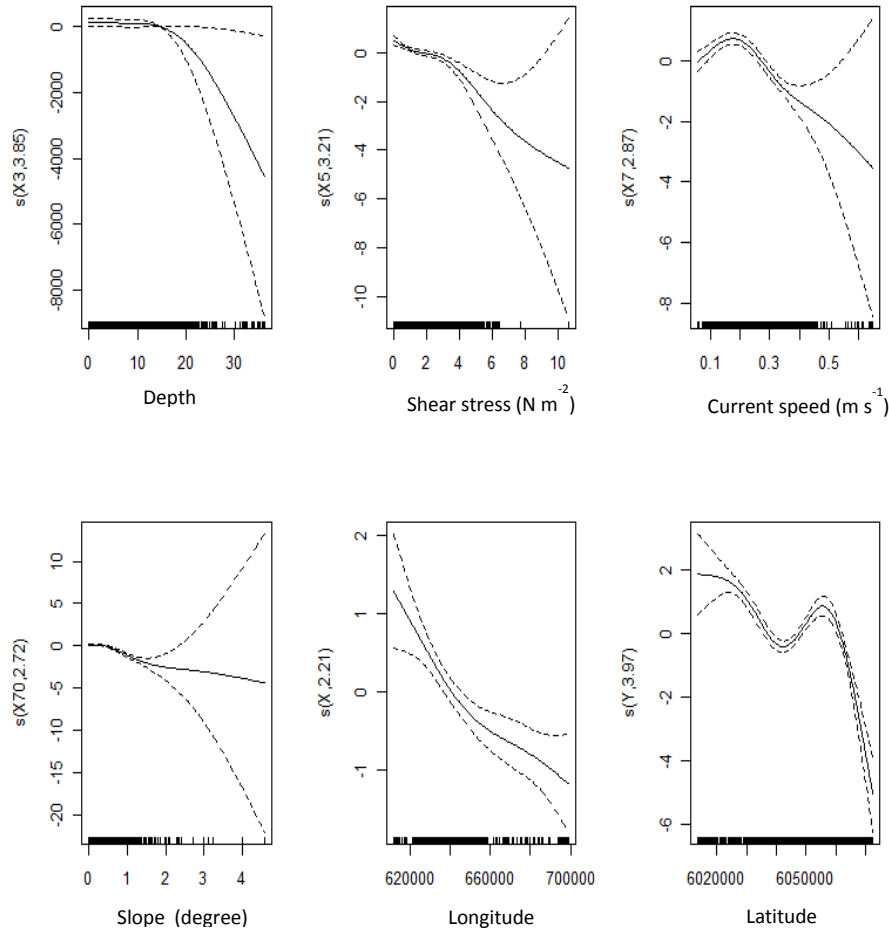


Figure App. 10- 3 Partial GAM plots for the eelgrass model. The values of the environmental variables are shown on the X-axis and the probability on the Y-axis in logit scale. The degree of smoothing is indicated in the legend of the Y-axis. The dotted lines indicate the 95 % confidence bands.

The GAM model explained 63.1% of the variability in eelgrass cover (deviance explained). There was no spatial auto-correlation in the model residuals.

However, the model under-estimated the coverage. To increase predicted cover a scaling factor of two was included in the model. Thereby we obtained higher agreement between observed and predicted values.

There was high agreement between observed and predicted cover values using 30% of the data for validation and 60% of the data for modelling (Pearson's correlation = 0.66, Spearman rank correlation = 0.66). The linear regression was highly significant with a slope of 0.99 and an intercept of 0.003 ($R^2 = 0.44$).



A P P E N D I X 1 1

Identification and evaluation of proposed reference areas



As outlined in chapter 2.1 the identification and evaluation of reference areas is not part of the baseline report itself but is necessary to ensure a contemporary transition to a possible future monitoring programme, which demands comparable baseline data between reference areas and the proposed impact area.

Reference areas must be comparable in terms of abiotic conditions (e. g. salinity, substrate) and the occurring biological communities to the proposed impact area. To ensure comparable abiotic conditions reference areas should be located as near to the impact area as possible, but clearly outside of the proposed impact zone.

Regarding the variety of vegetation communities evaluated during the baseline investigation, reference areas should inhabit the following plant communities:

- Macroalgae: *Fucus*-community, *Furcellaria*-community, *Phycodrys/Delesseria*-community, *Saccharina*-community
- Angiosperms: Tasselweed/dwarf-eelgrass community, eelgrass-community

The filamentous algae community has a minor importance and is not a stable community in terms of spatial distribution, species composition and biomass. Therefore reference areas will not be defined for this community. The mixed eelgrass/algae-community occurs only in areas far in the south of Fehmarn and north of Großenbrode, which are located so far away from the proposed alignment, that impacts have been excluded. Therefore no reference area for this community is necessary.

Ideally one reference area should be defined and evaluated inhabiting all of the above described communities in sufficient spatial resolution and coverage. But due to the various substrate and depth specifications of the communities this was not possible and reference areas had to be splitted according to sediment and depth specifications. Some of the above mentioned communities inhabit a comparable broad depth scale. For example the *Phycodrys/Delesseria*-community can be found in depths between 5 and 20 m. Species composition, coverage and especially biomass values differ significantly between these depth intervals although the characteristic key-species of the community are consistent. Each proposed reference area must therefore take into account the depth level.

For most of the communities it was possible to find comparable areas in the vicinity of the proposed Fehmarnbelt link – areas already part of the investigation area of the baseline surveys. But especially for the *Saccharina*-community and the deep occurrences of the *Phycodrys/Delesseria*-community it was necessary to evaluate areas further away of the investigation area. Table App. 11-1 gives an overview of the proposed reference areas and Table App. 11-2 shows the extent of the investigations per area.

Table App.11-1 Proposed reference areas and their representative vegetation communities and surveyed depth intervals.

Community	Außenschlei	Hohwacht Bight	Orth Bight	Sagasbank
<i>Fucus</i>		2–5 m		
<i>Furcellaria</i>		5–10 m		
<i>Phycodrys/Delesseria</i>	15–20 m	5–10 m		10–15 m
<i>Saccharina</i>	15–20 m			
Tasselweed/dwarf eel.			0.25–2 m	
Eelgrass			2–6 m	



Orth Bight is a proposed reference area for tasselweed/dwarf eelgrass and eelgrass. But as all relevant data analyses are already part of the baseline report (see chapter 5) it is not specifically listed and analysed within this appendix.

Table App. 11-2 Overview of vegetation sampling in reference areas.

Activity	Video transects	Site cover estimates (25 m ²)	Frame cover estimates (0.25 m ²)	Frame biomass sampling (0.0625 m ²)
	2010	2010	2010	2010
Außenschlei	3	9	6x5=30	6x5=30
Hohwacht Bight	3	20	12x5=60	12x5=60
Sagasbank	2	6	6x5=30	6x5=30
Variables measured	Cover of macroalgae, mussel, stone and sand	Cover of sub- strate, total veg- etation and key species	Species composi- tion, cover	Species composi- tion, biomass

Außenschlei

The area Außenschlei lies in the Western Kiel Bight, approximately 72 km west from the proposed Fehmarnbelt link. Beside Fehmarnbelt and the east coast of Fehmarn it is the only other marine region within the Western Baltic providing hard substrates in depths over 15 m. Although it is located so far away from the proposed link it represents the only possibility for a reference of deep occurring vegetation and the analysis of the depth limit of vegetation within a comparable salinity range.

Different survey methods have been conducted all according to the methods already described in the FEMA benthic vegetation baseline report. Three video transects have been tracked in order to get information about the spatial distribution of vegetation, including the depth limit of phytobenthos. The depths of the recorded videos lay between 14 and 20 m at all transects. Nine coverage estimations (25 m²) have been made by divers. 30 coverage estimations in 0.25 m²-frames and 30 biomass samples out of ¼ (0.0625 m²) of these frames have also been taken (Figure App. 11-2).

The *Phycodrys/Delesseria*-community as well as the *Saccharina*-community did occur in this area (Figure App. 11-3). Overall 18 species could be identified (Table App. 11-3). The overall depth limit of vegetation could be determined at 18.0 to 18.5 m. The mean species number was 10.3, the mean Total cover value 31.7 and the mean biomass 78 g m⁻².

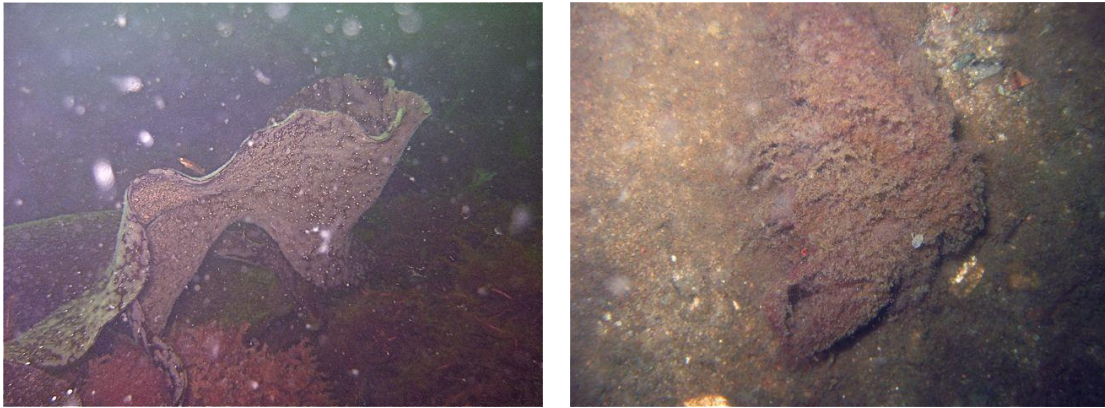
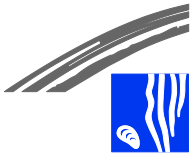


Figure App.11-1: *Saccharina latissima* is regularly occurring at Außenschlei (left side). Between 18 and 18.5 m depth the vegetation is getting scarce and the lower depth limit is reached (right side).

