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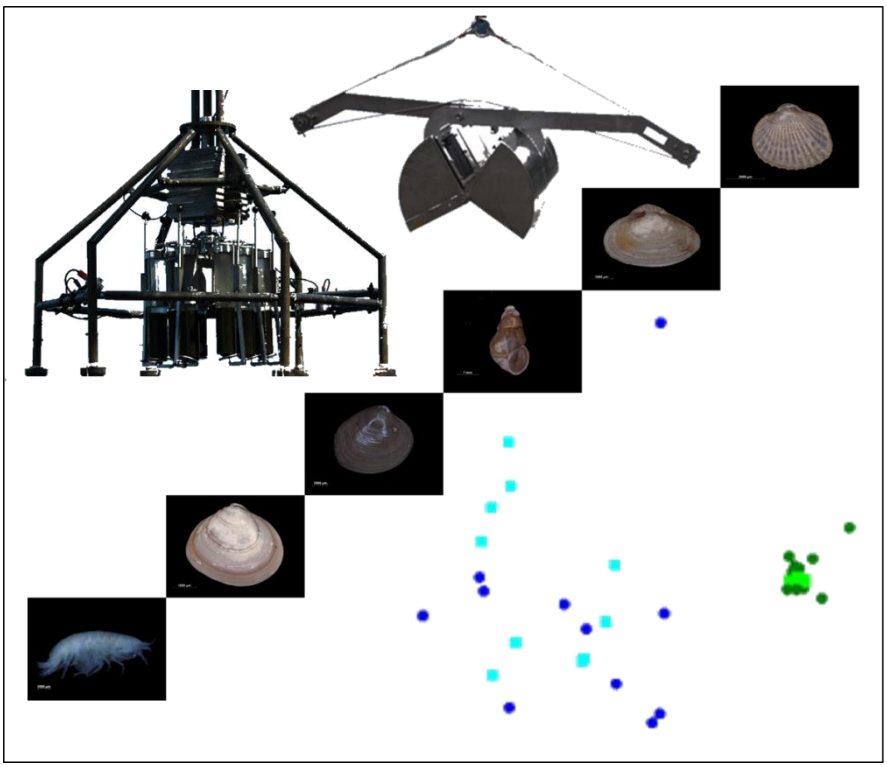
Influence of the sampling strategy on the description of benthic ecosystem functioning



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List of abbreviations

MUC:	Multicorer
vV:	van Veen grab sampler
SECOS:	The Service of Sediments in German Coastal Seas
HELCOM:	Commission based on the Helsinki-convention
ICES:	International Council for the Exploration of the Sea
WFD:	EU Water Framework Directive
BMBF:	Bundesministerium für Bildung und Forschung
MSFD:	Marine Strategy Framework Directive
SAR:	Species-area relationship
IfAÖ:	Institut für Angewandte Ökosystemforschung
SAC:	Species-area curve
AB:	Station Arkona Basin
OB:	Station Oder Bank
CTD:	Instrument used to determine the conductivity, temperature, and depth of the ocean
ind:	Individuals
SD:	Standard deviation
ANOVA:	Analysis of variance
FCA:	Fuzzy Component Analysis
rvEMB:	Research vessel Elisabeth Mann Borgese

Abstract

In national monitoring programs Multicorer (0.01 m²) and van Veen grab (0.1 m²) samples, with different sample sizes, are used to record the ecological status of the Baltic Sea (ISO 16665, 2014). As a part of the ecological status, ecosystem functioning is investigated, while common benthic community descriptors, such as abundance, biomass, species richness and biological traits, are used. Therefore, the influence of the gear types, with different sample unit sizes and number of replicates, on the description of ecosystem functioning needs to be addressed. This is done in order to find a sampling approach, that is sufficiently accurate without losing representative status for macrozoobenthic monitoring.

In this study, 12 Multicorer and 10 van Veen grabs samples were taken at two homogenous sampling sites in the Baltic Sea. In order to sample two different benthic communities, sites with varying environmental conditions, the muddy Arkona Basin and the sandy Oder Bank were chosen. To detect the influence of the gear types, comparisons of the area-adjusted abundance, biomass and functional traits were performed and cumulative species-area curves were generated.

The results showed that the influence of the gear type depends on the benthic community structure. In heterogeneous communities smaller sample sizes possess a higher influence on the data quality than in homogenous communities. Overall, the use of Multicorer samples, with smaller sample sizes, represents higher variations in are-adjusted studies and is not able to detect the same proportion of biodiversity in terms of species richness, as van Veen grab samples with lager sample sizes. Thus, the possibility to compare information of benthic communities, sampled by different gear types was discussed. Considering the results it is advisable to use the standard van Veen sampling procedure to get sufficiently accurate and representative data.

1. Introduction

Costanza et al. (1997) have assessed that estuarine and coastal ecosystems provide many benefits and services for human welfare. Since then the conservation of coastal and estuarine waters is getting attention on a national and international level. Therefore, the European Water Framework Directive was established in 2000 with the aim of realising a good ecological status of all significant European water bodies by 2015 (WFD, 2000). The implementation of WFD should be supported by investigations integrating physiochemical and biological measurements (WFD, 2000; Borja et al., 2003). As part of biological measurements, benthic macroinvertebrates are used as suitable bio-indicators for water ecosystem monitoring (Pearson & Rosenberg, 1978; Ponti et al., 2009; Zettler et al., 2013).

Macroinvertebrates are qualified for ecosystem assessments, because they are comparatively stationary and regulated by the environmental conditions over long periods (Pearson & Rosenberg, 1978; Borja et al., 2003) and therefore useful to identify several kinds of natural and anthropogenic stresses (e.g. Pearson & Rosenberg, 1978; Bilyard, 1987; Ponti et al., 2009). Changes of environmental factors, like food supply, water salinity, oxygen concentration, current energy, temperature, turbidity, substrate composition and the sedimentation rate induce changes in the distribution of macroinvertebrates (e.g. Olenin, 1997; Laine, 2003; Ellis et al., 2006; Gogina et al., 2010). These responses can be assessed by exploring the variation in benthic macrofauna community descriptors like abundance, biomass, body size, taxonomic richness and composition (e.g. Pinna & Basset, 2004; Bremner, 2008). Other features relevant for the assessment of ecosystem functioning are species functional traits, that can be studied using biological trait analysis (Kristensen et al., 2014; Bremner et al., 2006). Per definition, ecosystem functioning is the transfer of matter and energy through various levels of biological organization (Bonsdorff et al., 1995) affected by biological, physical and chemical processes (Paterson et al., 2012). Due to behavioural strategies, morphology and life history of macroinvertebrates and environmental factors (Gogina et al., 2014) ecosystem functioning results in different ecosystem services generating significant components of ecosystem health (Tett et al., 2013)

and benefiting society. Thus, it is advised to include ecosystem functioning assessments to detect the ecological status of European water bodies.

Abundance and biomass are essential values to describe marine benthic communities, at which the abundance describes the number of individuals and the biomass the weight of organisms (e.g. wet weight, dry weight, ash-free dry weight) per square meter or sample (Ruhmor, 1990). Thus, abundance and biomass of macroinvertebrates are selected as indicators characterising biodiversity-related descriptors of Marine Strategy Framework Directive (MSFD) (Berg et al., 2015).

The species richness describes the biological diversity of habitats based on species-area relationships (SAR). The species-area relationship is the perception that, with an increasing sampling area, the number of species that will be detected rises (Schreiner, 2003). Species-area relationships were recognized about a 100 year ago by Arrhenius (1921) and studies of this kind have a long tradition (MacArthur & Wilson, 1967; Rosenzweig, 1995; Connor & McCoy, 2001). Today SARs are among fundamental laws in community ecologies (Schreiner, 2003). SARs are used in different fields of application: to detect regions that represent species richness hotspots (Fattorini, 2006; Mashayekhi et al., 2014) to identify the human impact on biodiversity (Tittensor et al., 2007), and to estimate the extinction rates of species depending on the habitat loss (Engen, 2007). Furthermore SARs are used to define the optimal sizes for Marine Protected Areas (Mashayekhi et al., 2014) and to investigate the species richness of larger regions (Plotkin et al., 2000). Species-area curves (SAC) are the graphical description of SARs depending on species richness and sampled area (Connor & McCoy, 2001). SACs are required to find the minimum area which is needed to be sampled to generate expectations for larger areas (Rumohr et al, 2001). Basically, the course of the function shows that if the sample size increases, abundant taxa multiply quickly and rare taxa occur progressively and slowly as they are only found in larger samples (Jones et al., 1983). By this the SAC rises steeply and gradually levels off. Pigolotti and Cencini (2009) suggested that the number of species of small areas and large areas increases rapidly but not for intermediate areas (Fig. 1). This is due to the fact that larger regions provide diverse habitats and consequently possess a higher species diversity (Kohn & Walsh, 1994).

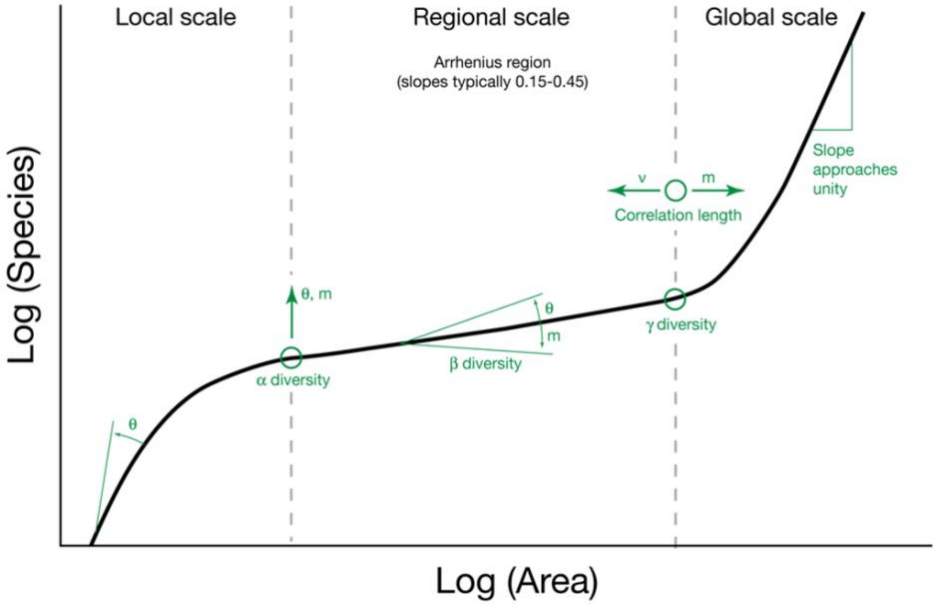


Fig. 1. Species-area curve with the triphasic relationship on, local (alpha), regional (beta), and global (gamma) scales. The effects of θ and m on the shape of the function are indicated by arrows (Hubbell, 2001).

Thus, the size of the area is the most important assignment of species-area curves (Palmer & White, 1994), especially because of habitat heterogeneity which leads to aggregate species spatial distribution and species turnover changes (Harte et al., 2009). Therefore, in SARs the assumption exists that the species are randomly distributed, in a homogenous environment (Ulrich & Buszko, 2007) and heterogeneity needs to be excluded or special SAR models for heterogeneous habitats need to be applied (Colwell et al., 2004). Furthermore, SAR could be influenced by demographic processes such as colonization, dispersal, speciation and local extinction (Pigolotti & Cencini, 2009). As a consequence, a large pool of samples, at random design and generally without replacement should be used (Gotelli & Colwell, 2001) to reveal assumptions. This is especially relevant for research programs to specify which area should receive conservation priority based on species diversity (Myers et al., 2000) and ecosystem functioning.

Biological Trait analyses are an additional way to analyse ecosystem functioning. Thereby, biological traits that characterise the way species affect physical, chemical and biological structures, resulting in different qualities and rates of ecological processes, are investigated (Christiansen et al., 2002). In Biological Trait Analyses to each species, functional traits like, the food web position, the regulation of carbon, bioturbation and habitat alteration, are attached and differences in functional diversity

are analysed (Gogina et al., 2014). The functional diversity is defined as “the distribution and range of functional traits of organisms present in a community or ecosystem” by Diaz and Cabido (2001) and is often expressed in functional group richness (Tilman et al., 1997). Furthermore, functional diversity, which affects ecosystem functioning is based on the amount of resources (Song et al., 2014). Due to that, changes of resources can induce the loss of biodiversity, which leads to an overall reduction of functional richness (Törnroos et al., 2015). Thus, functional diversity is a factor that detects changes in ecosystem functioning by the variation of environmental factors due to natural and anthropogenic stresses (Strong et al., 2015) and directly transmits those to ecosystem services.

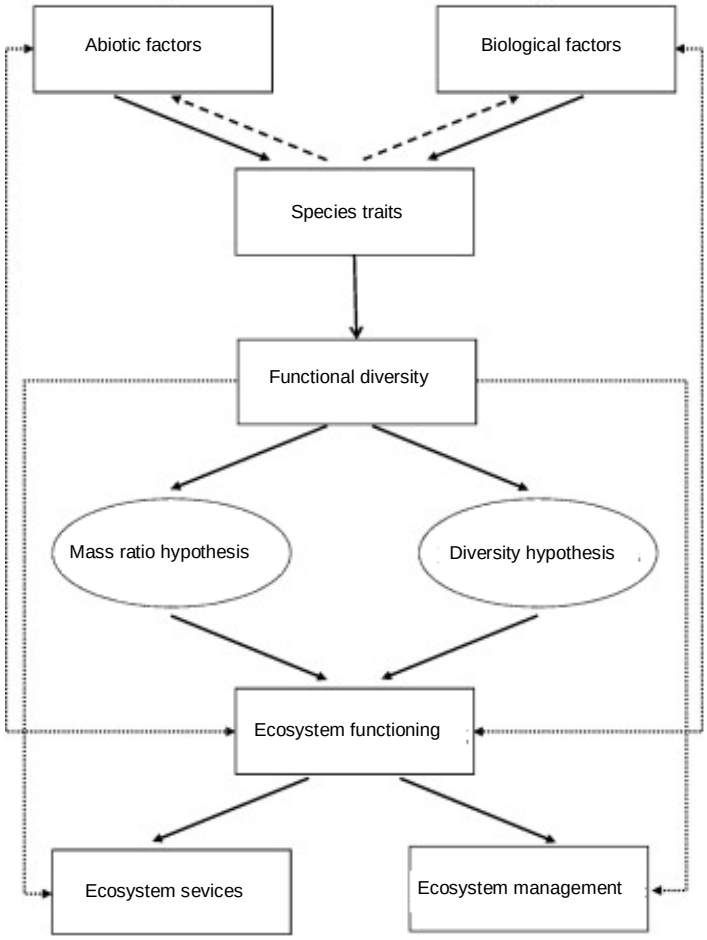


Fig. 2. The relationships between abiotic factors, biological factors, functional diversity, ecosystem functions, ecosystem services and ecosystem management. Changes in abiotic and biotic factors can affect species traits, resulting in varying functional diversity and ecosystem functioning, that influence ecosystem services and ecosystem management with feedback to abiotic and biotic conditions. The mass ration hypothesis and diversity hypothesis transmit functional diversity into ecosystem functioning (Song et al., 2014).

Overall, a high effort is required to characterize those benthic community descriptors, which are relevant for ecosystem functioning. Most of the work consists of collecting samples, sorting, identification of species, counting individuals and weighing the biomass, which requires a lot of effort and is time and money consuming (Ferraro et al., 1989). For this reason, the Water Framework Directive is searching for a rapid and cost-effective sampling procedure (Lampadariou et al., 2005; Pinna & Basset, 2004) to improve the standard sampling procedure of 3 to 5 van Veen grab samples utilised by the Water Framework Directive (WFD), the International Council for the Exploration of the Sea (ICES) and the Commission based on the Helsinki-convention (HELCOM). But a rapid approach is only feasible, if it does not compromise the ecological validity and accuracy of the results (Oliveira et al., 2011). As possibilities to reduce the sampling effort of macrozoobenthic sampling, the use of larger sieve mesh sizes, the reduction of the taxonomic identification level, and the diminution of the sampling area by limiting the number of replicates or using gear types with a smaller sampling unit size are considered (Ruhmor, 1990; Lampadariou et al., 2005; Pinna & Basset, 2004).

Ruhmor (1990) remarked, that the choice of the sample procedure is influenced by sampling characteristics, like the suitability for different sampling sites (e.g. boat, bridge, scuba), the weight of equipment and the lifting capacity of the winch as well as financial limitations. Furthermore, the sediment regimes need to be considered when selecting the gear type, because the sediment type affects the disturbance of sediment, the retention of fine-grained sediments and the penetration depth of the tool depending on the particle size (Sola et al., 1989; Ruhmor, 1990; HELCOM, 2010). Another factor that needs to be evaluated by the choice of gear type is the occurrence of macrozoobenthic species. Because of the feeding habits of macrozoobenthic species most of them are found in the upper 10 to 15 centimeters (Ruhmor, 1990; HELCOM, 2010; Schumacher, 2003) and at least the sample size and volume needs to be considered, because they are correlated with the number of species (Ruhmor et al., 2001).