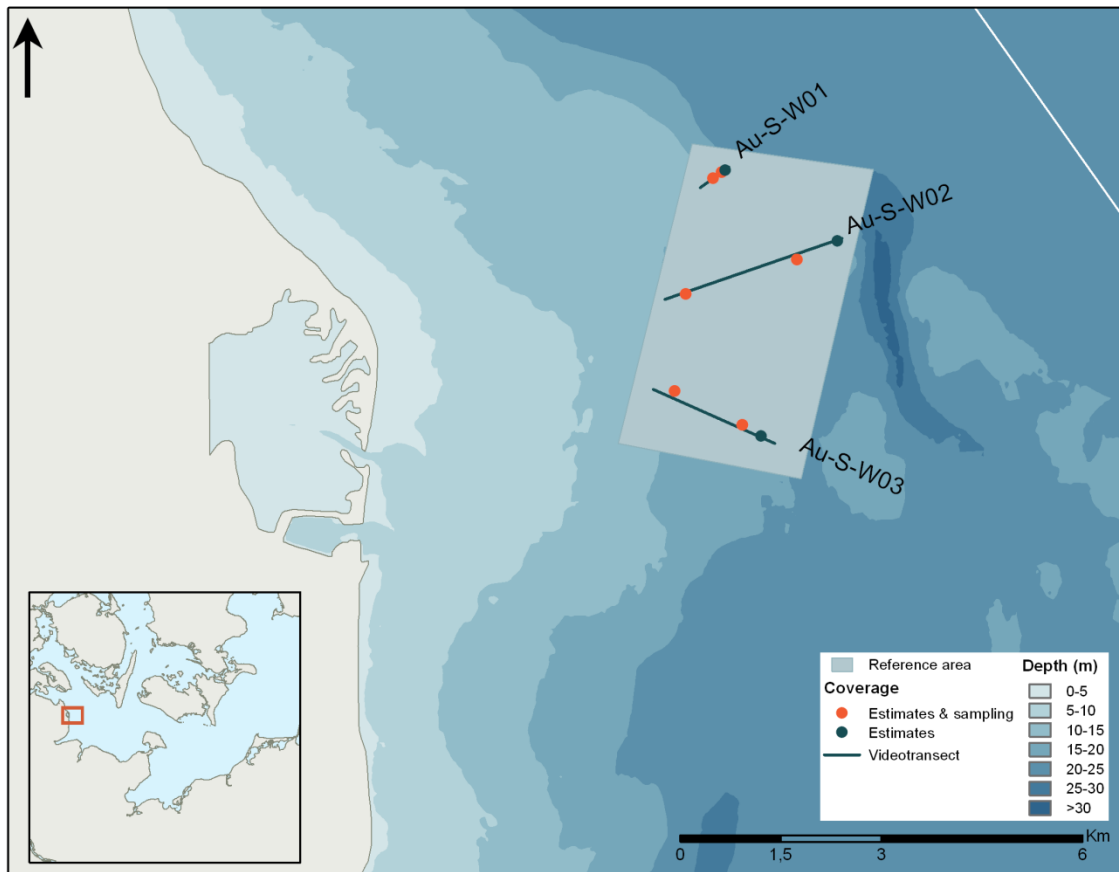


Figure App.11-2 Video transects, coverage estimates and biomass sample sites in the reference area 'Außenschlei' in the summer of 2010.

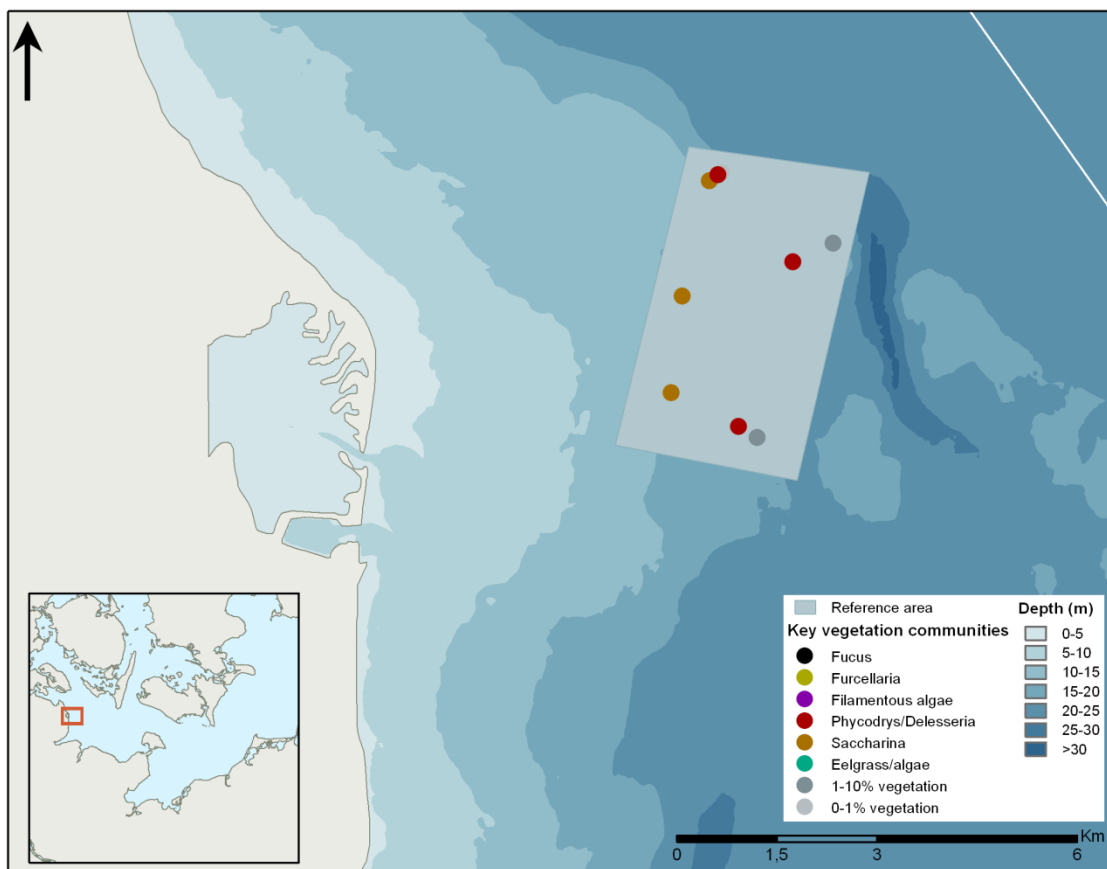


Figure App.11-3 Macroalgae communities in the reference area Außenschlei.



Table App.11-3 Species list from Außenschlei. K = key species, AP = accompanying species.

Spermatophytes	Charophytes	Chlorophytes	Phaeophytes	Rhodophytes
-	-	-	<i>Desmarestia aculeata</i>	<i>Aglaothamnion/ Callithamnion</i>
			<i>Desmarestia viridis</i>	<i>Brongniartella byssoides</i>
			<i>Ectocarpus siliculosus</i>	<i>Coccotylus truncatus</i> (AP)
			<i>Saccharina latissima</i> (K)	<i>Cystoclonium purpureum</i>
				<i>Dasya baillouviana</i>
				<i>Delesseria sanguinea</i> (K)
				<i>Membranoptera alata</i> (AP)
				<i>Phycodrys rubens</i> (K)
				<i>Polysiphonia elongata</i>
				<i>Polysiphonia fibrillosa</i>
				<i>Polysiphonia fucoides</i>
				<i>Polysiphonia stricta</i>
				<i>Rhodochorton purpureum</i>
				<i>Spermothamnion repens</i>
0 taxa	0 taxa	0 taxa	4 taxa	14 taxa
Red listed species			4 taxa	
Mean (range) / Median species number			10.3 (4-14) / 12.0	
Mean (range) / Median total cover			31.7 (1-85) / 15.0	
Mean (range) / Median total biomass			78.0 (1.4-187.6) / 48.7	

The *Saccharina*-community and *Phycodrys/Delesseria*-community (15–20 m) occur mainly at the east coast of Fehmarn and in Fehmarnbelt. An appropriate reference area lies at Außenschlei. Those results have been compared to the results from the Fehmarn coast.

In Figure App. 11-4 the MDS and Cluster analyses of these data are shown. Three clusters can be recognized: one with *Laminaria gigitata*, one with the *Saccharina*-community and one with the *Phycodrys/Delesseria*-community. Beside the *Laminaria digitata* cluster all clusters include reference as well as impact sites.

The statistical tests ANOSIM (R = 0.154, p = 0.004) as well as SIMPER (50.5% dissimilarity) also state that the reference and impact group are not separable at all.

Phycodrys/Delesseria- (15-20m) and Saccharina-community

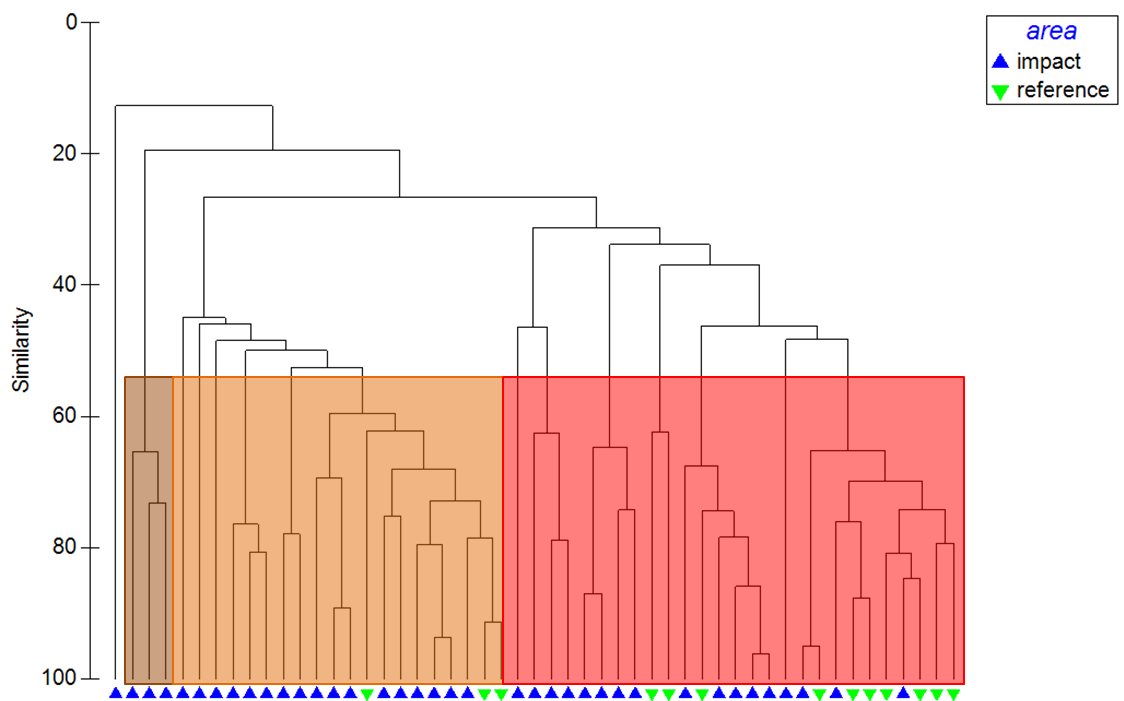
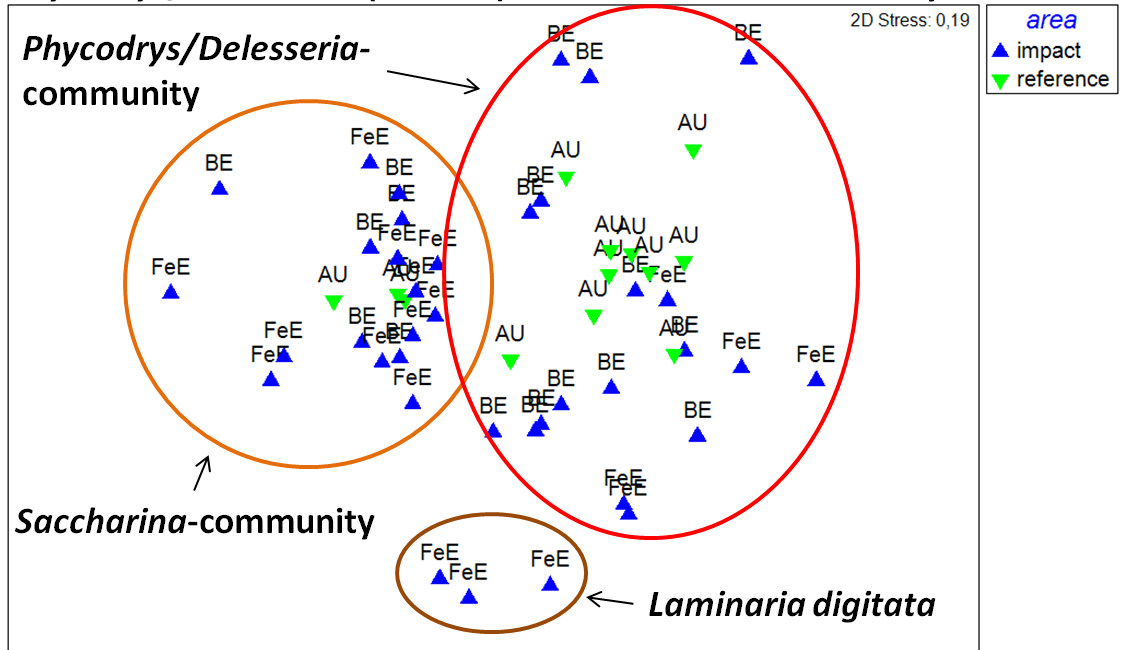


Figure App.11-4 MDS and Cluster-Analysis of Außenschlei macroalgae communities.



Hohwacht Bight

The Hohwacht Bight is a part of the Natura 2000 area Eastern Kiel Bight and lies at its south-western margin. Different survey methods have been conducted all according to the methods already described in the FEMA benthic vegetation baseline report. The area is approximately 48 km away from the proposed Fehmarnbelt link and is located at the south-western boundary of the vegetation baseline investigation area.

Three video transects have been tracked in order to get information about the spatial distribution of vegetation, including depth limits. The depths of the recorded videos laid between 2 and 10 m at all transects.

20 coverage estimations (25 m²) have been made by divers. 60 Coverage estimations in 0.25 m²-frames and 60 biomass samples out of ¼ (0.0625 m²) of these frames have also been taken: 30 for the *Fucus*-community (2-5 m) and 30 for the *Furcellaria*- and shallow *Phycodrys/Delesseria*-community (5-10 m) (Figure App. 11-6).

The *Fucus*-community, the *Furcellaria*-community and the *Phycodrys/Delesseria*-community (5–10 m) did occur in this area (Figure App. 11-7). Additionally an eel-grass/algae-community could be detected. Overall 30 species could be identified (Table App. 11-4). The mean species number was 15.1, the mean Total cover value was 43.3 and the mean biomass was 1053.0 g m⁻².

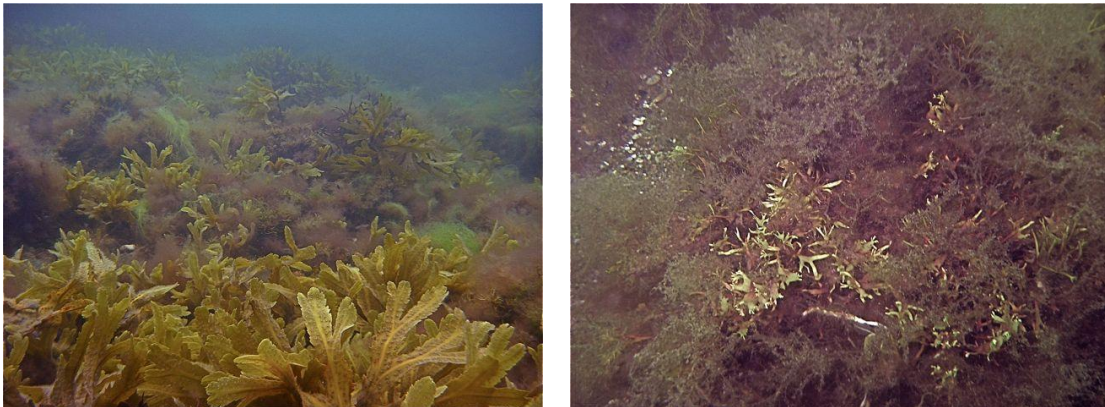


Figure App.11-5 Between 2–5 m a dense *Fucus* zone occurs locally at Hohwacht Bight (left side). Deeper occurring hard substrates (5–10 m) are representing the *Phycodrys/Delesseria*-community (right side).