In macroinvertebrate sampling technologies, commonly two different kinds of sediment sample gear types are used: grab samplers and core samplers (Fig. 3). The van Veen grab sampler is the standard tool to sample macroinvertebrates of soft-bottom communities, due to its reliability and simplicity of handling at sea

(Ruhmor, 1990; HELCOM, 2010). The advantages of the van Veen grab are the ability to sample most types of substrate (25-35 kg sampler weight for fine grained sediments and up to 80 kg in sandy bottoms). It provides high sample integrity, it is less vulnerable to blockage or loss of sample, and it forms fewer bow waves then other samplers (HELCOM, 2010; Schuhmacher, 2003). The standard procedure by van Veen grab includes 3 to 5 replicates with a sample area of about 0.1 m, to ensure statistical integrity. By comparison, the Multicorer samples a smaller area of 0.01 m² and probably needs more replicates to ensure statistical integrity. However, the HELCOM proposes the use of core samples in habitats with a very dense and uniform fauna. Furthermore, core samples may represent better results for habitats, where the burrowing depths of the fauna are beyond the penetration depth of the grab sampler (HELCOM, 2010).

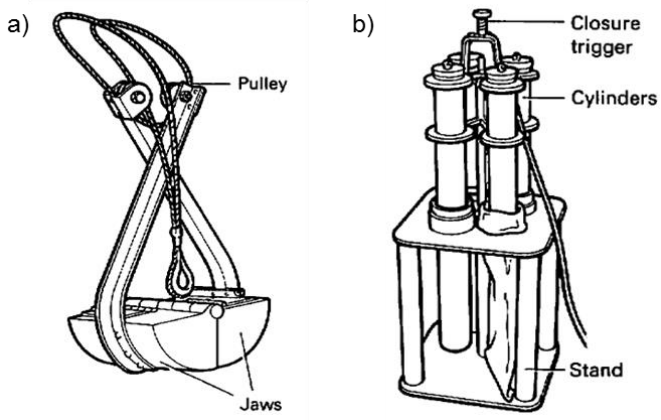


Fig. 3. Surface-sediment sampler: a) van Veen grab sampler and b) Multicorer by Downing (1984).

All this leads to the question, if it is possible to use the sampling approach of core sampling by keeping the high ecological validity and accuracy of the van Veen grab results. Several studies were performed in the Mediterranean Sea to investigate the influence of gear types with different sample sizes to analyse the potential of forecasts for the abundances and biomasses of larger sample areas (Lampadariou et al., 2005; Karakassis et al., 2013; Pinna et al., 2014). Moreover, as both types of samplers are broadly used in different national monitoring programs (ISO 16665, 2014) around the Baltic Sea, for large scale investigations on joint datasets the comparability of results obtained by different gears needs to be addressed in the Baltic Sea.

The Baltic Sea is one of the world largest brackish water basins (area 373 000 km²) consisting of a very young and geologically semi-enclosed sea area (Laine, 2002; Ojaveer & Kalejs, 2008) (Fig. 4). The sea surface temperature, subject to northern climatological seasonality, varies annually from 0 °C to 20 °C (Laine, 2002). The depth zonation is composed of shallow coastal areas, narrow sills with 8-15 m depth, an average depth of 54 m and maximum depths of 459 m (Gustafsson, 2001). The western part of the semi-enclosed sea area is connected to the North Sea through the Kattegat and the Skagerrak, with infrequent inflow events of oxygen enriched high saline waters (around 14 PSU) (Schinke & Matthäus, 1998; Gustafsson, 2001). In addition, the Baltic Sea represents a drainage basin with a freshwater surplus by river discharge (Lass et al., 2001). The freshwater supply, with an increased load of organic matter and nutrients (38 000 t/year phosphorus, 977 000 t/year nitrogen), is about 16 000 m²/s (Bergström & Carlsson, 1994; Omstedt et al., 1997; Miltner & Emeis, 2000; HELCOM, 2013). As consequence, by the freshwater surplus and the density difference between the Baltic Sea and Kattegat, an estuarine circulation is driven (Lass et al., 2001), resulting in gradual decrease in salinities from the Kattegat and Skagerrak, with salinities of 25-30 PSU, to 5 PSU at the Baltic proper and finally to freshwater conditions in the North (Zettler et al., 2007). The sea surface sediments are characterized by a mosaic of rocks, till, gravel and coarser sand. With increasing depth the sediments become finer. Muddy sediments, enriched with organic loads dominate the basins and deeper parts of the trenches (Darr et al., 2014).

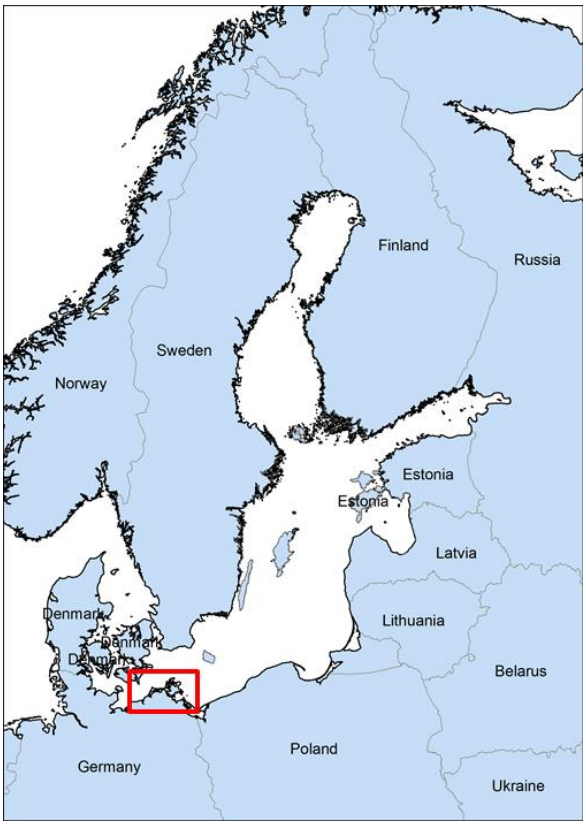


Fig. 4. The Baltic Sea with its adjoining countries. The red box shows the investigation area, Pomeranian Bight and Arkona Basin.

This work is done within the framework of the “Bundesministerium für Bildung und Forschung” (BMBF) - SECOS project (“The Service of Sediments in German Coastal Seas – evaluating the function of marine benthic systems in the context of human use”). In order to sample different benthic communities of relatively homogenous areas, two SECOS stations with different environmental conditions affecting the species composition were chosen. The sandy Oder Bank station (OB) located in the Pomeranian Bight and the muddy Arkona Basin station (AB) adjoning to the Pomeranian Bight in the North. At each station 10 van Veen grab samples and 12 Multicorer samples were taken.

It is assumed, that the influence of the sampling strategy on the description of ecosystem functioning, will be vary between the different communities, subject to different community structures. Furthermore, the size of the sampled area, as a combination of different gear types and the number of replicates will influence the description of ecosystem functioning.

Therefore, the objectives of the study are to investigate the influence of different gear types with varying sample unit sizes and number of replicates on the conclusions regarding to the ecosystem functioning descriptors, abundance, biomass, species richness and biological traits of two different benthic communities. This is done in order to find a sampling approach that is sufficiently accurate without losing representative status for macrozoobenthic monitoring.

2. Material and methods

2.1. Study area

In this study the sandy Oder Bank station (OB) and the muddy Arkona Basin station (AB), with different environmental conditions composition were chosen. Both stations are a part of the Pomeranian Bight that is located in the south-western Baltic Sea and consists of shallow brackish waters with a mean depth of 13 m (Fig.5 ; Lass et al., 2001; Glockzin & Zettler, 2008). The Pomeranian Bight combines two typical coastal basins of glacial origin the Arkona Basin and the Bornholm basin (Neumann & Bublitz, 1968). The area is bordered by the German and Polish Coast in the South and by the 25 m depth line in the North (Glockzin & Zettler, 2008). The Pomeranian Bight is affected by a large freshwater discharge of the Oder River through the Swine, Peene and Dzwina (18 km²/year) (Lass et al., 2001; Mikulski 1966; Bergström & Carlsson, 1994), with organic material and high nutrient load (39-99 kt/year nitrogen, 4.7-8.4 kt/year phosphorus) (Pastuszak et al., 1998). Transported river loads are mixed into the water column by wind driven currents (Pastuszak et al., 1998) and accumulate at deeper areas such as the Arkona Basin (Christiansen et al., 2002; Neumann et al., 1996) and at the slopes and in ripples on the plateau of the Oder Bank, but in much smaller amounts as in the Arkona Bank (Bobertz & Harff, 2004). At both stations the oxygen availability is given at all times because the water column is well mixed down to a depth of 30 m (Kuhrts et al., 2006). The salinity ranges from 0 to 2.5 PSU in the Oder lagoon and shows a mean value of 8 PSU in the Pomeranian Bight, to 15 PSU at the Arkona Basin (Leipe et al., 1998). The texture of sediments in the Pomeranian Bight changes gradually from sand at the Oder Bank, to mud at the Arkona Basin (Fig. 5). The macrozoobenthic species composition is influenced by these environmental factors and should vary between the stations.

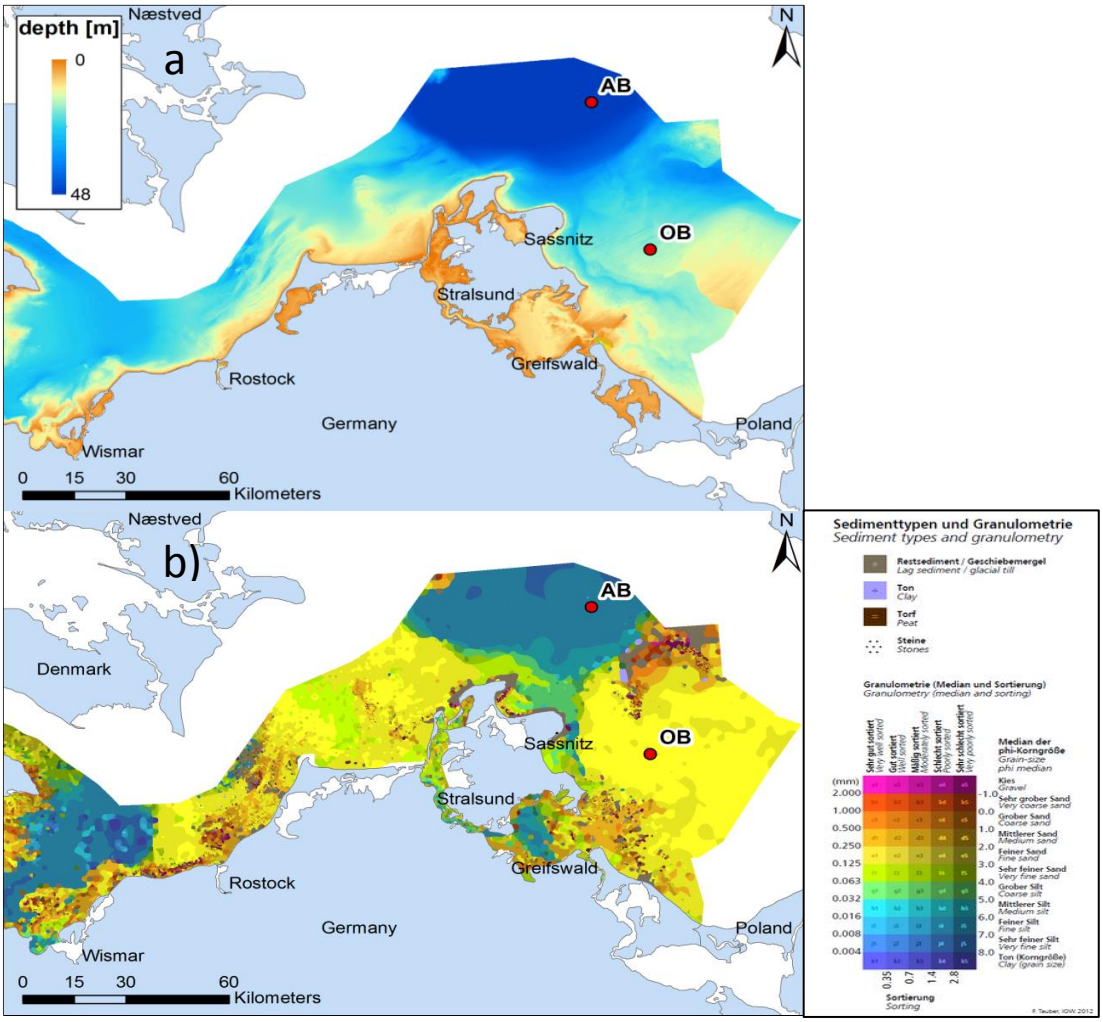


Fig. 5. South eastern part of the German Baltic Sea, with the sampling sites Arkona Basin (AB) and Oder Bank (OB), a) shows the depth zonation and b) the Sediment types and granulometry by Tauber (2012).

2.2. Sampling strategies and design

In this study two different gear types were used to investigate the effect of sampling methods on the description of macrozoobenthic communities. These are the grab and the core samplers, a van Veen grab (vV) and a Multicorer (MUC), typically used for surface-sediment sampling in the Baltic Sea region. These are recommended gears for benthic macrofauna sampling according to the HELCOM (2010) and ICES guidelines (Ruhmor, 1990). Grab samplers like van Veen grab are used to collect horizontal surface sediments when large volumes of sediment or a large surface area is needed and for coarse-grained sediments (U.S. EPA, 2001). The sampler consists of two jaws, which shut when the van Veen grab is hauled up. The van Veen grab is often selected for monitoring programs, because it can sample

most types of substrate, it provides high sample integrity, it is less vulnerable to blockage or loss of sample and it forms fewer bow waves then other samplers (HELCOM, 2010; Schumacher, 2003). In this study, a van Veen grab with a sample area of 0.0976 m² (≈0.1 m²), a weight of 70-75 kg and a 10-15 cm penetration depth was used. Core samplers were typically selected to sample vertical profiles of the sediment to characterize deeper sediments, to document historical changes (U.S. GS, 1997), and if soft fine-grained sediments are expected. In this study, a Multicorer with 8 cores of 1 m length and a sample area of 0.0079 m² (≈0.01 m²) per core was used. The weight was about 700 kg and the penetration depth varied between 9 and 27 cm.

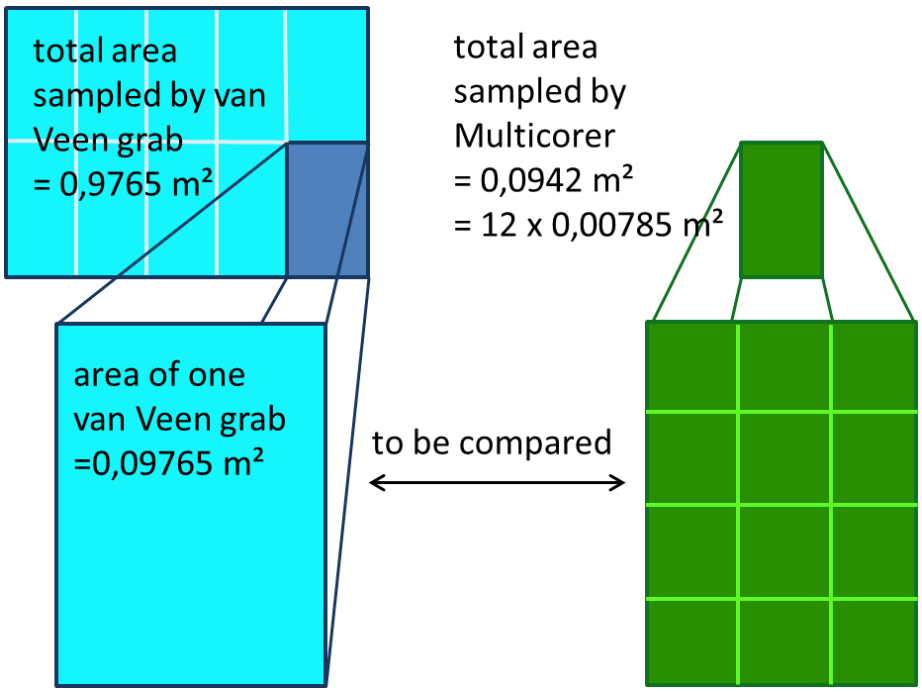


Fig. 6. Surface-sediment sampler used in this study a) van Veen grab sampler (pictured by IfAÖ) and b) Multicorer (pictured by Geomar). The planned and realized sampling design, of this investigation, with the areas sampled by van Veen grab and Multicorer.

At each station 10 replicates of van Veen grab (0.1 m²) had to be sampled. Thereafter around 1 m² of sediment were taken by van Veen grab at the Arkona Basin just as at the Oder Bank. In addition 12 cores (0.01 m²) with a total area of around 0.1 m² were planned to be taken; this area is comparable to one van Veen grab sample (Fig. 6).