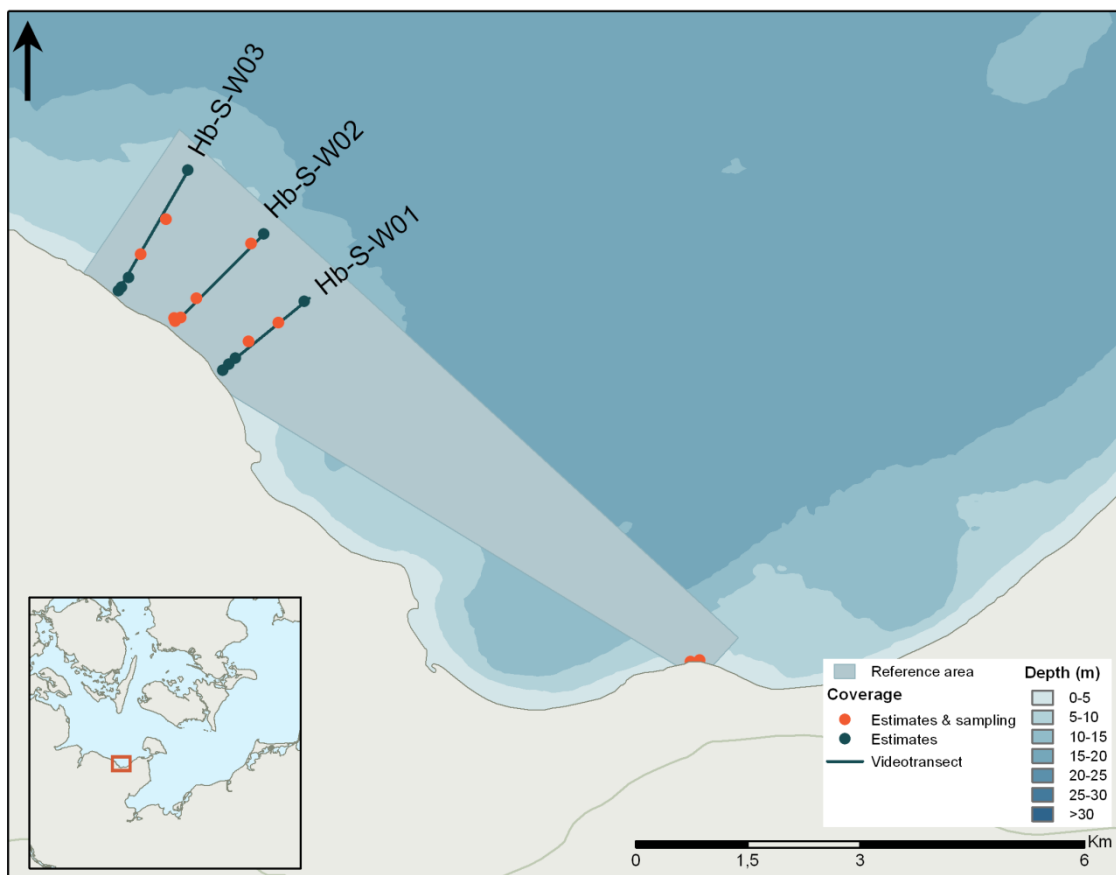


Figure App. 11-6 Video transects, coverage estimates and biomass sample sites in the reference area 'Hohwacht Bight' in the summer 2010.

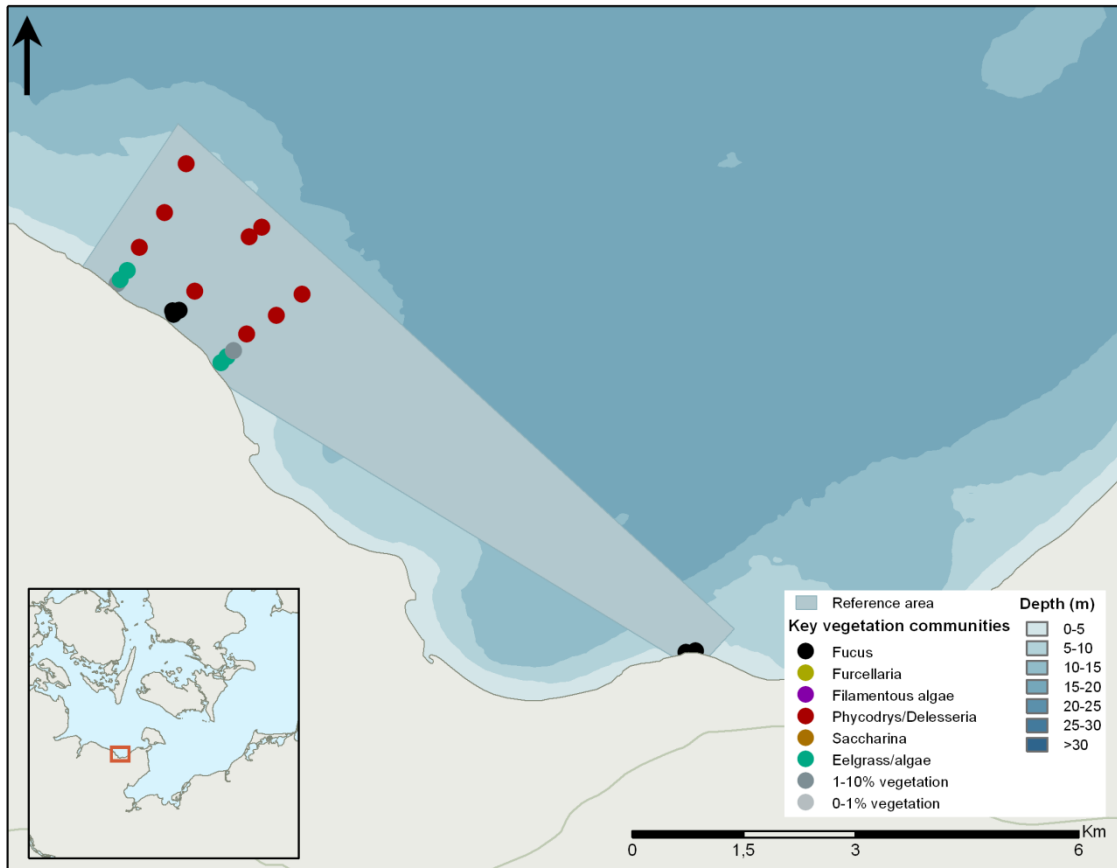


Figure App.11-7 Vegetation communities in the reference area Hohwacht Bight.



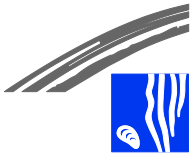
Table App.11-4 Species list from Hohwacht Bight. K = key species, AP = accompanying species.

Spermatophytes	Charophytes	Chlorophytes	Phaeophytes	Rhodophytes
-	-	<i>Chaetomorpha linum</i>	<i>Chorda filum</i>	<i>Aglaothamnion/ Callithamnion</i>
		<i>Chaetomorpha melagonium</i>	<i>Ectocarpus siliculosus</i>	<i>Ahnfeltia plicata</i> (AP)
		<i>Cladophora rupestris</i>	<i>Elachista fucicola</i>	<i>Brongniartella byssoides</i>
		<i>Cladophora</i> sp.	<i>Fucus serratus</i> (K)	<i>Ceramium tenuicorne</i>
			<i>Fucus vesiculosus</i> (K)	<i>Ceramium virgatum</i>
			<i>Pylaiella littoralis</i>	<i>Coccotylus truncatus</i> (AP)
			<i>Sphacelaria rigidula</i>	<i>Cystoclonium purpureum</i>
			<i>Sphacelaria</i> sp.	<i>Delesseria sanguinea</i> (K)
				<i>Dumontia contorta</i>
				<i>Furcellaria lumbricalis</i> (K)
				<i>Membranoptera alata</i> (AP)
				<i>Phycodryis rubens</i> (K)
				<i>Polysiphonia elongata</i>
				<i>Polysiphonia fibrillosa</i>
				<i>Polysiphonia fucoides</i>
				<i>Polysiphonia stricta</i>
				<i>Rhodomela confervoides</i>
				<i>Spermothamnion repens</i>
0 taxa	0 taxa	4 taxa	8 taxa	18 taxa
Red listed species		6 taxa		
Mean (range) / Median species number		15.1 (8-21) / 14.0		
Mean (range) / Median total cover		43.6 (5-90) / 40.0		
Mean (range) / Median total biomass		1053.0 (42.2-2573.2) / 400.8		

Fucus-community

The *Fucus*-community occurs mainly on the westcoast of Fehmarn. An appropriate reference area lies in the Hohwacht Bight. Those results have been compared to the results from the Fehmarn coast.

In Figure App. 11-8 the MDS and Cluster analysis of these data are shown. Two clusters can be recognized: one with *Fucus serratus* and the other one with *Fucus vesiculosus*. Both include reference as well as impact sites.



The statistical tests ANOSIM ($R = 0.154$, $p = 0.004$) as well as SIMPER (50.5 % dissimilarity) also state that the reference and impact group are not separable at all.

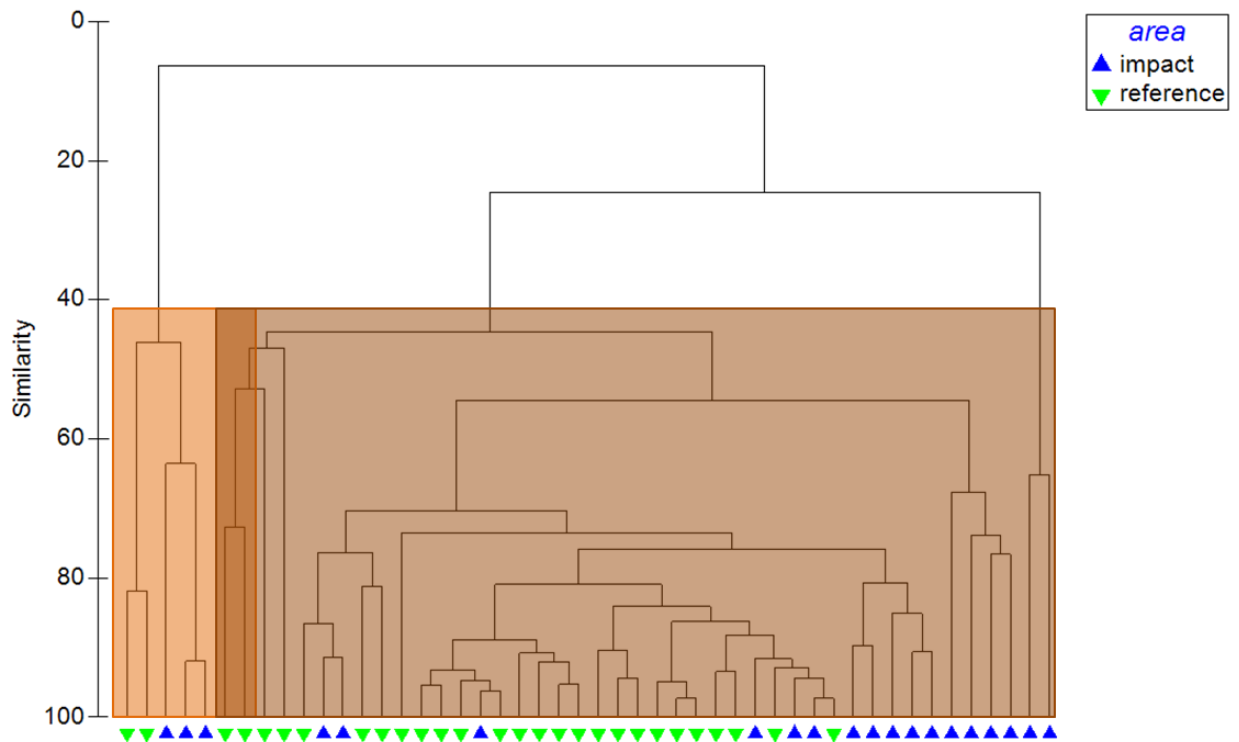
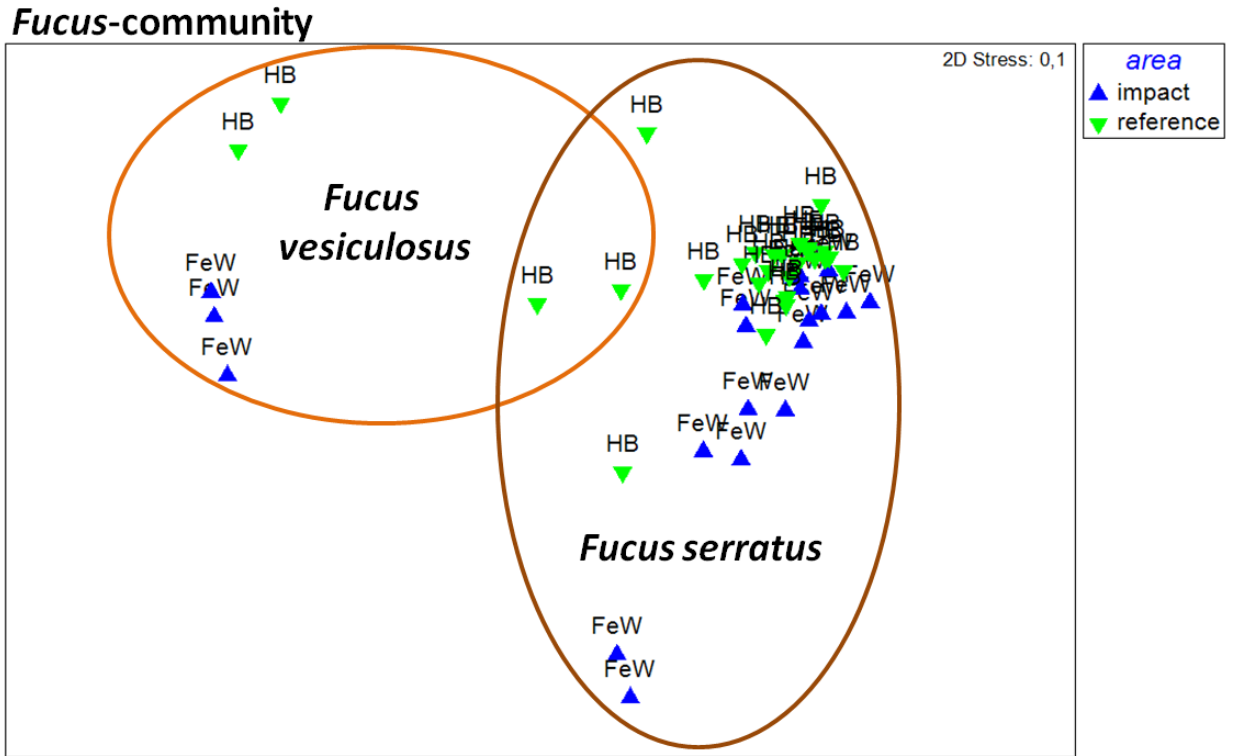


Figure App.11-8 MDS and Cluster-Analysis of the Fucus community in Hohwacht Bight and impact zone.



Furcellaria-community

The *Furcellaria*-community occurs only at few sites around Fehmarn. Nevertheless, an appropriate reference area lies approximately in the Hohwacht Bight. The results have been compared to the results from the Fehmarn coast.

In Figure App. 9-11 the MDS and Cluster analysis of these data are shown. No incisive clusters can be recognized. It is obvious, that reference as well as impact area sites mix themselves.

The statistical tests ANOSIM ($R = -0.04$, $p = 0.671$) as well as SIMPER (54.5% dissimilarity) also state that the reference and impact area are barely separable due to the fact that the differences in the reference and impact area itself are greater than the differences between those two.



Furcellaria-community

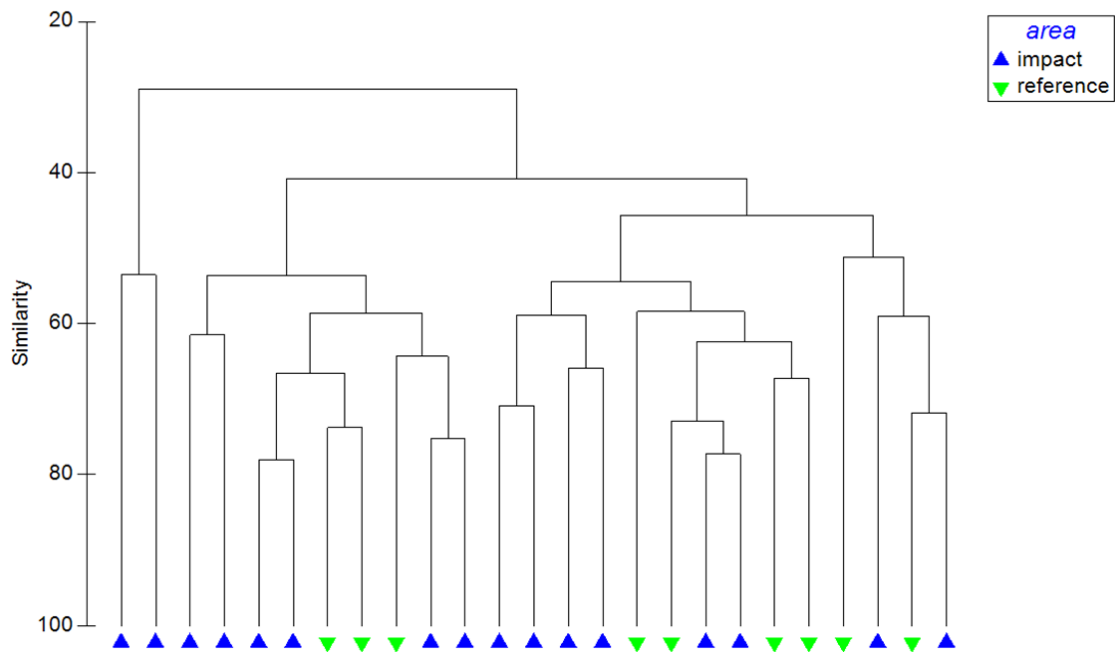
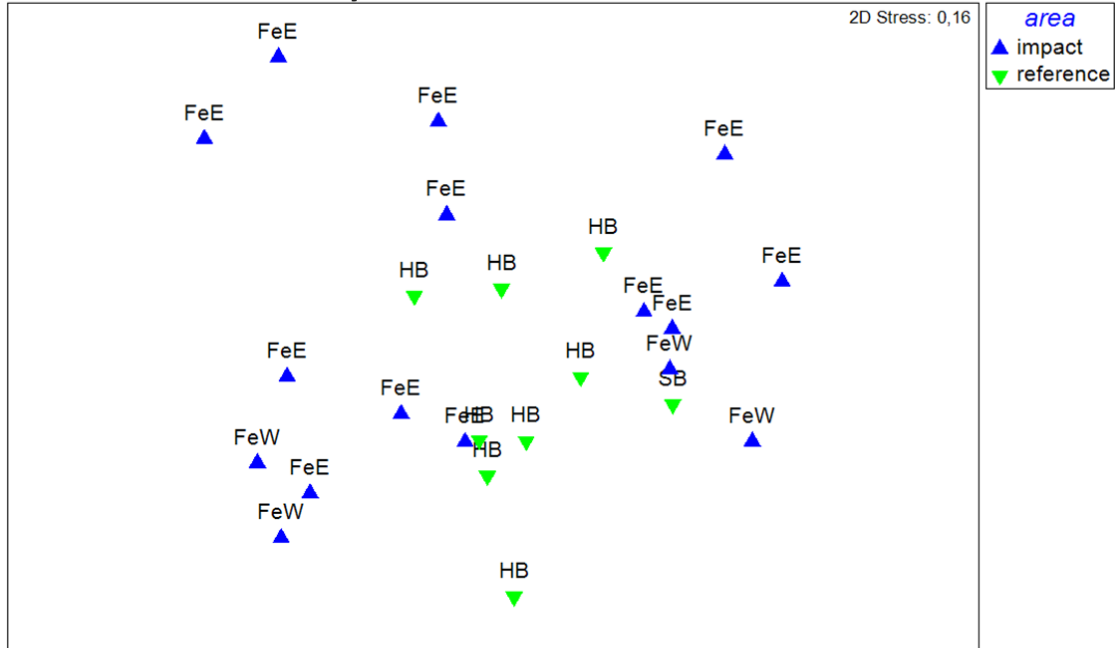