2.3. Macrozoobenthic sampling

The samples analysed in this work were collected on the cruise of the research vessel Elisabeth Mann Borgese (EMB100) within the framework of the BMBF project SECOS, in the period from 9th to 23rd of April, 2015. The sampling procedure included 10 replicates of van Veen grab samples and 12 replicates of the Multicorer samples at the stations Arkona Basin and Oder Bank as shown in Fig. 7. The van Veen grabs were taken while the rv Elisabeth Mann Borgese was drifting. The cores were sampled as pairs at 6 positions with a distance of about 50 meters (Fig. x.1).

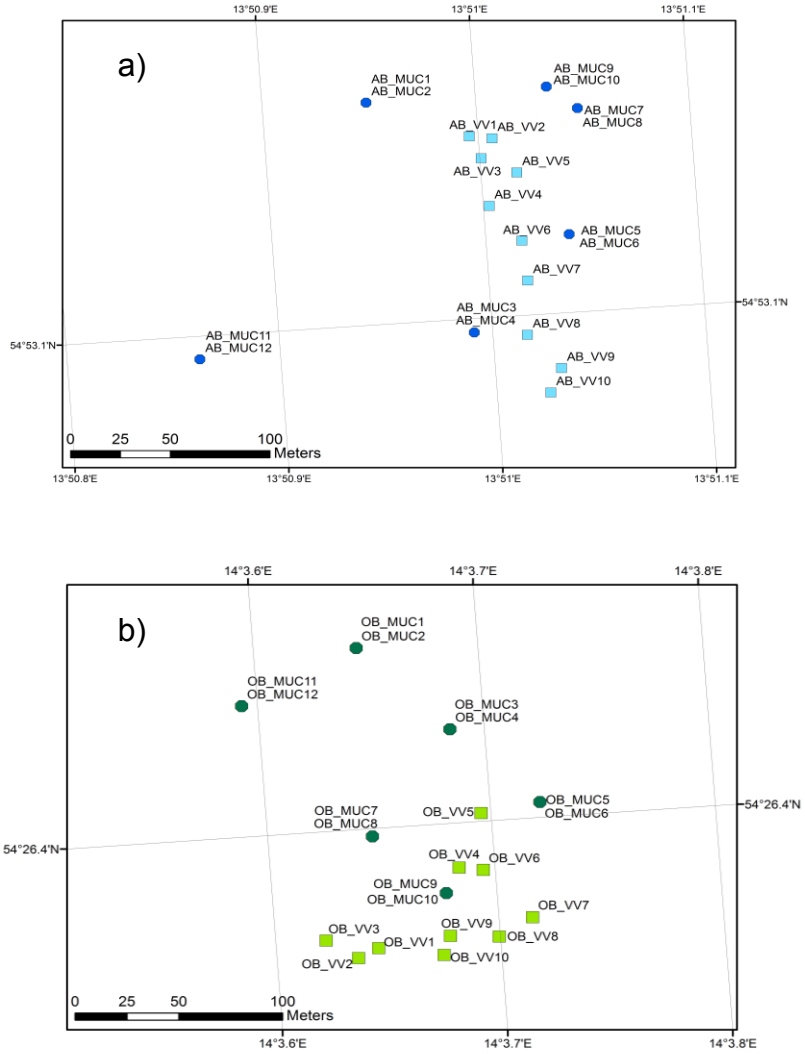


Fig. 7. Exact positions of samples (replicates) collected at a) the Arkona Basin (dark blue circles: Multicorer samples at Arkona Basin; light blue quadrates: van Veen samples at Arkona Basin) and b) the Oder Bank (dark green circles: Multicorer samples at Oder Bank; light green quadrate: van Veen samples at Oder Bank).

The samples were washed through a sieve with a mesh size of 1 mm and preserved in a 4% buffered formaldehyde-seawater solution following the HELCOM-guidelines (HELCOM, 2013). In the laboratory, the macrozoobenthic organisms were sorted and identified to the lowest possible taxonomic level, after the formalin was washed out. Thereafter, the species were counted and the wet weight per species was determined. For colonizing species like bryozoan and hydrozoan these treatments are not possible. Accordingly, they were excluded from the following calculations of abundances and biomass.

Environmental parameters of the sites like salinity and water temperature were measured by the ship-based CTD (instrument used to determine the conductivity, temperature, and depth of the ocean) and water depth by the ship-based acoustic systems during the sampling. To identify the sediment characteristics, an additional sample of the surface layer was taken at each station. The median grain size, the sorting and the organic content were determined (Tab. 1.).

Tab. 1. Environmental parameters measured of the sediment samples taken Arkona Basin and Oder Bank: organic content [%], grain size [µm], oxygen content [mg/l], salinity over ground [PSU], depth [m], water temperature [°C].

Environmental parameter	Arkona Basin	Oder Bank
Organic content [%]	12.42	0.21
Grain size [µm]	18	194
Oxygen content [mg/l]	6.31	8.53
Salinity over ground [PSU]	15.0	8.3
Depth [m]	45.7	15.2
Water temperature [°C]	4.7	5.8

2.4. Statistical methods and data treatment

The analyses of macrozoobenthic communities were performed with the Primer package (v6; Clarke & Gorley, 2006). Thereby, multivariate analyses of the similarity among species of the two stations and the two gear types were carried out. In order to reduce the impact of species with high abundances on the comparison of the community similarities the data was square-root-transformed (Clarke and Warwick, 2001). Non-metric multidimensional scaling (nMDS) and cluster analyses based on Bray-Curtis similarity and group average linking were calculated.

To compare the average values of the abundance in individuals per sample and square meter (ind/sample and ind/m²), the biomass in gram per sample and gram per square meter (g/sample and g/m²) and the number of species per sample (taxa/sample) between the two gear types (van Veen grab and MUC) at both stations (Arkona Basin and Oder Bank) were analysed with the software R (3.0.2) and the

package “Rcmdr” (Fox, 2005). The median, the arithmetic mean and the standard deviation (SD) were calculated. To test the average values by the analysis of variance (ANOVA), the data needs to be normally distributed and the homogeneity of variance needs to be fulfilled (Legendre & Legendre, 1998). If the conditions are not fulfilled it is advisable to use non-parametric test procedures. The homogeneity of variance was verified by using the Levene-test for each station by the gear factors. The normal distribution was tested by the Shapiro-Wilk-test. According as, the data were normal distributed an analysis of variance or a non-parametrical Kruskal-Wallis-test was performed to test the average values for significant differences. Results are represented in Box-Whisker-plots trough quartiles. In Box-Whisker-plots the median value, the boxes between the 25% and 75% quartiles including 50% of the data points and the whiskers indicating the variability outside the boxes within the 95% confidence interval, are visualised (Tukey, 1977).

Species-area curves were generated. Thereby successive samples were added cumulatively to determine if new samples provide unique or redundant information compared to earlier samples (Kindt, 2003; Lyman & Ames, 2007). Species-area curves are generated by plotting a measure of sampling effort, like the number of species on the x-axis and a measure of ecological property of interest, like species richness on the y-axis. The species-area function persists with an intercept representing alpha diversity (MacArthur & Wilson, 1965) and the slope beta diversity (Whittaker, 1960). The species-area curves were computed with the software R (3.0.2) by utilising the package “vegan” (Okasanen et al., 2015). For this the function “specaccum” was used to find species-accumulation-curves or the number of species for a certain number of samples (Kindt & Oksanen, 2015). The „random” method developed by Gotelli & Colwell (2001), was used to find the expected species-area constellation. The number of all possible permutations was calculated by the binomial coefficient:

$$\binom{n}{r} = \frac{n!}{r! \quad (n-r)!}$$

In order to calculate for 10 van Veen grab samples, 1022 permutations and for 12 MUC samples, 4094 permutations needed to be generated. As output, the species-area curves with standard deviations were given.

To detect the influence of the sampling strategy on the representativness of the description of ecosystem functioning by biological traits “Fuzzy Component Analysis” (FCA) was used. It was implemented using R (3.0.2) by the package “ade4” (Dray & Dufour, 2007). The FCA is used to ordinate biological traits by stations on a multidimensional scale (Chevenet et al., 1994). Thereby functional characteristics of the communities were determined by 9 biological traits with 35 modalities which are important for ecosystem processes (Tab. 2). With a “fuzzy coding” calculation (Chevenet et al., 1994) the affinity of each species to the specific modality of each trait was computed. The scores were set in the range from 0 (no affinity) to 1 (total affinity), so the sum of all scores for each species becomes one. With the result that each taxon and each biological trait will have the same weight in further analyses (Gogina et al., 2014). To receive the information about the functional traits of each species, the internal IOW Biological Trait Database was used (Gogina et al., 2014). Prior to perform the FCA, the data of abundance per square meter and biomass per square meter was log10(x+1) transformed to level off the dominant taxa. In the first part FCAs of each site with both sampling gears (MUC and vV) and all stations for abundance per square meter and biomass per square meter were performed to investigate the influence of the gear type. The results, generated by Euclidian distances, are shown in the ordination plots at which each point indicate the abundance- or biomass-weighted trait composition of different gear type at each station. In the second part, the single replicates, all possible combinations of 3 replicate samples and a combination of all sampled replicates of each gear were tested for each station by the biomass per square meter, to determine the influence of the number of replicates considered for the description of functional structure. The 3 samples were chosen, because it is according to the standard procedure of the HELCOM monitoring and due to statistic stability (HELCOM, 2010). The results generated by Euclidian distances are shown in the ordination plots at which each point indicates biomass-weighted trait composition of each combination of replicates collected, using different gear type at each station.

Tab. 2. Trait classes with modalities and attendant code used in the Fuzzy Component Analysis.

Trait class	Modalities	Code
Motility	Sedentary	mod.sed
	Limited free movement	mot.lim
	Freely motile in/on sediment	mot.fre
	Semi-pelagic	mot.spel
Feeding	Suspension	feed.sus
	Deposit feeder	feed.dep
	Predator	feed.pre
	Scavenger	feed.sca
	Grazer	feed.gra
	Parasite or commensal	feed.com
Habitat structure	Permanent burrow	struc.bur
	Hole, pit or non-permanent burrow	struc.pit
	Tube	struc.tub
	Creating troughs or trampling across	struc.tra
Sediment transport	Forming biogenic epibenthic	struc.epi
	Surface-to-deep	sed.sd
	Deep-to-surface	sed.ds
	Surface mixing	sed.sm
	Deep mixing	sed.dm
	No transport	sed.no
Position in sediment	Protruding surface	pos.pro
	Attached	pos.att
	Oxygenated zone	pos.oxy
	Below the oxygenated zone	pos.sox
Size	Small	size.s
	Medium	size.m
	Large	size.l
Reproductive technique	Asexual	sex.asex
	Spawn	sex.spa
	Attached eggs	sex.egg
	Brood	sex.bro
Larvae	Planktonic	lar.pla
	Benthic	lar.ben
Longevity (years)	<2	long.2
	2-5	long.5
	6-10	long.10
	10+	long.10p

3. Results

The data of 44 samples was analysed, 10 van Veen grab and 12 MUC samples taken at each of the two sites: Arkona Basin and Oder Bank. Overall 309 data points for abundance and wet weight of species were generated by 31 species at 44 sample points.

3.1. Analysis of communities at Arkona Basin and Oder Bank

Non-metric multidimensional scaling (nMDS) and cluster analysis of species at all 44 sample stations were performed to define benthic communities. The data was square-root-transformed before the similarity matrices were calculated. The multivariate analyses were based on Bray-Curtis similarity and group average linking. On the one hand, the abundance of species per square meter (ind/m², Fig.8) and on the other hand, the wet weight of species per square meter (g/m², Fig.9) were compared. Thereby, the data was classified into the 4 groups: MUCAB (MUC samples at Arkona Basin), vVAB (vV samples at Arkona Basin), MUCOB (MUC samples at Oder Bank) and vVOB (vV samples at Oder Bank).

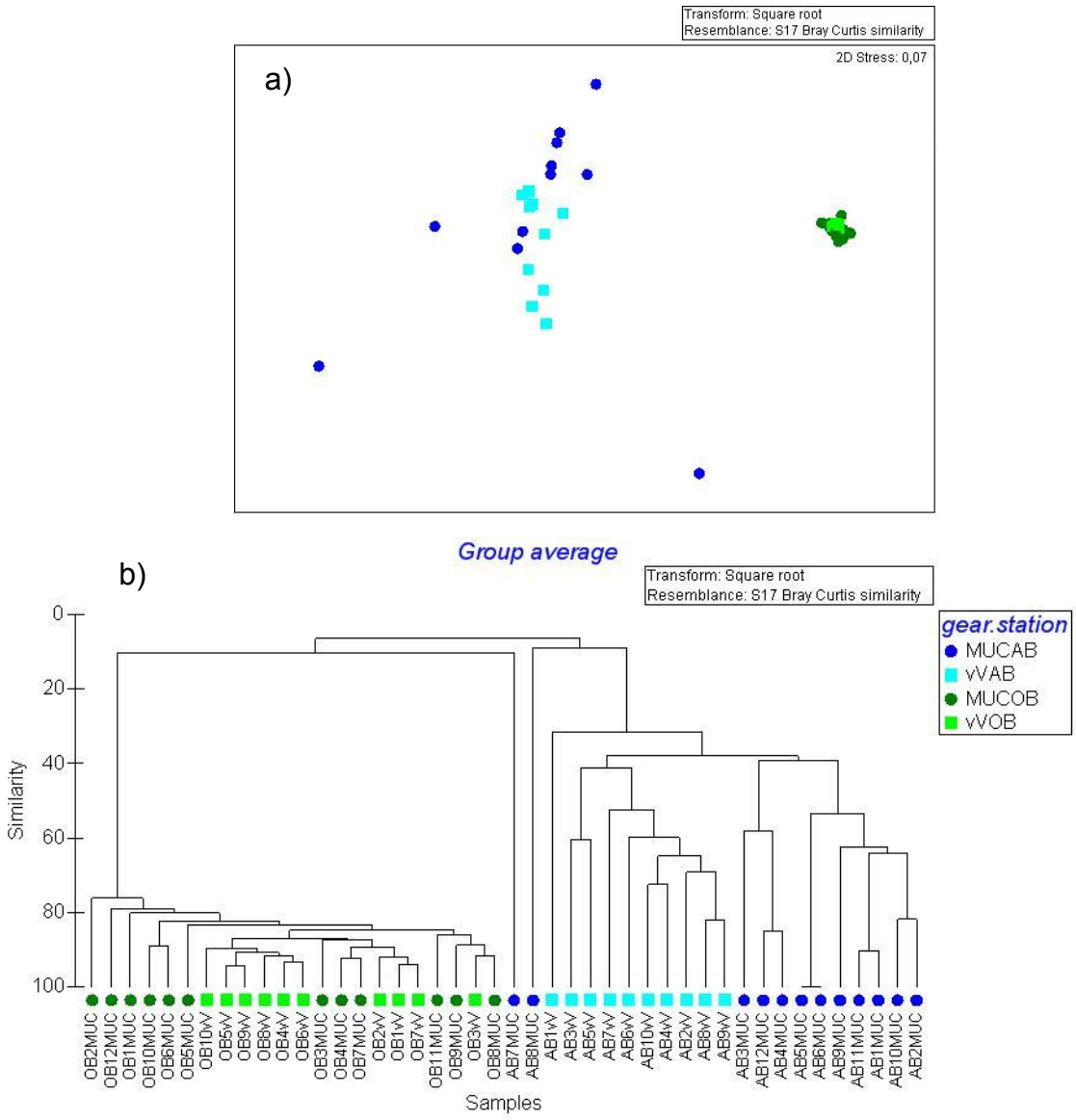


Fig. 8. The results of the a) nMDS plot and b) cluster analysis of the abundance per square meter are shown. As factors the gear type and station was used resulting in four categories (dark green circles: Multicorer samples at Oder Bank; light green quadrate: van Veen samples at Oder Bank; dark blue circles: Multicorer samples at Arkona Basin; light blue quadrates: van Veen samples at Arkona Basin).

In Fig. 8 the nMDS plot and the cluster analysis of the abundance of species per square meter are shown. The nMDS analysis shows two groups and two single stations as outliers. Low stress value of 0.07 indicates good reliability of ordination (as a rule of thumb stress value above 0.2 is deemed suspect). The first group reflects the compact Oder Bank community, whereas the second one displays the more scattered Arkona Basin community. The outliers arise at the samples AB7MUC and AB8MUC. The cluster analysis supports the nMDS results. At the similarity level

of less than 10% a division between the two groups of samples corresponding to two different study sites and two single outliers emerged. Disregarding the two obvious outliers, the Arkona Basin community shows a high variability, clustering in subgroups at the similarity level of 40 to 80%. In addition, at the 50% similarity level, the Arkona Basin community splits into two divisions, the van Veen sampled and the Multicorer sampled fraction. The Oder Bank community holds a high similarity up to the 80% level, afterwards the data clusters into no apparent groups defined by the gear type.

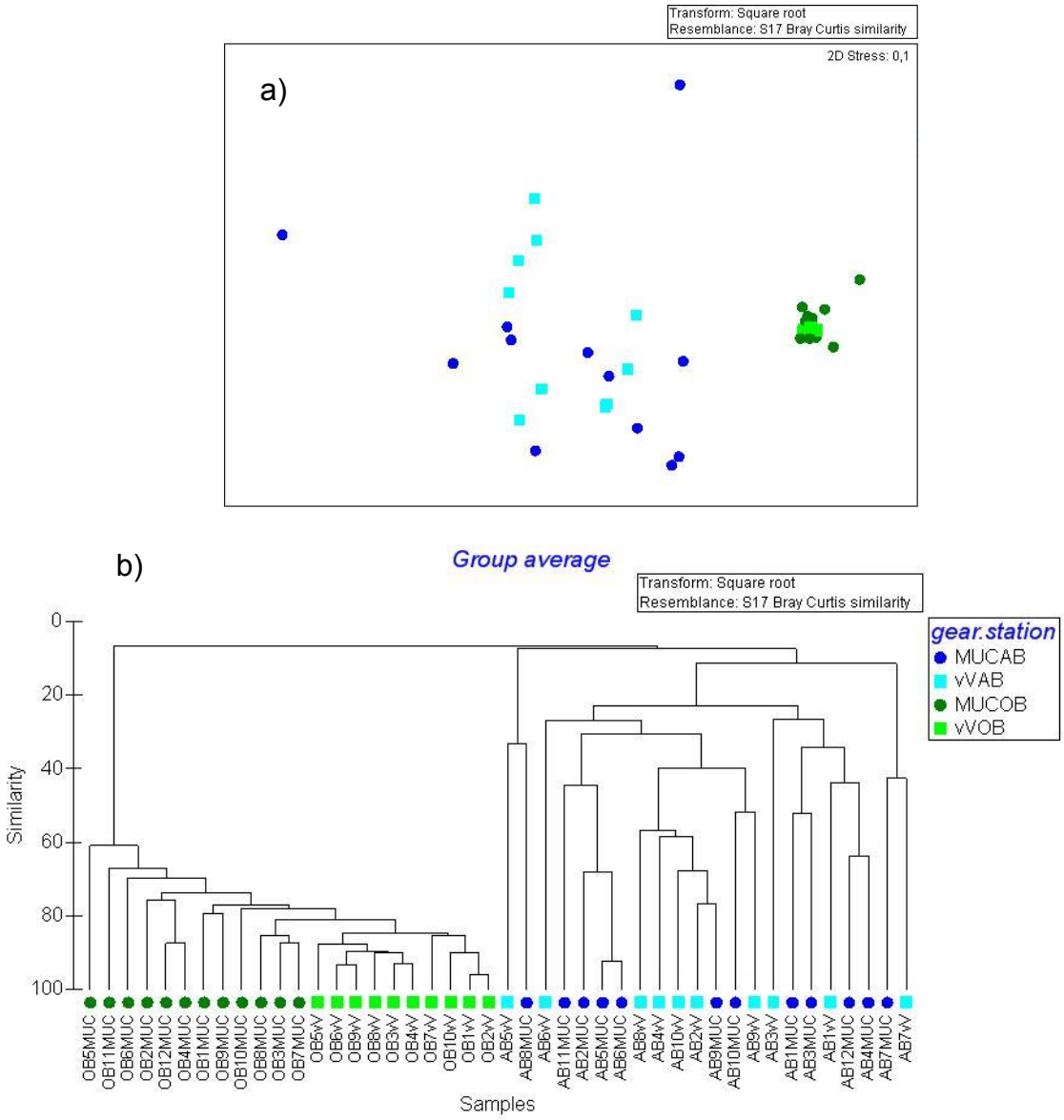


Fig. 9. The results of the a) nMDS plot and b) cluster analysis of the species wet weight per square meter are shown. As factors the gear type and station was used resulting in four categories (dark green circles: Multicorer samples at Oder Bank; light green quadrate: van Veen samples at Oder Bank; dark blue circles: Multicorer samples at Arkona Basin; light blue quadrates: van Veen samples at Arkona Basin).

Figure 9 shows the nMDS plot and cluster analysis of the species wet weight per square meter. With nMDS the same groups (Oder Bank community, Arkona Basin community, outliers: AB7MUC, AB8MUC) were evident as in the nMDS of the species abundance per square meter. However, the observed spreading was higher. Yet a stress value of 0.1 also indicated good reliability of ordination. The cluster analysis supports the nMDS but represents different results than the cluster analysis of the species abundance per square meter. The cluster analysis of the species wet weight per square meter shows a division into two groups, the Arkona Basin community and the Oder Bank community at the 10% similarity level. The Arkona Basin community clusters in many subgroups below the 30% similarity level. Stations sampled by different gear types appear in disordered arrangements. In contrast the Oder Bank community shows a similarity to the 60% level and clusters at the 80% similarity level into two subdivisions, the van Veen sampled and the Multicorer sampled group.

For the two sites differences in benthic communities, similarities within the communities and different abilities to form subsamples were identified. For this reason and due to highly different mean values the sites Arkona Basin and Oder Bank are treated separately below to analyse the effect of gear types and to estimate the minimal sampling unit size.

3.2. Analysis of abundance and biomass

The average values of abundance (n/sample and n/m²), biomass (g/sample and g/m²) and number of species per sample between the two gear types (van Veen grab and MUC) at both stations (Arkona Basin and Oder Bank) were compared. Subject to the test requirements, in all cases the variances were homogenously distributed. The normal distribution was tested by the Shapiro-Wilk-test with the result, that the abundance per sample and per square meter (MUC: AB p=0.5904, OB p=0.8411, vV: AB p=0.4377, OB p=0.6889), just as the number of species per square meter (MUC: AB p=0.2851, OB p=0.4387, vV: AB p=0.1446, OB p=0.2915) were normally distributed. In contrast the wet weight per sample and per square meter was not normally distributed (MUC: AB p=0.0003, OB p=0.002, vV: AB p=0.0087,

OB p=0.0026). According as, the data were followed a Gausschen distribution an analysis of variance or a non-parametrical Kruskal-Wallis-test was performed to test the average values on significant differences.

3.2.1. Comparison of the average values of the Arkona Basin community

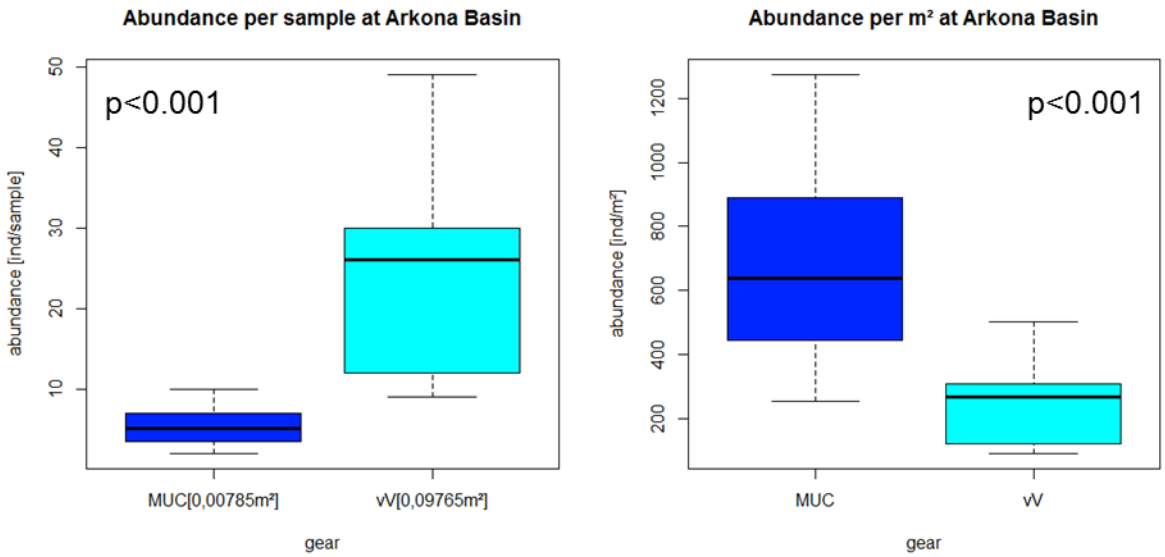


Fig. 10. Comparison of the average values of the abundance per sample [ind/sample] and abundance per square meter [ind/m²] by the factor gear type (Multicorer: dark blue, van Veen: light blue) of the Arkona Basin community, with p-values of the analysis of variance.

For the abundance of species per sample at the Arkona Basin an arithmetic mean of 5±2 (mean ± SD) ind/sample for the gear type MUC and 24±13 (mean ± SD) ind/sample for the gear type vV was determined. The median value mapped in Fig. 10 represents a value of 5 ind/sample for the MUC samples and of 26 ind/sample for the vV samples. The abundance of species per square meter shows a median value of 637 ind/m² for the MUC samples and a value of 266 ind/m² for the vV samples. The arithmetic mean constitute 679±304 (mean ± SD) ind/m² for the gear type MUC and 246±129 (mean ± SD) ind/m² for the gear type vV. The analysis of variance for the abundance per sample computed between the gear types MUC (0.01 m²) and vV (0.1 m²) shows a significant difference ($p<0.001$) among the average values. Likewise, the comparison of abundance values adjusted to the area of 1 square meter shows a significant difference between the gear types MUC and vV ($p<0.001$).

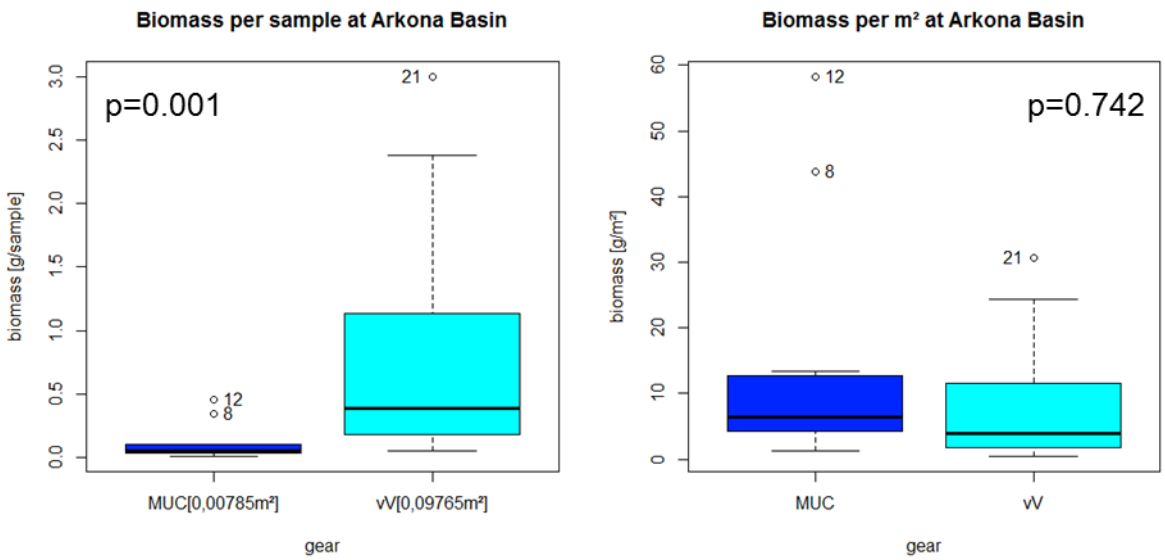


Fig. 11. Comparison of the average values of the biomass measured in wet weight per sample [g/sample] and wet weight per square meter [g/m²] by the factor gear type (Multicorer: dark blue, van Veen: light blue) of the Arkona Basin community, with p-values of the Kruskal-Wallis test.

The arithmetic mean of the species biomass per sample at Arkona Basin was calculated as 0.11±0.14 (mean ± SD) g/sample for the gear type MUC and 2.92±6.27 (mean ± SD) g/sample for the vV samples. In Fig. 11 the median values of the species biomass per sample constitute 0.05 g/sample for the MUC samples and 0.72 g/sample for vV samples are show, whereat the outlier number 18, originated by one large (40-45 mm, 18.78g) *Arctica islandica*, was excluded. The biomass per square meter shows an arithmetic mean of 13.99±17.80 (mean ± SD) g/m² for the gear type MUC and 29.88±64.28 (mean ± SD) g/m² for the gear type vV. The median values represent a value of 6.45 g/m² for MUC samples and 7.37 g/m² for vV samples. The non-parametrical Kruskal-Wallis test shows significant differences (p=0.001) of the average values for the biomass per sample between the factors MUC (0.01 m²) and vV (0.1 m²). For the calculation of average values for the biomass per square meter no significant differences (p=0.7416) were found.

3.2.2. Comparison of the average values of the Oder Bank community

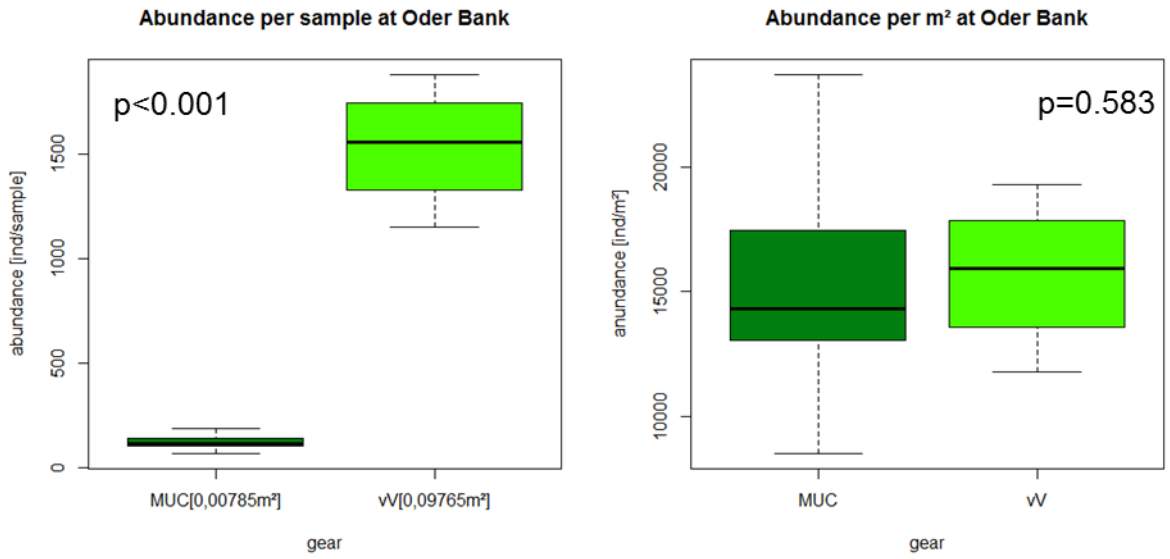


Fig. 12. Comparison of the average values of the abundance per sample [ind/sample] and abundance per square meter [ind/m²] by the factor gear type (Multicorer: dark green, van Veen: light green) of the Oder Bank community, with p-values of the analysis of variance.

The arithmetic mean of the species abundance per sample at Oder Bank constitutes 117±32 (mean ± SD) ind/sample for the MUC samples and 1547±248 (mean ± SD) ind/sample for the vV samples. The median values were 113 ind/sample for the gear type MUC and 1558 ind/sample for the gear type vV (Fig. 12). The abundance of species per square meter gives values of 15021±4079 (mean ± SD) ind/m² for MUC samples and 15850±2535 (mean ± SD) ind/m² for vV samples. As median values of the abundance 14331 ind/m² at MUC samples and 15950 ind/m² at vV samples were determined. The ANOVA reveals significant differences ($p<0.001$) between the mean values of the abundance per sample by the factors MUC (0.01 m²) and vV samples (0.1 m²). The abundance per square meter do not represent significant differences of the mean values ($p=0.583$) between the factors vV and MUC.