Figure App.11-9 MDS and Cluster-Analysis of the Furcellaria-community in Hohwacht Bight and impact zone.

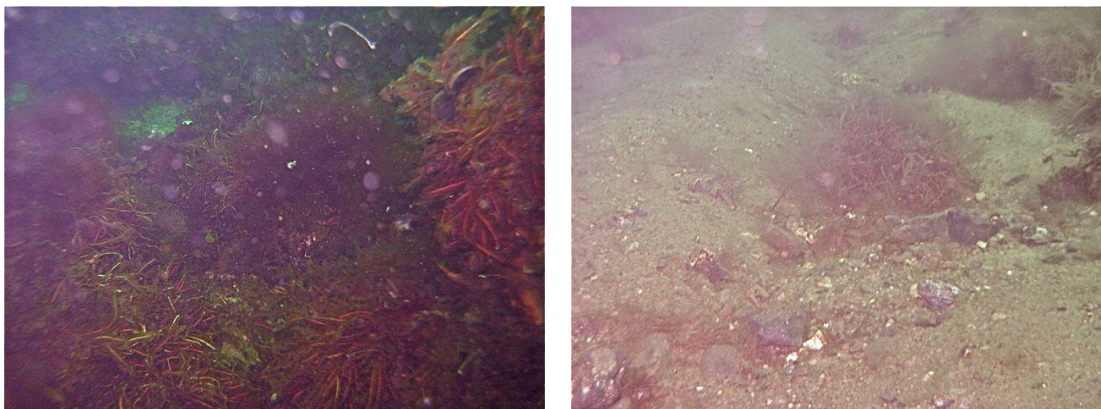


Sagasbank

In the Natura 2000 area Sagasbank, different survey methods have been conducted all according to the methods already described in the FEMA benthic vegetation baseline report.

Two video transects have been tracked in order to get information about the spatial distribution of vegetation, including depth limits. The depths of the recorded videos lay between 8-16 m at the easterly transect and between 9-14 m at the westerly transect. Six coverage estimations (25 m²) have been made by divers. 30 Coverage estimations in 0.25 m²-frames and 30 biomass samples out of ¼ (0.0625 m²) of these frames have also been taken (Figure App. 9 - 1).

Only one macroalgae community could be detected at Sagasbank in 2010: the *Phycodrys/Delesseria*-community (Figure App.) with 21 species overall (Table App. 9 - 1). The mean species number was 12.2, the mean Total macroalgae cover was 59.8 and the mean biomass was 235.4 g m⁻².



*Figure App. 11-10: Vegetation coverage varies strongly at Sagasbank. Sites with a high coverage of the *Phycodrys/Delesseria*-community (left side) and sites with a very low vegetation coverage (right side) are alternating on small scale.*

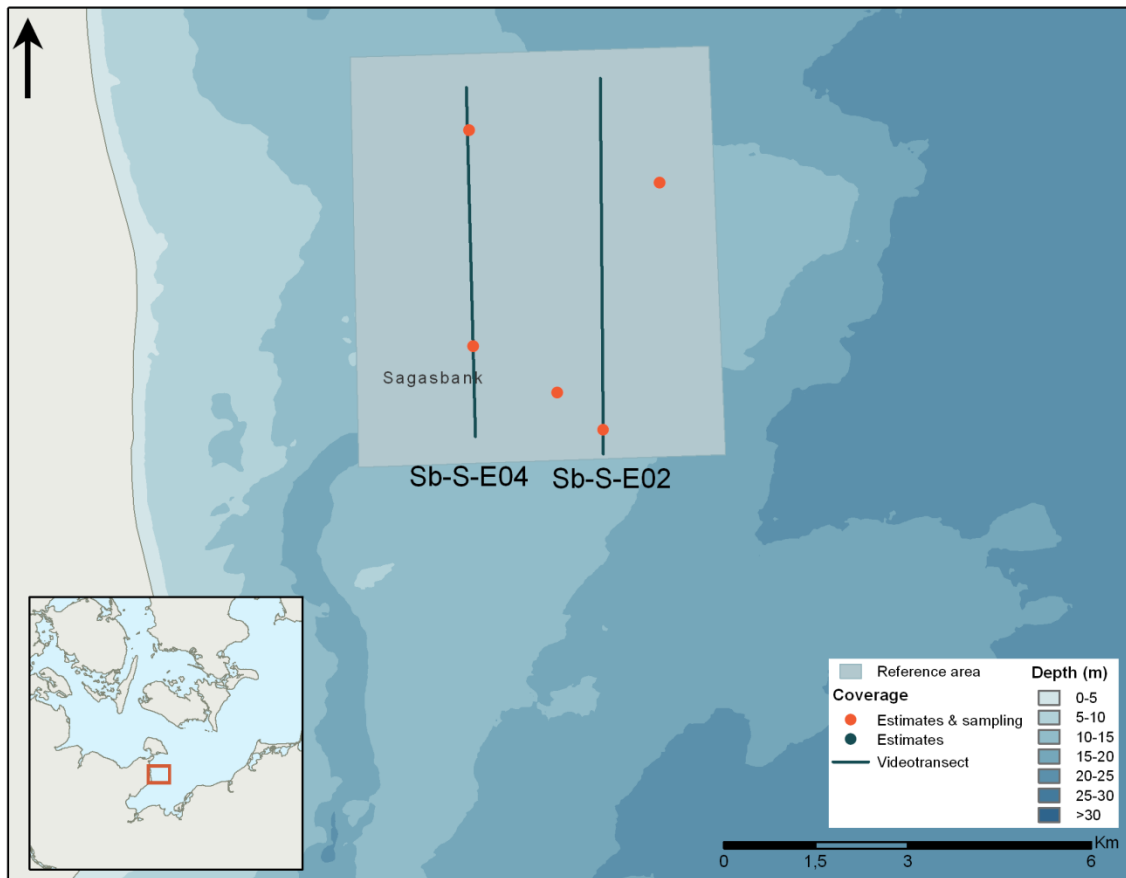


Figure App. 9 - 1 Video transects, coverage estimates (at one site two coverage estimates have been made) and biomass sample sites in the reference area 'Sagasbank' in the summer 2010.