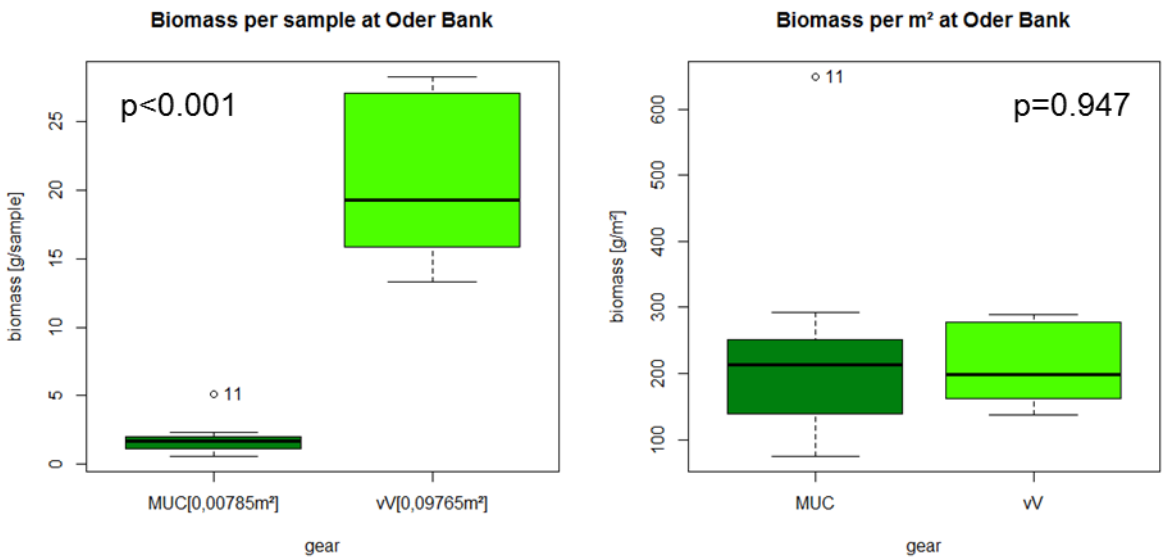


Fig. 13. Comparison of the average values of the biomass measured in wet weight per sample [g/sample] and wet weight per square meter [g/m²] by the factor gear type (Multicorer: dark green, van Veen: light green) of the Oder Bank community, with p-values of the Kruskal-Wallis test.

For the species biomass per sample at the Oder Bank an arithmetic mean of 1.79±1.15 (mean ± SD) g/sample for the MUC samples and of 20.36±5.56 (mean ± SD) g/sample for the vV samples was calculated. The median values of the species biomass per sample represent values of 1.67 g/sample for the gear type MUC and 19.31 g/sample for the gear type vV (Fig. 13). An arithmetic mean of the species biomass per square meter of 228.31±146.48 (mean ± SD) g/m² for MUC samples and of 208.45±56.90 (mean ± SD) g/m² for vV samples was determined. The median values constitute 212.64 g/m² for MUC samples and 197.77 g/m² for vV samples. The Kruskal-Wallis test measured a significant difference ($p<0.001$) between the biomass per sample of the gear type MUC (0.01 m²) and the gear type van Veen (0.1 m²). For the biomass per square meter no significant differences ($p=0.9474$) among the gear types MUC and vV were found.

3.3. Analysis of species richness

3.3.1. Comparison of the average values of the species richness

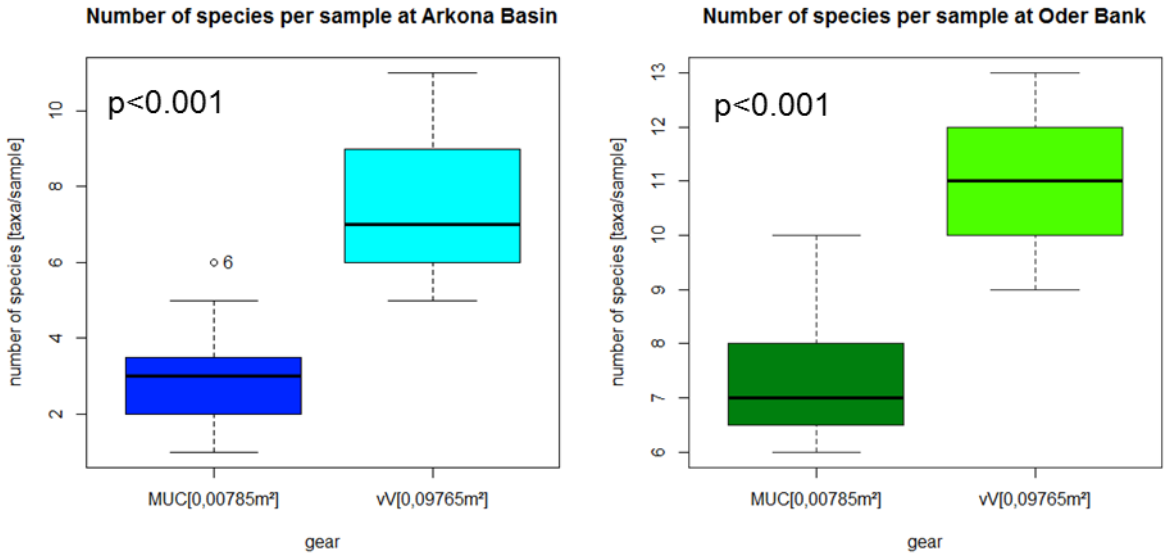
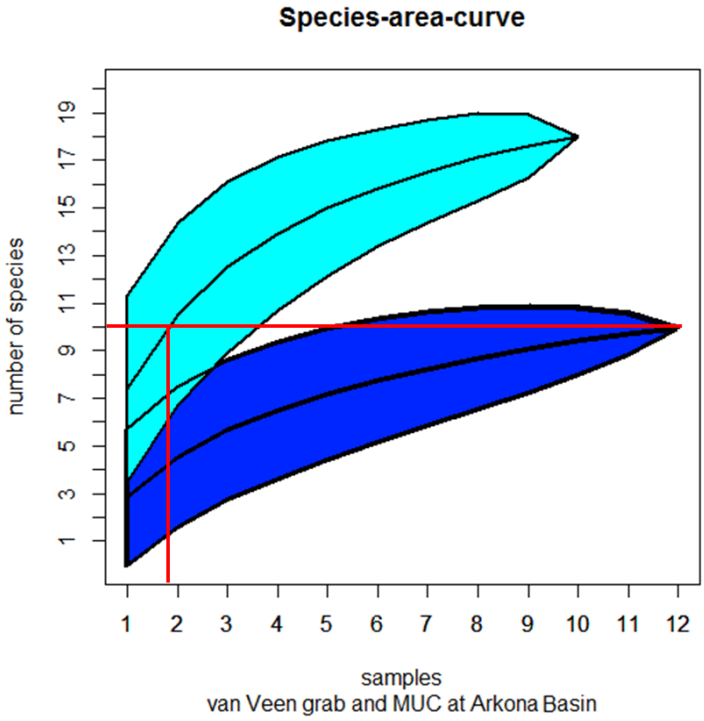


Fig. 14. Comparison of the average values of the number of species [taxa/sample] of the Multicorer samples with an area of 0.01 m² (dark) and van Veen samples with an area of 0.1 m² (light) at the Arkona Basin (blue) and Oder Bank (green).

The calculation of arithmetic mean of the number of species at the Arkona Basin resulted in 3±1 (mean ± SD) taxa/sample for the Multicorer samples and 8±2 (mean ± SD) taxa/sample for the van Veen grab samples (Fig. 14). The median values in Fig. 10 represent a value of 3 taxa/sample for MUC samples and 7 taxa/sample for vV samples. At the Oder Bank the arithmetic mean of the number of species constitutes 8±1 (mean ± SD) taxa/sample by Multicorer sampling and 11±1 (mean ± SD) taxa/sample by van Veen sampling. As median values the number of 7 taxa/sample at MUC samples and 11 taxa/sample at vV samples were determined. The analysis of variance for the number of species per sample computed between the gear types MUC (0.01 m²) and vV (0.1 m²) shows a significant difference ($p<0.001$) among the average values of the Arkona Basin, such as among the average values of the Oder Bank.

3.3.2. Analysis of species-area curves

To analyse the effect of the sample size as a factor of the number of species cumulative species-area curves were generated. The species-area curve represents the cumulative number of species against the cumulative number of samples. In the Figures 15 and 16 the van Veen grab and MUC samples are shown on the x-axis and the number of species on the y-axis. The area which arises by the number of samples for the gear type is shown in the legend.

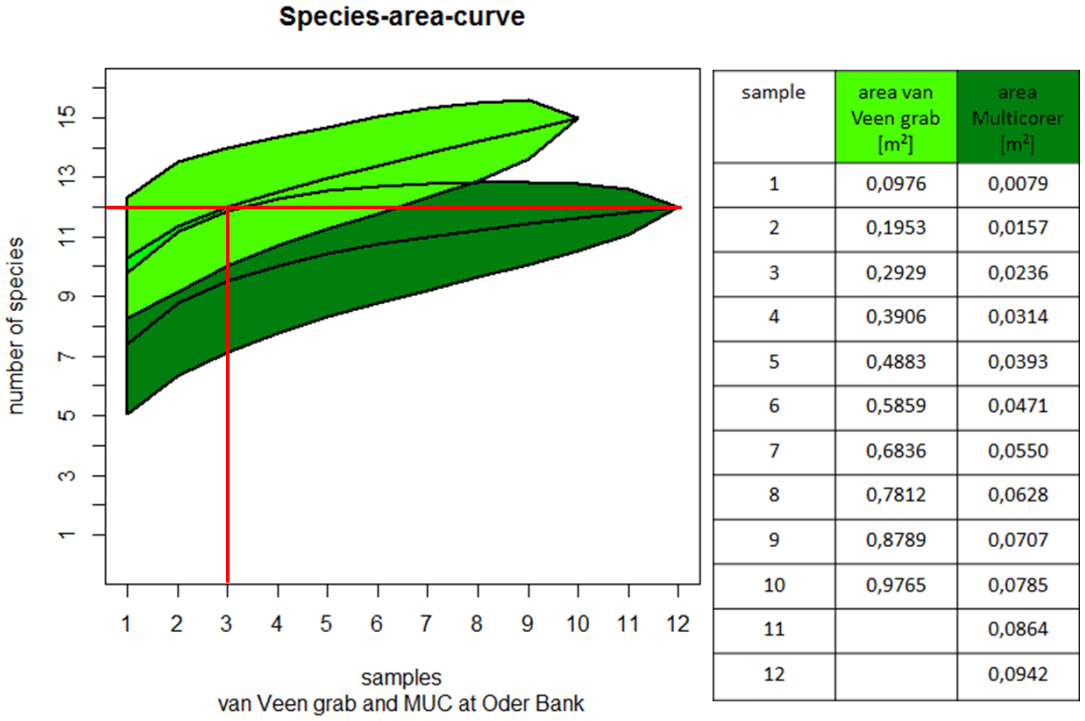


sample	area van Veen grab [m²]	area Multicorer [m²]
1	0,0976	0,0079
2	0,1953	0,0157
3	0,2929	0,0236
4	0,3906	0,0314
5	0,4883	0,0393
6	0,5859	0,0471
7	0,6836	0,0550
8	0,7812	0,0628
9	0,8789	0,0707
10	0,9765	0,0785
11		0,0864
12		0,0942

Fig. 15. Species-area curve of the number of species over the number of van Veen samples (light blue) and the Multicorer samples (dark blue) at Arkona Basin. The legend represents the sample area created by the number and type (van Veen and Multicorer) of samples. The red lines are showing the point, at which the same number of species sampled by 12 Multicorer are sampled by van Veen grab.

In Fig. 15 species-area curves with the number of species detected by the number of samples taken at the Arkona Basin are shown. Furthermore, the standard deviations of 1023 permutations for the van Veen grab and 4094 permutations for the Multicorer are specified. The curve that corresponds to Multicorer samples starts with 3±1.5 (mean ± SD) species at the first sample and rises to the maximum of

10±0.4 (mean ± SD) species in 12 samples. The van Veen grab curve is rising steeper than the MUC function. The van Veen curve represents a number of 7±1.9 (mean ± SD) species at the first sample to the number of 18±0.7 (mean ± SD) species in 10 samples. The MUC sampled 10 species in 12 samples with an area of 0.1 m². Notice that to sample the same number of species by van Veen grab, 2 samples with a total area of 0.2 m² are required. The functions increase quickly with the first 4 samples and progress slowly with the following samples. Both functions don't reach the asymptote so the number of species populating the habitat is not accomplished.



sample	area van Veen grab [m²]	area Multicorer [m²]
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8	0,7812	0,0628
9	0,8789	0,0707
10	0,9765	0,0785
11		0,0864
12		0,0942

Fig. 16. Species-area curve of the number of species over the number of van Veen samples (light green) and the Multicorer samples (dark green) at the Oder Bank. The legend represents the sample area created by the number and type (van Veen and Multicorer) of samples. The red lines are showing the point, at which the same number of species sampled by 12 Multicorer are sampled by van Veen grab.

In Fig. 16 the species-area curves shows the number of species found by the number of samples taken at the Oder Bank. In addition the standard deviations of 1023 permutations for the van Veen grab and 4094 permutations for the Multicorer are illustrated. The Multicorer function starts with 7±1.2 (mean ± SD) species at the first sample and rises to the maximum of 12±0.4 (mean ± SD) species in 12 samples.

The van Veen grab function and the MUC function are raising similar. The van Veen function represents a number of 10±0.5 (mean ± SD) species at the first sample to the number of 15±0.7 (mean ± SD) species in 10 samples. In 12 Multicorer samples with an area of 0.1 m² 12 species were found to the same number of species by van Veen grab three samples with an area of 0.3 m² needs to be sampled (red lines). The functions rise quickly with the first two samples than slowly. The functions don't reach the asymptote like the functions of the Arkona Basin.

3.4. Biological trait analysis

Fuzzy Component Analyses were performed to detect the influence of the sampling strategies on biological traits. To detect a general effect of the gear types Multicorer and van Veen grab, the abundance per square meter and the biomass per square meter of the species at the Arkona Basin and the Oder Bank were investigated (Fig. 17+18). Furthermore, the effect of the number of replicates was investigated (Fig. 19-22). Therefore, single FCAs of the species biomass per square meter for each station (Arkona Basin and Oder Bank) and each gear type were carried out. Fuzzy Component Analyses were performed by 9 biological traits with 35 modalities (Tab.2).

3.4.1.1. FCA of the abundance per m² of both sample types and stations

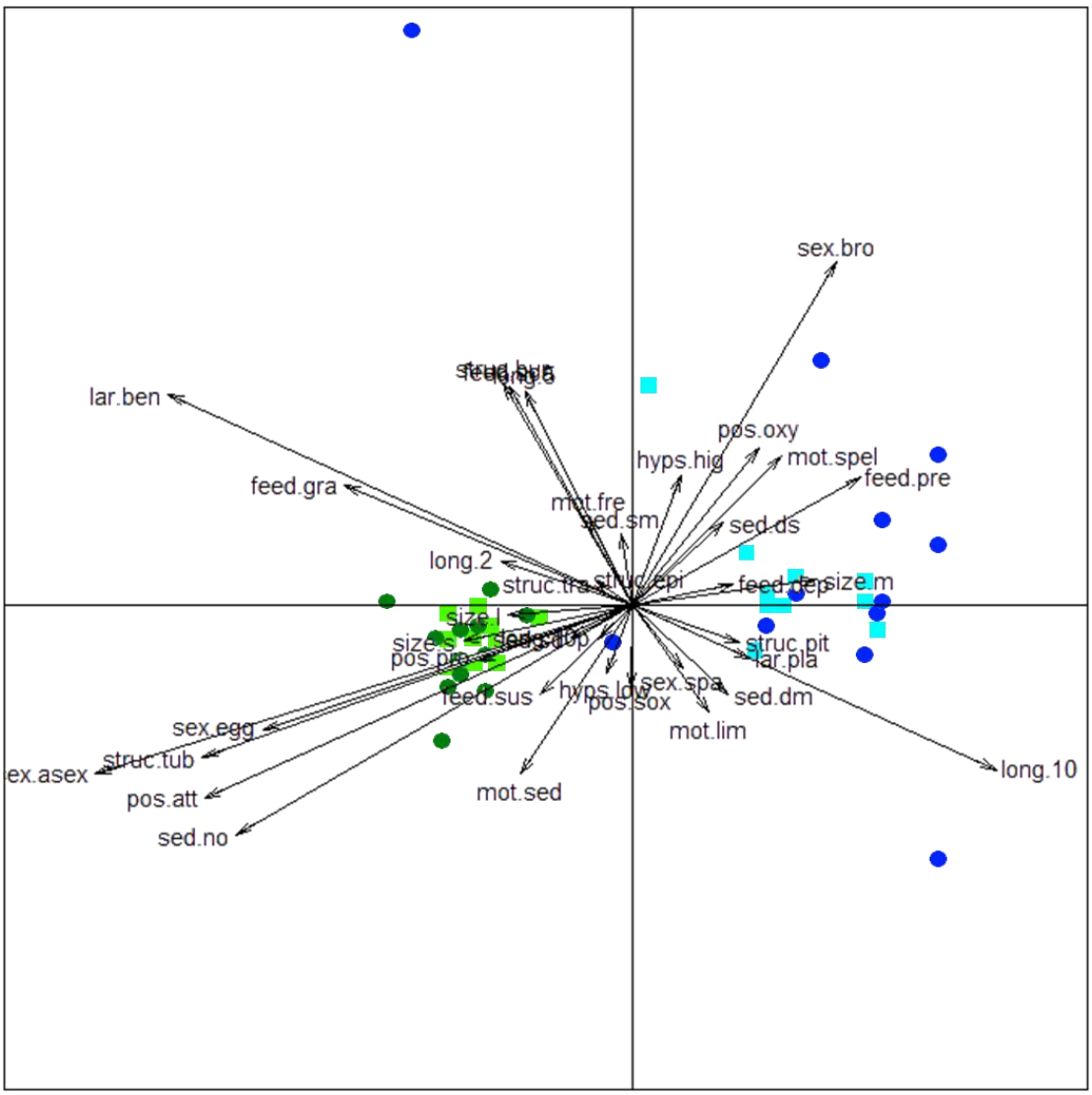

Fig. 17. The Fuzzy Component Analysis of the abundance per square meter of single replicates by the functional traits (Tab 2.) is mapped. Results of both sample types (Multicorer, van Veen) at Arkona Basin and Oder Bank are shown (dark green circles: Multicorer samples at Oder Bank; light green quadrate: van Veen samples at Oder Bank; dark blue circles: Multicorer samples at Arkona Basin; light blue quadrates: van Veen samples at Arkona Basin).

The Fuzzy Component Analysis of the abundance per square meter of single replicates by the functional traits shows two clusters: The compact Oder Bank cluster and the higher scattered Arkona Basin cluster (Fig. 17). At the Oder Bank the samples of the gear types are well mixed, thus no influence of the gear types appears. The Oder Bank community is characterised by the functional traits, no sediment transport (sed.no), attached position in sediment (pos.att), tube habitat structures (stuct.tub) and the reproductive techniques attached eggs (sex.egg) and asexual (sex.asex). The Arkona Basin community is higher scattered whereas the

Multicorer samples show higher differences than the van Veen grab samples. Apart from functional traits no clusters are formed. The main part of the Arkona Basin community depends on the functional traits, the feeding type predator (feed.pre) and deposit feeder (feed.dep), the reproductive technique brood (sex.bro), a medium body size (size.m) and longevity greater than 10 years (long.10). Furthermore, two outliers were found at the Arkona Basin sampled by Multicorer.

3.4.1.2. FCA of the biomass per m² of both sample types and stations

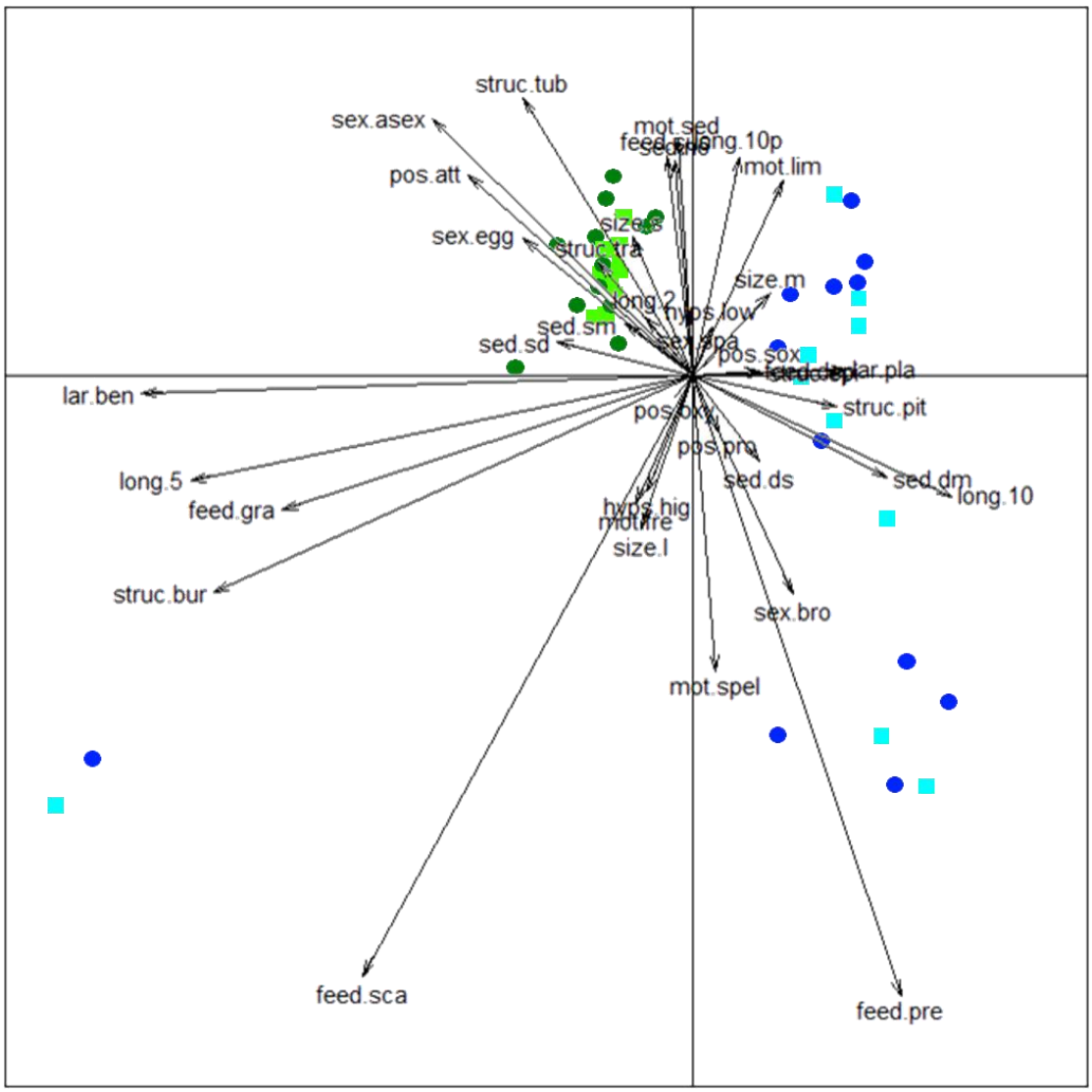

Fig. 18. The Fuzzy Component Analysis of the biomass in wet weight per square meter of single replicates by the functional traits (Tab 2.) is mapped. Results of both sample types (Multicorer, van Veen) at Arkona Basin and Oder Bank are shown (dark green circles: Multicorer samples at Oder Bank; light green quadrate: van Veen samples at Oder Bank; dark blue circles: Multicorer samples at Arkona Basin; light blue quadrates: van Veen samples at Arkona Basin).

The Fuzzy Component Analysis of the biomass per square meter of single replicates by the functional traits represents two clusters and two outliers (Fig. 18). The Oder Bank cluster is closer than the Arkona Basin cluster. At both sites the gear types MUC and vV are mixed. At the Oder Bank cluster the Multicorer samples are showing higher variances than the vV samples. But according to the functional traits no differences by the gear types were found.

The Oder Bank community is characterised by the functional traits habitat structure tube (struc.tub), an attached position in sediment (pos.att) and the reproductive techniques attached eggs (sex.egg) and asexual (sex.asex). The Arkona Basin cluster is drawn out so it is feasible to subdivide two clusters. The first cluster is explained by the functional traits, medium size (size.m), planktonic larvae (lar.pla), a habitat structure with hole, pit or non-permanent burrows (struct.pit) and a deep mixing sediment transport (sed.dm). The second cluster is characterised by the functional traits, reproductive technique brood (sex.bro) and the feeding type predator (feed.pre). The two outliers of the Arkona Basin are represented by one MUC and one vV sample and are depending on the functional traits, habitat structure burrow (struc.bur) and the feeding type scavenger (feed.sca).

3.4.2.1 FCA of the biomass per m² sampled by Multicorer at Arkona Basin

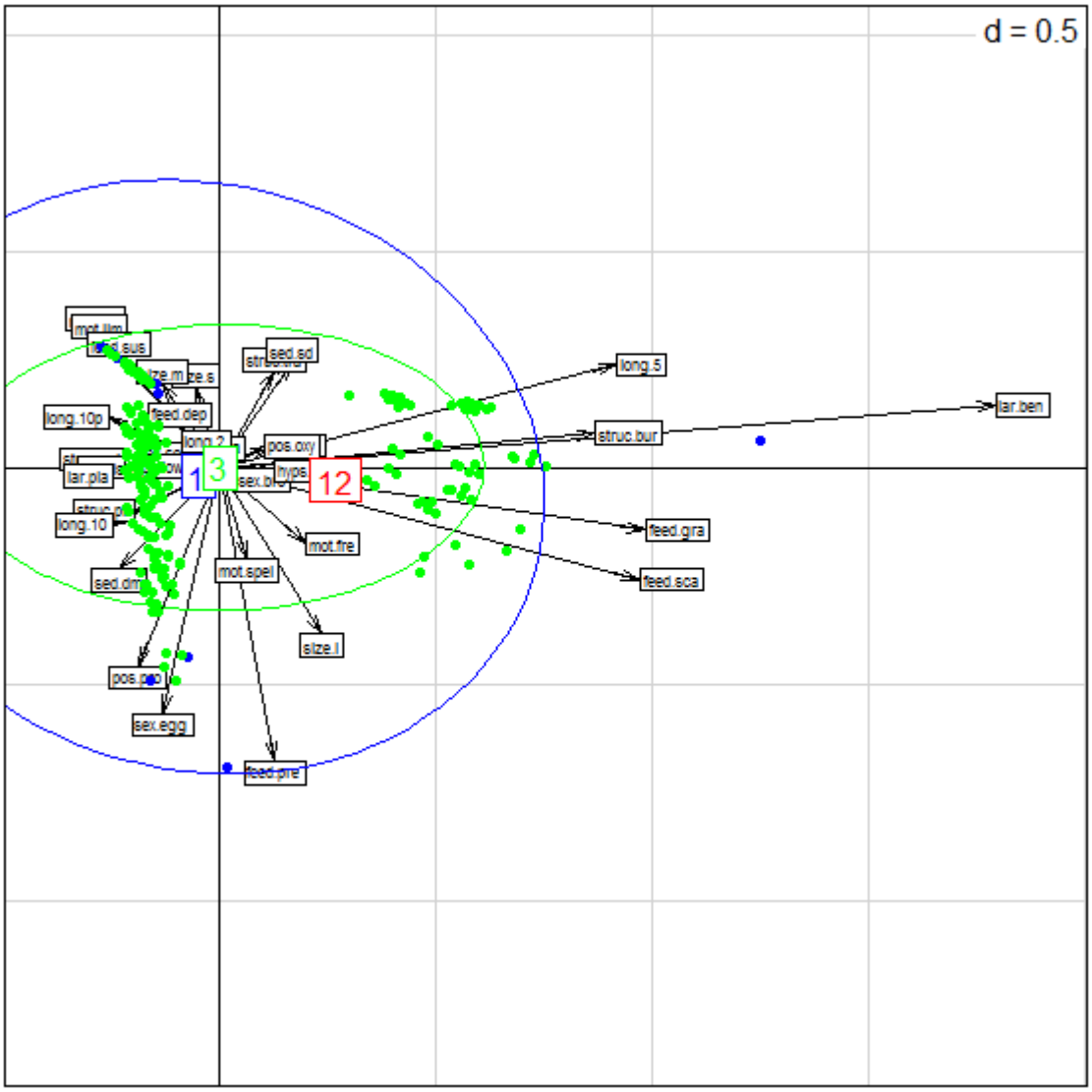

Fig. 19. The Fuzzy Component Analysis of the biomass in wet weight per square meter sampled by Multicorer at the Arkona Basin, by the functional traits (Tab 2.) is mapped. Thereby the distribution of the sample points by one replicate (blue), 3 replicates (green) and 12 replicates (red) are represented.

The Fuzzy Component Analysis of the biomass per square meter, sampled by Multicorer at the Arkona Basin, shows the distributions of the sample points by one replicate, 3 replicates and 12 replicates (Fig. 19). The sample points of the investigations by one replicate are scattered to 1.5. In contrast the sample points of the combination of 3 replicates are less scattered and drawn-out, up to 1 in the length and 0.5 in height. The combination of 12 Multicorer replicates combined to the central points of the single and 3 replicates is displaced to the height.

3.4.2.2. FCA of the biomass per m² sampled by van Veen grab at Arkona Basin

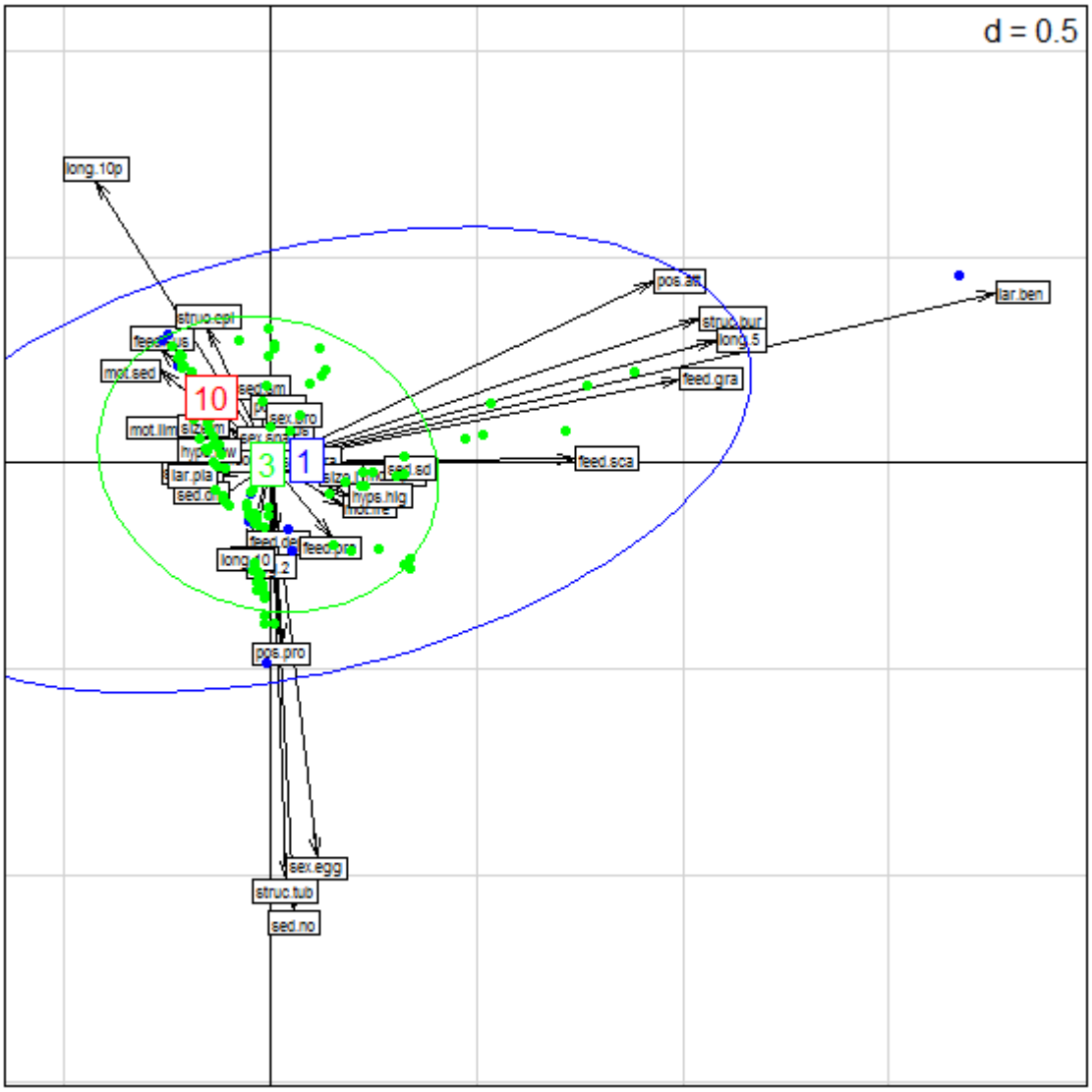

Fig. 20. The Fuzzy Component Analysis of the biomass in wet weight per square meter sampled by van Veen grab at the Arkona Basin, by the functional traits (Tab 2.) is mapped. Thereby the distribution of the sample points by one replicate (blue), 3 replicates (green) and 10 replicates (red) is represented.

In the Fuzzy Component Analysis of the biomass per square meter sampled by van Veen grab at the Arkona Basin, the distributions of the sample points by one replicate, 3 replicates and 12 replicates are represented (Fig. 20). The sample points of the investigations by 3 replicates are scattered to 0.8. This time the single replicate data points are drawn-out, to 2 in the length and 1 in the height. The combination of 10 van Veen grab samples is displaced to the upper left according to the central points.

By the comparison of the Fuzzy Component Analyses of the biomass per square meter at the Arkona Basin it becomes apparent that the biological traits of the species sampled by Multicorer and van Veen grab representing the same orientation. Further, with both gear types the combination of 3 replicates shows slighter variances in data points than the single replicates. But the variation of the data points sampled by Multicorer for the single and the 3 replicates are 20-25% higher than the variances of the data points sampled by van Veen grab.