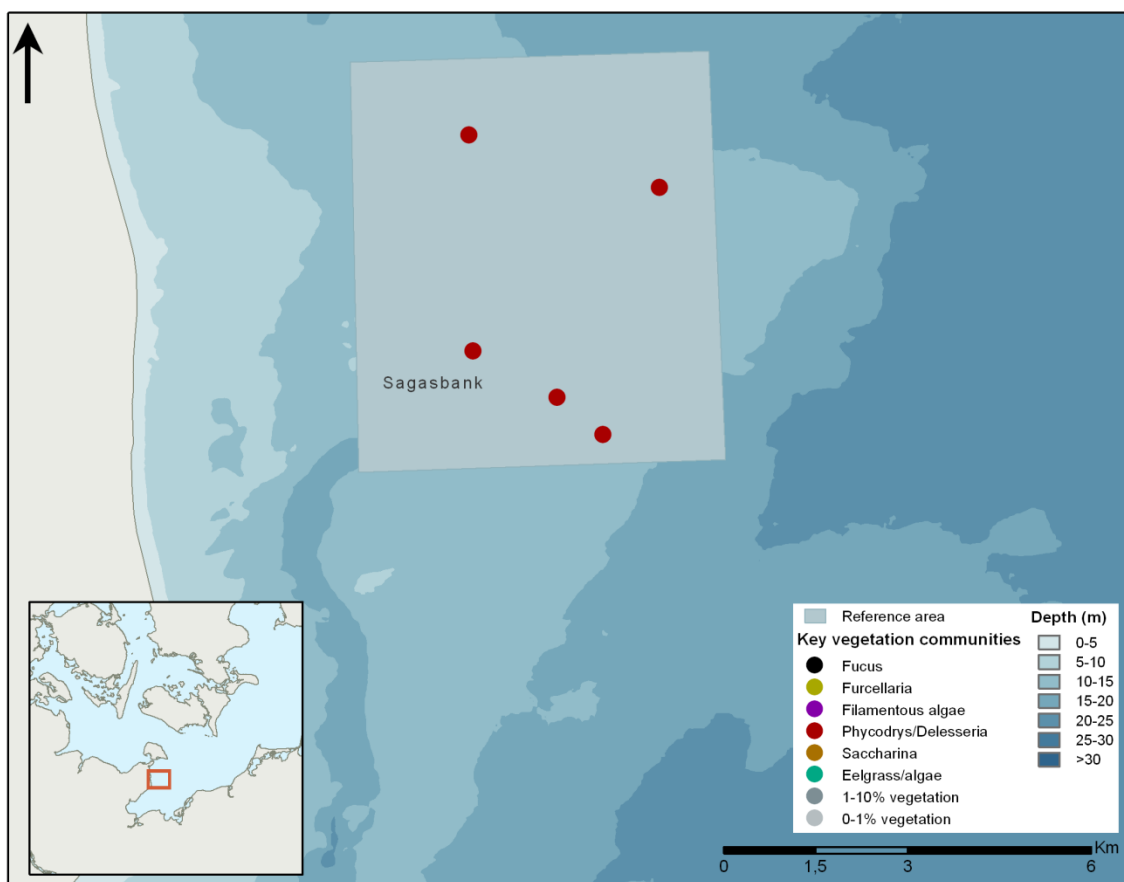


Figure App. 9 - 2 Vegetation communities in the reference area Sagasbank.



Table App. 9 - 1 Species list from Sagasbank. K = key species, AP = accompanying species.

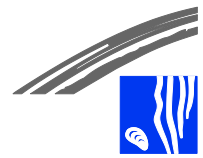
Spermatophytes	Charophytes	Chlorophytes	Phaeophytes	Rhodophytes
-	-	<i>Chaetomorpha linum</i>	<i>Desmarestia viridis</i>	<i>Aglaothamnion/ Callithamnion</i>
		<i>Chaetomorpha melagonium</i>	<i>Saccharina latissima</i> (K)	<i>Ceramium tenuicorne</i>
				<i>Ceramium virgatum</i>
				<i>Coccotylus truncatus</i> (AP)
				<i>Cystoclonium purpureum</i>
				<i>Delesseria sanguinea</i> (K)
				<i>Furcellaria lumbricalis</i> (K)
				<i>Membranoptera alata</i> (AP)
				<i>Membranoptera cf. Pantoneura</i>
				<i>Phycodrys rubens</i> (K)
				<i>Polyides rotundus</i>
				<i>Polysiphonia elongata</i>
				<i>Polysiphonia fibrillosa</i>
				<i>Polysiphonia fucoides</i>
				<i>Polysiphonia sp.</i>
				<i>Polysiphonia stricta</i>
				<i>Rhodomela confervoides</i>
0 taxa	0 taxa	2 taxa	2 taxa	17 taxa
Red listed species		2 taxa		
Mean (range) / Median species number		12.2 (8-16) / 13		
Mean (range) / Median total cover		59.8 (20-95) / 63.8		
Mean (range) / Median total biomass		235.4 (161.1-333.8) / 213.8		

Phycodrys/Delesseria-community in 5-15 m

The shallow *Phycodrys/Delesseria*-community occurs at many sites around Fehmarn. Appropriate reference areas lie in the Hohwacht Bight (5–10 m) and at Sagasbank (10–15 m). The results have been compared to the results from the Fehmarn coast.

In Figure App. 9 - 3 the MDS and Cluster analyses of these data are shown. No incisive clusters can be recognized. It is obvious, that reference as well as impact area sites mix themselves.

The statistical tests ANOSIM (R = 0.391, p = 0.001) as well as SIMPER (49.8% dissimilarity) also state that the reference and impact area are barely separable.



Phycodrys/Delesseria-community (5-15m)

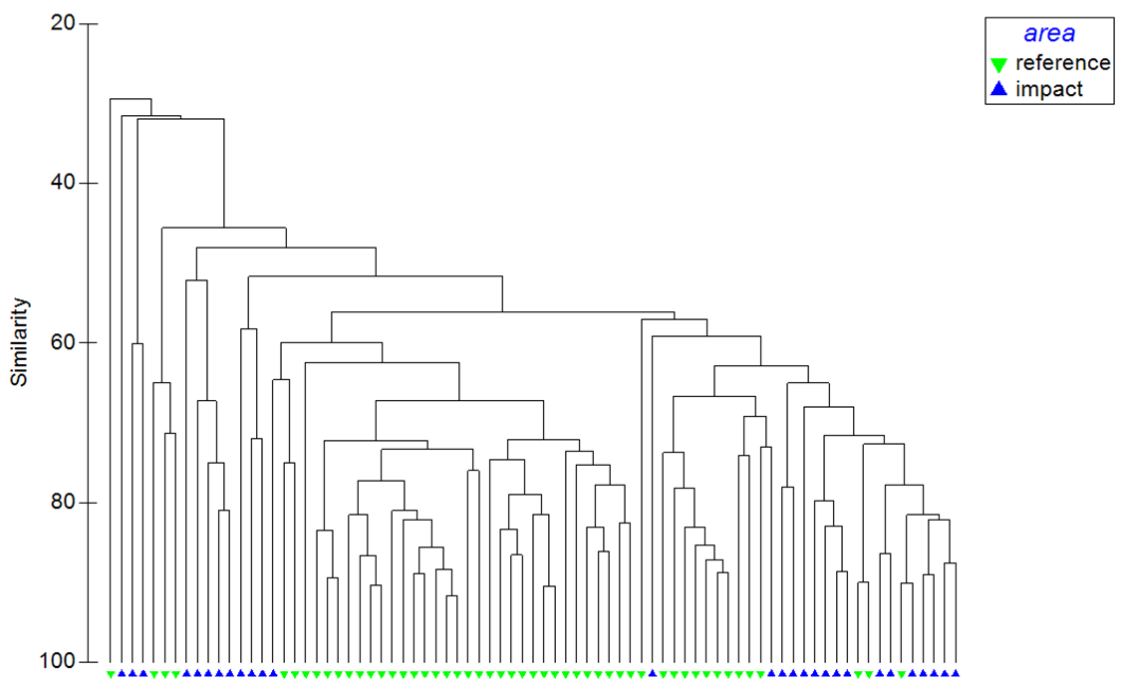
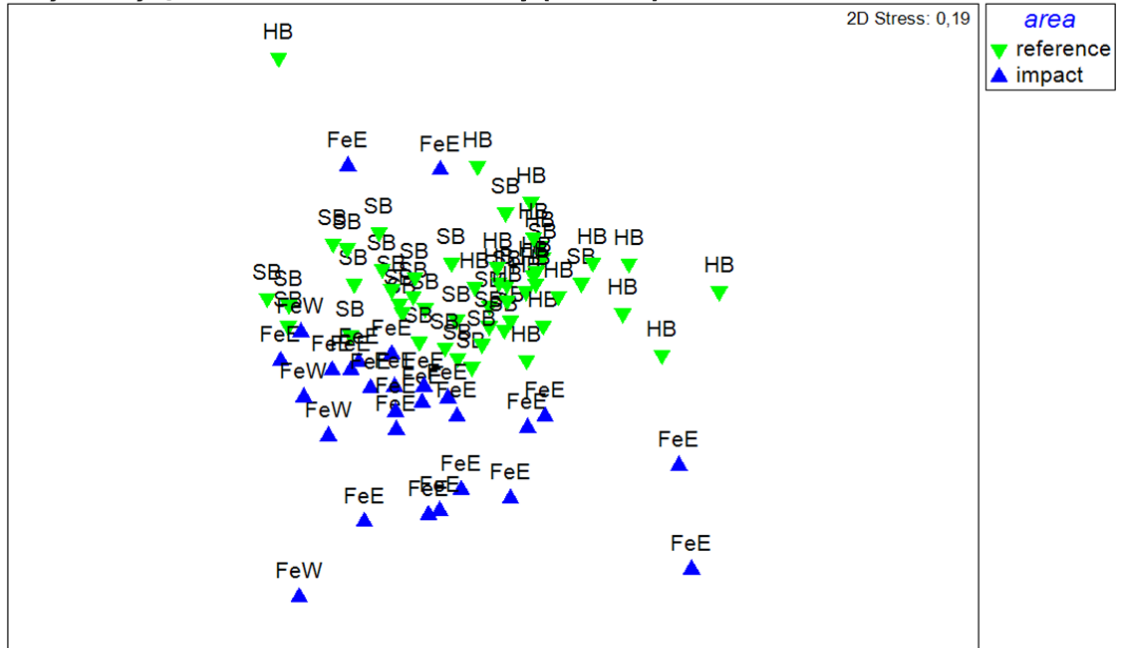
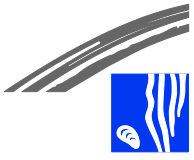


Figure App. 9 - 3 MDS and Cluster-Analysis of the Phycodrys/Delesseria-community in Hohwacht Bight (5-10 m), Sagasbank (10-15 m) and the impact zone.