3.4.2.3. FCA of the biomass per m² sampled by Multicorer at Oder Bank

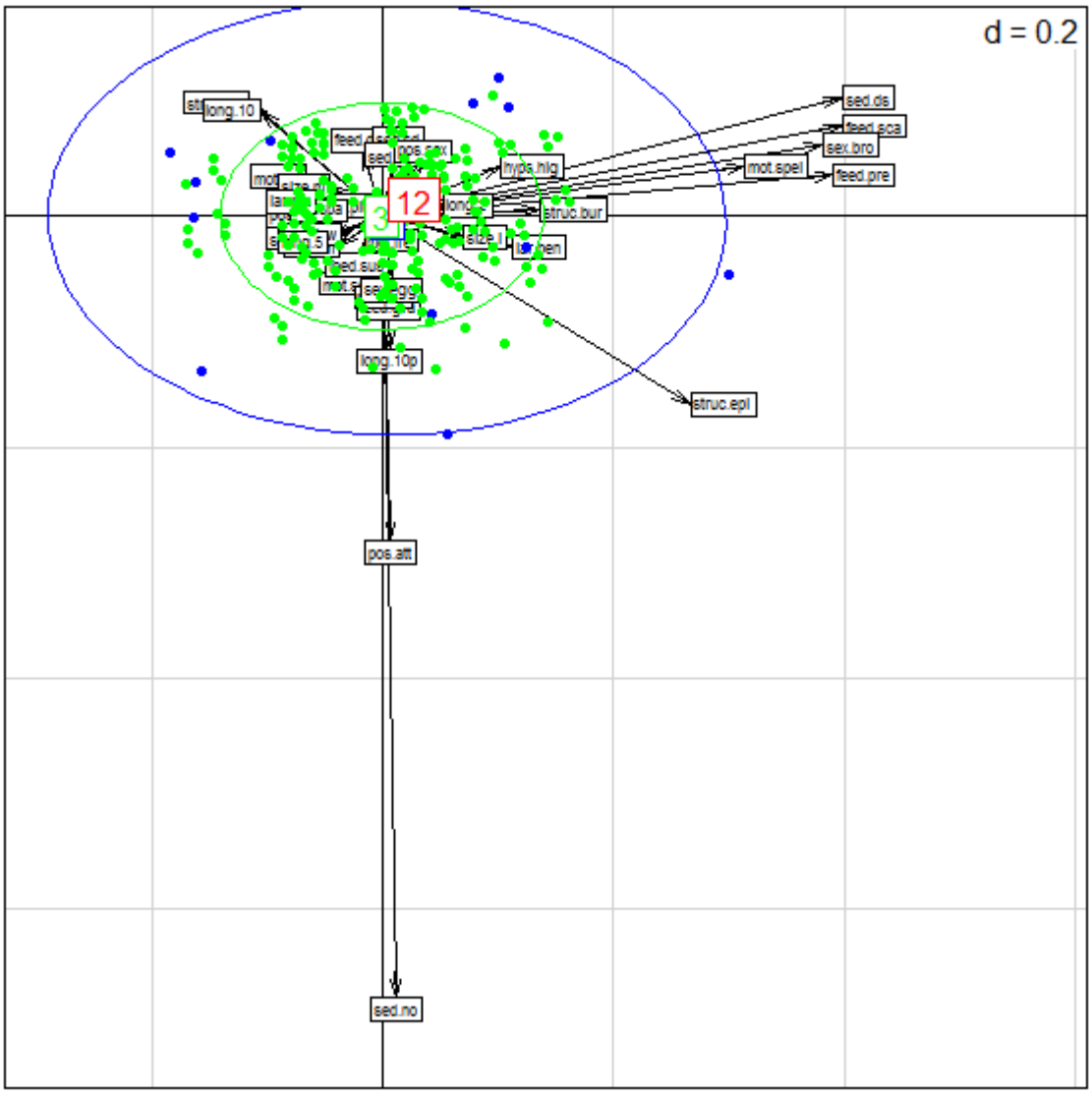

Fig. 21. The Fuzzy Component Analysis of the biomass in wet weight per square meter sampled by Multicorer at the Oder Bank, by the functional traits (Tab 2.) is mapped. Thereby the distribution of the sample points by one replicate (blue), 3 replicates (green) and 12 replicates (red) is represented.

The Fuzzy Component Analysis of the biomass per square meter sampled by Multicorer at the Oder Bank, represents the distributions of the sample points by one replicate, 3 replicates and 12 replicates (Fig. 21). The sample points of the investigations by 3 replicates are scattered to 0.3 and the sample points of the single replicates to 0.6. The scatterplots of both replicate combinations are oblate in the height (1 replicate: 0.4, 3 replicates: 0.2). This time the single replicate data points are drawn-out, to 2 in the length and 1 in the height. The combination of 12 Multicorer replicates is central located.

3.4.2.4. FCA of the biomass per m² sampled by van Veen grab at Oder Bank

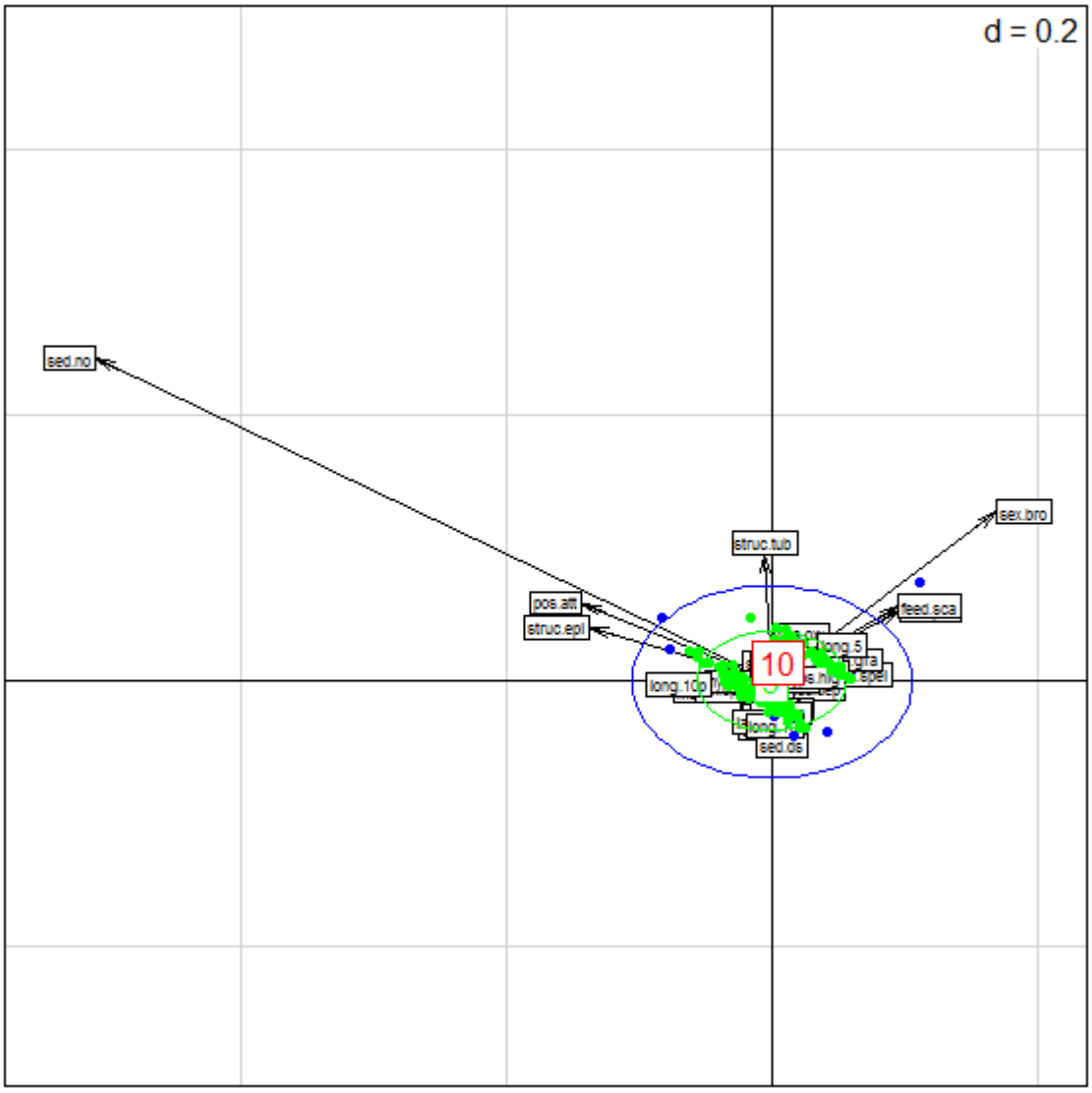

Fig. 22. The Fuzzy Component Analysis of the biomass in wet weight per square meter sampled by van Veen grab at the Oder Bank, by the functional traits (Tab 2.) is mapped. Thereby the distribution of the sample points by one replicate (blue), 3 replicates (green) and 10 replicates (red) is represented.

In the Fuzzy Component Analysis of the biomass per square meter sampled by van Veen grab at the Oder Bank, the distributions of the sample points by one replicate, 3 replicates and 12 replicates are represented (Fig. 22). The sample points of the investigations by 3 replicates are scattered to 0.1 and the single replicate data points are scattered to 0.2. Again both distributions are oblate in the height. The combination of 10 van Veen grab samples is mapped in the centre of the scatter-plot.

When comparing the Fuzzy Component Analyses of the biomass per square meter at the Oder Bank, it becomes obvious that the same biological traits are showing main effects of distribution, by Multicorer and van Veen grab. In both approaches with different gear types, the combination of 3 replicates shows smaller variances of the sample points, than the single replicates. According to the gear type the van Veen grab shows 50-60% slighter variances of the data points, than the Multicorer.

4. Discussion

The aim of this study was to investigate the influence of the gear types, Multicorer and van Veen grab, each with different sample sizes, on the description of ecosystem functioning expressed by the benthic community descriptors abundance, biomass, species richness and biological traits of two different sample sites. In order to find the best sampling strategy for those communities, without compromising between data accuracy and sampling effort, samples of two different benthic communities were taken with both gear types. The mean values of abundance and biomass between the sample types have been compared, species-area curves were constructed and Fuzzy Component Analyses were performed on data for different communities and gear types, in order to determine the influence of the sampling strategy.

4.1. Examination of the benthic communities

To explore differences between benthic communities, community analyses were performed. By multivariate analyses two different benthic communities were detected. On the similarity level of 10% the data splits into the Arkona Basin and Oder Bank community based on the abundance per square meter (stress: 0.07) and wet weight per square meter (stress: 0.1). That classification develops for the reason of different environmental factors as expected (e.g. Olenin, 1997; Laine, 2003; Ellis et al., 2006; Gogina et al., 2010). At the Arkona Basin an organic content of 12.42%, a grain size of 18 µm, a salinity of 15 PSU and oxygen contend of 6.31 mg/l were measured in 45.7 m depth. The Arkona Basin community includes 18 species with *Pontoporeia femorata*, *Macoma balthica* and *Arctica islandica* dominating (Fig. 23).

Fig. 23. Species dominating the Arkona Basin community: *Pontoporeia femorata*, *Macoma balthica* and *Arctica islandica* (pictured by Natalie Steiner).

Based on the abundance per square meter, the Arkona Basin community clusters into two groups, sampled by van Veen grab and sampled by Multicorer, and two outliers. The outliers AB7MUC and AB8MUC were taken by the same Multicorer haul (13°51.0382, 54°53.1228). That leads to the possible concern that local heterogeneity was detected, with a random chance to capture individuals that are not included in that abundant species. On the other hand, the locations of SECOS sampling stations are chosen to be at relatively homogenous areas. While reviewing the raw data it became apparent that at these samples only one species (*Alitta succianea*) is recorded that appears to be absent from other samples of the Multicorer sampled at Arkona Basin. However, the main species representing the community are missing, which is the reason for the outlying data points. As the other occurring species show no difference by comparing with the other samples, taken by Multicorer at the Arkona Basin, the outlying samples were not excluded of the following analyses to preserve natural data. The cluster analysis of the Arkona Basin by the abundance per square meter shows two clusters: the Multicorer sampled cluster and the van Veen sampled cluster (see explanation in section 4.2). As for the biomass per square meter no specific clusters were found. The Arkona Basin community shows higher variability of the abundance and biomass than the Oder Bank community.

The Oder Bank community shows a very high similarity, of up to 80% for the abundance per square meter and 60% for the biomass per square meter. At the Oder Bank environmental factors of 0.21% of organic content, 194 µm grainsize, 8.3 PSU salinity and 8.53 mg/l oxygen content in 15.2 m depth were recorded. In the Oder Bank community 16 species are occurring, here *Peringia ulvae*, *Mya arenaria* and *Cerastoderma glaucum* are the most abundant species (Fig. 24).

Fig. 24. Species dominating the Oder Bank community: *Peringia ulvae*, *Mya arenaria* and *Cerastoderma glaucum* (pictured by Natalie Steiner).

The cluster analysis of the biomass per square meter shows two groups by the factors van Veen grab and Multicorer, indicating that the van Veen grab samples are more equal, than the Multicorer samples. The reason for these clusters could not be identified, due to the fact that the two clusters are quite similar, holding a similarity of more than 80%. Looking at the abundance per square meter, no obvious clusters were detected by cluster analysis and nMDS ordination at the Oder Bank. Thus, it is apparent that variability of species composition between the two different habitats is obviously higher than the variability within samples of one benthic community obtained by different gear type. Therefore, the following analyses of the influence of gear type and sample unit size on the description of ecosystem functioning was performed separately for the two different and typical benthic communities, the more heterogeneous Arkona Basin community and the more homogenous Oder Bank community.

4.2. The influence of sampling strategies on the abundance and biomass

To discover the influence of the gear type with different sampling sizes on the abundance and biomass, comparisons of average value were undertaken. Thereby the effect of the factor gear type (van Veen grab, sampling area of 0.1 m^2, and Multicorer, sampling area of 0.01 m^2) on the distribution of variables abundance and biomass was tested. As to be expected, in every approach comparing values per sample, i.e. not adjusted to the same area, significant effect of the factor gear was identified. At both sites, Arkona Basin and Oder Bank, both abundance and biomass were significantly higher in van Veen grab samples (0.1 m^2) than the Multicorer samples (0.01 m^2). These results show that in samples with larger sample size and volume higher abundances and biomasses are found (U.S. EPA, 2001).

In the next step the sampling data were extrapolated to the area of 1 m^2. In order to test the possibility of comparing the results of Multicorer and grab samples, whereat no influence of the gear types with different sample sizes is hypothesized for area-adjusted abundance and biomass. At the Arkona Basin significant differences ($p<0.001$) of the mean values of the abundance per square meter between the gear types were detected. Consequently the gear types with different sample sizes show an effect on the results. The mean value of the abundance per square meter sampled by the Multicorer (679/m^2) is higher than the mean value for the grab

samples (246/m²). In addition, this result causes the two clusters, of van Veen grab and Multicorer samples developed by the cluster analysis. Considering the raw data, it comes apparent that especially juvenile Mollusca like, *Arctica islandica*, *Macoma balthica* and *Peringia ulvae,* occur rarely compared to the area sampled by the grab. It leads to the assumption, that those fragile organisms with a size range of 0-5 mm were destroyed while washing the samples on board, as a strong water-jet was used to wash the muddy sediments trough the sieve and thereby the effect, destructive for fragile small individuals, lasted for longer time. This sampling procedure mistake or artefact was not evident in for Multicorer samples, because the sampling volume was smaller and easier to handle. Furthermore, it also did not appear at sandy sample sites, because sandy sediments are more permeable and less compact and are therefore easier to wash out. Due to that it is advised to be highly careful during the rinsing process of van Veen grab samples on muddy sediments, which are broadly used as standard for benthic monitoring as indicated in Ruhmor (1990) and HELCOM (2010).

The species biomass per square meter at the Arkona Basin shows similar median values between the gear types van Veen grab (7.37 g/m²) and Multicorer (6.45 g/m²) and no significant differences were detected during the Kruskal-Wallis test. This result is opposite to the results for abundance per square meter and was not expected. As a consequence it could be assumed that organisms sampled by van Veen grab have to be heavier, to accomplish the same mean wet weight per square meter with significantly lower abundance per square meter. But this is not the case: in fact the mean biomass per square meter sampled by van Veen grab is regulated by one organism. The 40-45 mm large individual of *Arctica islandica* is a singleton with a wet weight of 18.78 g and affects the calculation. After excluding the singleton the computation results still do not confirm the assumption of existence of significant differences ($p=0.291$) between the biomass per square meter sampled by van Veen grab and Multicorer sampler at the Arkona Basin.

The comparisons of average values per square meter for the Oder Bank community indicated no significant differences for the abundance ($p=0.583$), nor for the biomass ($p=0.947$) per square meter. Thus, it is possible to compare the area-adjusted biomass and abundance results, of a small area sampled by 12 Multicorer samples (0.01 m²) which accords to the area of just one van Veen grab sample (0.1 m²), to the

results as brought by 10 van Veen grab samples (1 m²). Therefore, the use of core samplers with smaller sample sizes to detect the biomass and abundance per square meter, is possible for macrozoobenthic communities with slight variances, like the Oder Bank community on sandy sediments. It is not feasible to give a statement for communities with higher variances, like the Arkona Basin community, because assumptions could not be tested with the dataset available in this study. However, it is advised to take samples with a higher sample unit size for those heterogeneous communities where variances of the mean values are high.