A P P E N D I X 1 2

Overview map with geographical locations

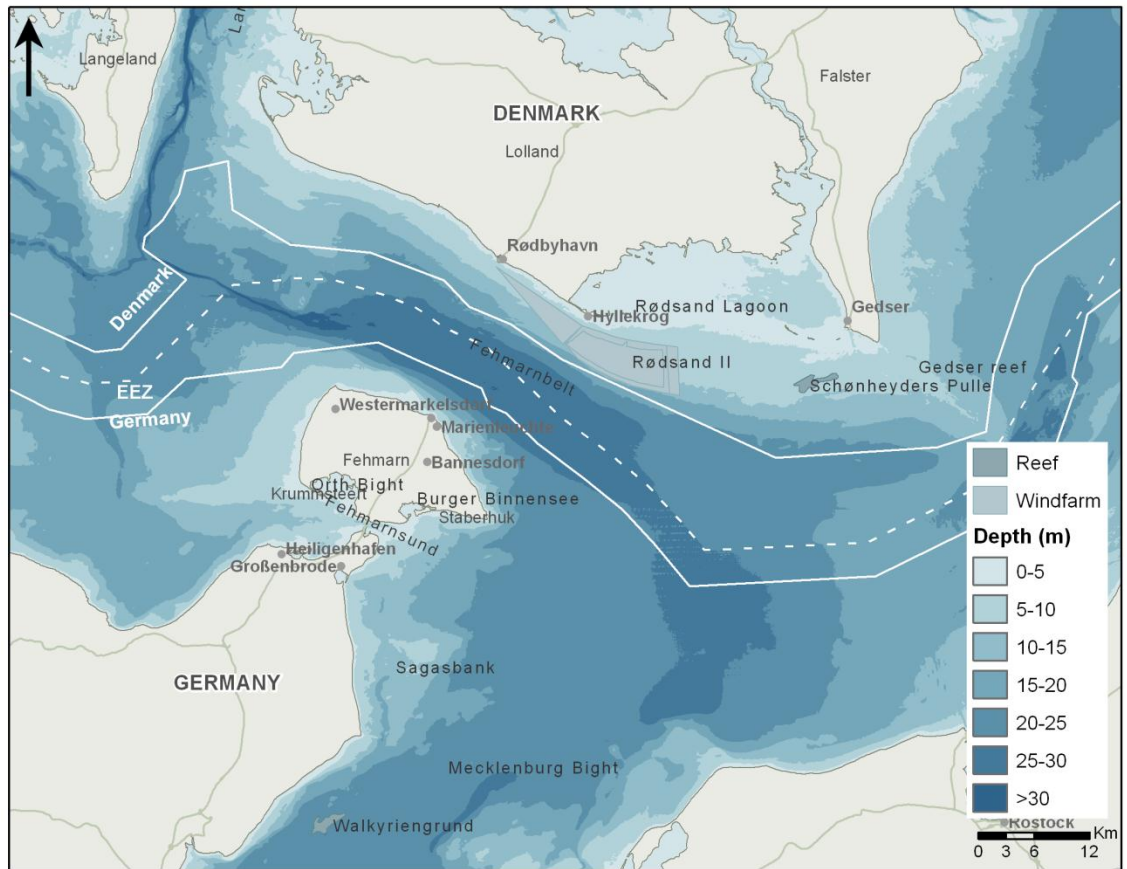
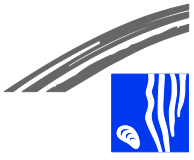


Figure App.12-1 Names of geographical locations used within the baseline descriptions.



A P P E N D I X 13

Distribution of Key Macroalgae Communities in 2010



Table App. 13-1 Number of sites with key communities in Danish and German areas in 2010.

Area	Filamen- tous algae	<i>Fucus</i>	<i>Furcellaria</i>	<i>Phycodrys/ Delesseria</i>	<i>Saccha- rina</i>
	2010	2010	2010	2010	2010
General	37	10	29	29	13
Danish waters	23	0	25	0	0
German waters	14	10	4	29	13
German coastal zone	14	10	4	24	10
German EEZ	0	0	0	5	3
DE 1332-01 Fehmarnbelt	0	0	0	5	3
DE 1533-301 Staberhuk	8	0	4	4	4
DE 1631-392 Eastern Kiel Bight	2	8	0	10	1
DE 1733-301 Sagasbank	0	0	0	6	0

The *Fucus*-community is distributed to a larger scale along the westcoast of Fehmarn and in Hohwacht Bight. Single sites with a *Fucus*-community also occur west of Puttgarden harbour. *Fucus* is distributed between 1 and 6 m depth. Overall 10 sites of the investigation area could be classified into a *Fucus*-community.

The *Furcellaria*-community is widely distributed along the coast of Lolland in depths of 2-10 m. This community occurs in a restricted spatial scale also at the eastcoast of Fehmarn. Overall 29 sites of the investigation area could be classified into a *Furcellaria*-community.

The *Phycodrys/Delesseria*-community occurs only in deeper areas between 7 and 20 m depth. It is widely distributed along the eastcoast of Fehmarn, the Hohwacht Bight, at Sagasbank, at Fehmarnbelt and Außenschlei as well as at one site at the westcoast of Fehmarn. Overall 29 sites of the investigation area could be classified into a *Phycodrys/Delesseria*-community.

The *Saccharina*-community also occurs only in deeper areas between 12 and 20 m depth. It is widely distributed along the eastcoast of Fehmarn and in a restricted spatial scale at Fehmarnbelt and Außenschlei and only at one site at the westcoast of Fehmarn. Overall 13 sites of the investigation area could be classified into a *Saccharina*-community.

The filamentous community is widely distributed within the whole investigation area and the majority of sites (37) could be classified into this community. It occurs in shallow areas as well as in intermediate depths; only in depths > 15 m it does not exist. This community is dominating along the Lolland coast (below the *Furcellaria*-community) and the south east coast of Fehmarn (Staberhuk). It also occurs at the west coast of Fehmarn between the *Fucus*- and *Phycodrys/Delesseria*-community. All of those areas are known to have a high coverage of blue mussels, often used as substrate by filamentous algae.

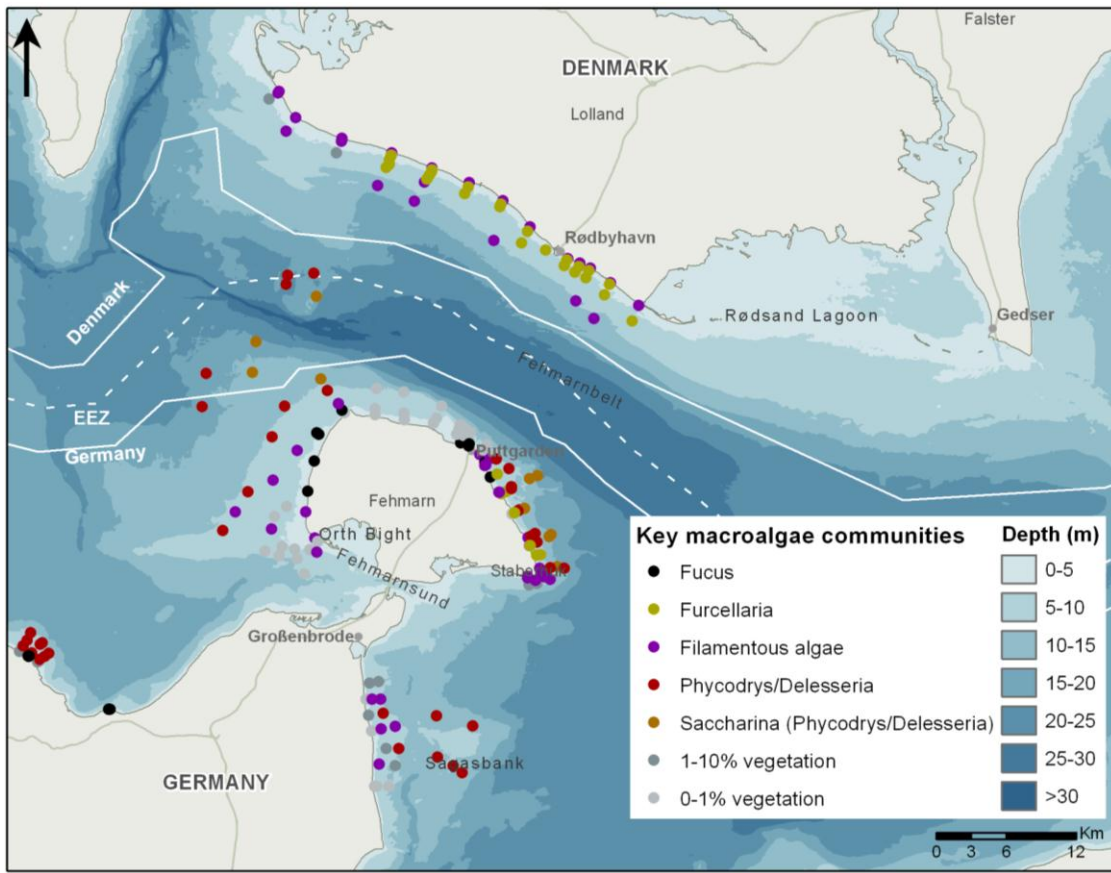


Figure App. 13 - 1 Site distribution of macroalgae communities within the investigation area.