In general this study demonstrates that it is an option to save sampling effort during the determination of abundance and biomass in homogenous communities like the Oder Bank by sampling a smaller area by smaller sample unit sizes (e.g. by the Multicorer), as suggested by the HELCOM (2010). The same results, that the sample size shows no significant differences in extrapolations per square meter for the abundance and biomass were reported by Pinna & Basset (2004) and Aguado-Gimenez et al. (2007). Different statements were given by Karakassis et al. (2013) and Lampadariou et al. (2005). Karakassis et al. (2013) showed that a large proportion of information of the abundance and biomass was lost when core samples were used, but with the addition that it was not feasible to exclude the possibility of methodological mistakes during the core sampling. Lampadariou et al. (2005) identified differences between the biomass values obtained by core sampling and van Veen sampling while sampling the same area.

In this section no instructions to coast-effectiveness approaches can be given because a high number of replicates was used. However, it is possible to compare area-adjusted abundance and biomass values of van Veen grab samples and core samples of homogenous communities as required in ISO 16665 (2014), but not for heterogeneous communities. To use the Multicorer sampling strategy actively to describe homogenous communities by smaller sample sizes, like suggested by HELCOM (2010), pre-testing of each community is essential. For investigations of heterogenic benthic communities with high variances in abundance, biomass and species richness it is advised against using smaller sample sizes.

4.3. The influence of sampling strategies on species richness

In order to determine the number of species, it is not possible to only compare mean values (Arkona Basin: MUC= 3/sample; vV= 8/sample; Oder Bank: MUC= 8/sample; vV= 11/sample) because the number of species recorded increases cumulatively with the cumulative number of samples. Therefore, species-area curves were constructed at which the cumulative number of species at the y-axis and the cumulative number of samples of the different gear types were plotted. At the Arkona Basin the species-area curve of Multicorer samples rises to 10 species in 12 samples with an area of 0.1 m². Compared to the Multicorer samples the van Veen sampled species-area curve rises steeper. The species-area curve sampled by van Veen grab found 18 species in 10 samples with an area of 1 m². Thus, to sample the same number of species that was found in the Multicorer samples 2 grab samples with an area of 0.19 m² are required. Similar results were found at the Oder Bank. The species-area curve shows 12 species in 12 Multicorer samples (0.1 m²) and 15 species in 10 van Veen grab samples (1 m²). At the Oder Bank, both functions rise quite similar but with the van Veen grab more species were found. It is expected to find the same number of species sampled by 12 Multicorer samples in three grab samples with a total area of 0.3 m² at the Oder Bank. So it is suggested that in the Multicorer samples more species were detected within a smaller sampling area. This confirms the result found by Sola et al. (1989) and can be attributed to the fact that with the increasing number of samples the number of recorded species increases. Due to the fact, that by multiple small samples more microhabitats with different species were sampled, than by fewer larger samples (Kon et al., 2015).

At both sites the functions increase quickly with the first samples (Arkona Basin: 4 samples, Oder Bank: 2 samples) and progress slowly with the following samples. So the species-area curve rises steeply and gradually levels off. Representing the relation that abundant taxa multiply quickly and rare taxa accrue slowly because they are only found in larger samples, as predicted by Jones et al. (1983). But neither the Multicorer function (that describes the sampled area up to 0.1 m²) nor the van Veen grab function (with higher number of species and with an area of 1 m² described) reaches the asymptote. That leads to the assumption that in this study the species richness of the different communities was not allocable, i.e. the

number of collected samples was not sufficient to satisfactorily describe species diversity. This effect is generated by singletons, species that occur just once per square meter or even more rarely. The same result was found by Ruhmor (2001), at which the number of singletons did not show any clear decrease with increasing sample effort. Riddle et al. (1989) proposes to exclude singletons from regression analyses and only include species that occur at densities >10 ind/m². In this study the raw data indicates that, especially at the Oder Bank station singletons are often composed of species living in the interface, such as *Bathyporeia pilosa, Crangon crangon or Neomysis integer*, which are difficult to sample by any sediment sampling technique. Therefore, it is advised to perform an additional dredge haul, to detect the highest level of species richness of a habitat (Jørgensen et al., 2011). However dredge sampling typically provides qualitative or semi-qualitative data. In any case, the species-area curves should be used as a criterion for decisions on sampling strategies with an objective to define the required minimum of sampling effort to obtain accurate results. Thus, the number of replicates for macrozoobenthic monitoring and especially for studies of ecosystem functioning should not be based on the total number of species, but more importantly should be targeted to include the dominant species which assign the ecosystem functions.

At the Arkona Basin total number of species found in 3 grab samples constituted 66% of all species found in 10 grab samples (18 taxa) and was higher than the overall number of species identified in all 12 Multicorer samples. Taking 4 grab samples resulted in the improvement of recording 77% of the total number of species found in 10 samples. Above 4 grab replicates the cost-efficiency of additional samples decreases because only one additional species per sample accrue. At the Oder Bank 3 grab samples provide 80% of the species that were found in 10 van Veen grab samples (15 taxa) and 100% of the species detected in 12 Multicorer samples. With additional samples, the cost-efficiency is reduced because less than one new species appear in each new sample. The most cost-effective sampling strategy for the van Veen grab samples at the Oder Bank is to take two samples by finding 73% of the species found in 10 van Veen grab samples, but thereby number of species recorded within the Multicorer samples summing to an area of one van Veen grab is not be reached. Therefore it is a good choice to sample an area of 0.3 m² by 3 van Veen grab samples to detect the number of abundant species in

heterogeneous communities like the Arkona Basin, but also in homogenous communities like Oder Bank community. Hence, the results of this investigation confirm the feasibility of the conventional approach to sample the species richness of abundant species to describe ecosystem functioning by 3 van Veen grab samples, just as recommended by ICES (Ruhmor, 1990) and HELCOM (2010).

4.4. The influence of the sampling strategies on biological trait analyses

The biological trait analysis was performed to investigate the influence of the gear type, with different sample unit sizes and the different combinations of replicates on the biological traits expression of two benthic communities. Thereby, Fuzzy Component Analyses of the abundance per square meter and the biomass per square meter showed high differences in biological traits by the benthic communities. In both calculations the Arkona Basin includes species, which are representing the functional traits, feeding type predator, reproduction technique brood, a medium body size and longevity greater than 10 years. The Oder Bank community is composed of species with the main functional traits, tube as habitat structure, an attached position in sediments and the reproductive techniques attached eggs and asexual. Furthermore, the influence of community homogeneity on the results of biological traits analyses becomes apparent. The highly homogenous Oder Bank community represents a compact scatter-plot and achieves the ordination of functional traits that is more straightforward, for interpreting compared with the ordination of traits for the Arkona Basin community. The latter is more scattered, and therefore the description of functional structure is more imprecise. In both calculations the sample points of the Multicorer and van Veen grab samples are mixed well within the communities. Thus, no influence of the gear type with different sample sizes on functional trait analyses by the abundance per square meter and biomass per square meter were identified.

In the next step the influence of different numbers of replicates was investigated. Fuzzy Component Analyses, of the biomass were undertaken, for each station and gear type with the different replicate combinations, single samples (MUC: 0.01 m^2, vV: 0.1 m^2), 3 replicates (MUC: 0.02 m^2, vV: 0.3 m^2) and 10 (vV: 1 m^2) or 12 (MUC: 0.1 m^2) replicates. In all approaches the data points of the combination of 3 replicates reflects more precise results than the single samples. At the Arkona Basin the combination of 10 grab samples and 12 Multicorer samples, as the most

precise measurements, showed variations of the central points of the single and the three replicate samples. This is explained by the heterogeneous community structure with high species richness proportional to low abundances and biomasses. At the Oder Bank station all central points of the approaches with different replicates are centred as a sign of high similarity of the community. As it is not possible for cost-effective and time-consuming reasons to sample 10 or 12 samples the number of 3 replicates is an opportunity to catch the functional variance of the community that is otherwise not sampled representatively by each one single sample. To take 3 replicates at each station confirms the HELCOM guidelines and allows computing statistical calculations, with statistical integrity ensured.

To investigate the influence of the gear type with different sample sizes, as a result of the combination of different sample unit sizes and replicates, the spread of the scatter-plots between the gear types was compared. At the Arkona Basin it becomes apparent that the main biological traits sampled by the different gear types represent the same orientation. However, the variances of the data points between the gear types are different, thus the single and 3 replicates sampled by Mulitorer showed 20-25% higher variances than the data points sampled by van Veen grab. At the Oder Bank station, it becomes obvious that both gear types are showing the same characteristic biological traits. According to the gear type 50-60% lower variances of data points were detected by van Veen grab sampling compared to Multicorer sampling.

In consequence of this investigation it is advised to sample at least 3 replicates to improve the results of the single samples. Furthermore, at both stations, with a homogenous and heterogeneous benthic community, the van Veen grab sampler showed 20-50% lower variance of the results than the Multicorer approach. Hence, a higher sampling area caused by van Veen grab should be accepted in order to achieve the accuracy of the results. Even if the analyses showed the same biological traits for both communities and gear types it is risky to sample smaller areas, because a smaller sampling area reduces the species richness recorded, which affects the description of functional diversity and ecosystem functioning (Törnroos et al., 2015) (Fig. 25).

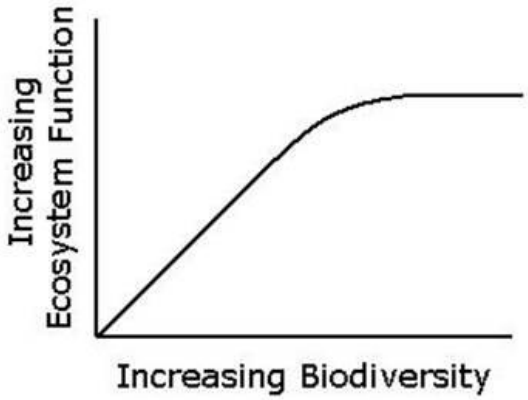

Fig. 25. The positive correlation of increasing ecosystem function and increasing biodiversity (Globalchange, 2006).

4.5. Conclusion

This study was undertaken to investigate the influence of different sampling strategies with different sampling sizes and the number of replicates on the description of ecosystem functioning. The possibility of comparable use of the core sampling approach and van Veen grab sampling, with keeping the ecological validity and accuracy was addressed. This is relevant, because both types of samplers are broadly used in different national monitoring programs (ISO 16665, 2014).

As it was expected, this study showed high influences of the benthic community structure on the description of the ecosystem functioning derived by different sampling strategies. For the homogenous Oder Bank community representative results are obtained for the investigated descriptors, even with a small area sampled by Multicorer. The less homogenous Arkona Basin community showed results with higher variance and absolute values of species richness, at the same time when total abundance and biomass were lower.

The influence of the sampling strategy on the description of ecosystem functioning by abundance, biomass, species richness and biological traits in both communities were estimated as followed. For the area-adjusted abundance and biomass derived by the two types of sampling gears similar mean values were found for the homogenous Oder Bank community. So, it is possible to compare the results of homogenous communities sampled by Multicorer and van Veen grab as described in

ISO 16665 (2014) and HELCOM (2010). But for the more heterogeneous community the gear type showed an effect resulting in variable mean values and lack of feasibility in comparable use. Thus, it is not advisable to use Multicorer samples with small areas for heterogeneous communities.

The cumulative species richness represents differences between the gear types, corresponding to the sampling sizes, as expected. Thereby, higher effectivities were indicated by the van Veen sampling strategy. The same number of species that were sampled by 12 Multicorer samples were found in 3 van Veen grab samples, which sampled a higher area but required lower amount of work at sea. Therefore, 3 samples of van Veen grab samples should be sampled to estimate the species richness.

No obvious effect of sampling strategy on the description of ecosystem functioning expressed by characteristic biological traits was detected, based on the single samples. On the other hand, the combination of 3 replicates sampled by van Veen grab seems to be the best approach to analyse biological traits. The combination of 3 replicates delivers better results in terms of capturing the functional variability, than the single sample approaches, and is more cost-efficient then sampling 10 replicates. Furthermore, the van Veen grab samples showed higher trait similarity within samples than the Multicorer sample results.

These results showed that it is advisable to use the standard sampling strategy, with 3 replicates of van Veen grab to describe ecological functioning, like recommended by HELCOM, ICES and WFD. Because the use of Multicorer samples, with a smaller sampling size showed higher variations in mean based studies and is not able to detect the same proportion of biodiversity in terms of species richness as van Veen grab samples. So, the Multicore sampling strategy is not able to keep the high accuracy given by van Veen grab samples. To summarize, it is possible to compare existing approaches of both sample types for homogenous communities. But, for further gain of data, required to describe ecosystem functioning and ecosystem services of different benthic communities, it is advised to use the standard sampling approach to get sufficiently accurate and representative data.

References

Aguado-Giménez, F., Marín, A., Montoya, S., Marín-Guirao, L., Piedecausa, A., García-García, B. (2007): Comparison between some procedures for monitoring offshore cage culture in western Mediterranean Sea: sampling methods and impact indicators in soft substrata, Aquaculture 271, 357-370

Arrhenius, O. (1921): Species and area, Journal of Ecology 4, 68-73

Berg, T., Fürhaupter, K., Teixeira, H., Uusitalo, L., Zampoukas, N. (2015): The Marine Strategy Framework Directive and the ecosystem-based approach - pitfalls and solutions, Marine Pollution Bulletin 96, 18-28

Bergström, S., Carlsson, B. (1994): River runoff to the Baltic Sea: 1950-1990, The American Biology 23, 280-287

Bilyard, G.R. (1987): The values of benthic infauna in marine pollution monitoring studies, Marine Pollution Bulletin 18, 581-585

Bobertz, B., Harff, J. (2004): Sediment facies and hydrodynamic setting, a study in the south western Baltic Sea, Ocean Dynamics 54, 39-48

Bonsdorff, E., Norkko, A., Boström, C. (1995): Recruitment and population maintenance of the bivalve Macoma balthica - factors affecting settling success and early survival on shallow sandy bottoms, Biology and Ecology of Shallow and Coastal Waters 28, 253-260

Borja, A., Muxilka, I., Franco, J. (2003): The applications of a marine biotic index to different , The application of a marine biotic index to different impact sources affecting soft-bottom benthic communities along European coasts, Marine Pollution Bulletin 46, 835-845

Bremner, J., Rogers, S., Frid, C. (2006): Methods for describing ecological functioning of marine benthic assemblages using biological traits analysis (BTA), Ecological Indicators6, 609-622

Bremner, J. (2008): Species traits and ecological functioning in marine conservation and management, Journal of Experimental Marine Biology and Ecology 366, 37-47

Chevenet, F.,Doledec, S., Chessel, D. (1994): A fuzzy coding approach for the analysis of long-term ecological data, Freshwater Biology 31, 295-309

Christiansen, C., Edelvang, K., Emeis, K., Graf., Jähmlich, S., Kozuch, J., Laima, M,, Leipe, T., Löffler, A., Lund-Hansen, L.C., Miltner, A., Pazdro, K., Pempkowiak, J., Shimmield, G., Shimmield, T. Smith, J., Voss, M., Witt, G. (2002): Material transport from the nearshore to the basin environment in the Southern Baltic Sea I: Processes and mass estimates, Journal of Marine Systems 35, 133-150

Clarke, K.R., Gorley, R.N. (2006): PRIMER v&: User Manual/Tutorial, PRIMER-E, Plymouth, 192pp

Clarke, K.R., Warwick, R.M. (2001): Change in marine communities: an approach to statistical analysis and interpretation, 2nd edition, PRIMER-E, Plymouth, 172pp

Colwell, R.K., Mao, C.X., Chang, J. (2004): Interpolating, extrapolation, and comparing incidence-based species accumulations curves, Ecology 85, 2717-2727

Connor, E.F., McCoy, E.D. (2001): Species-area Relationships, Encyclopaedia of Biodiversity 5, 397-411

Costanza, R., Darge, R., Degroot, R., Farber, S., Grasso, M., Hannon, B., Limburg, K., Naeem, S, Oneill, R.V., Paruelo, J., Raskin, R.G., Sutton, P., Vandenbelt, M. (1997): The value of the world's ecosystem sevices and natural capital, Nature 387, 253-260

Darr, A., Gogina, M., Zettler, M.L. (2014): Functional changes in benthic communities along a salinity gradient - a western Baltic case study, Journal of Sea research 85, 315-324

Darr, A., Gogina, M., Zettler, M.L. (2014): Detecting hot-spots of bivalve biomass in the south-western Baltic Sea, Journal of Marine Systems 134, 69-80

Diaz, S., Cabido, M. (2001): Vive la difference: plant functional diversity matters to ecosystem processes, Trends in Ecology & Evolution16, 646-655

Downing J. A. (1984): Sampling the Benthos of Standing Waters

Dray, S., Dufour, A.B. (2007): The ade4 package: implementing the duality diagram for ecologists, Journal of Statistical Software 22, 1-20

Ellis, J., Ysebaert, T., Hume, T., Norkko, A., Bult, T., Herman, P., Thrush, S., Oldman, J. (2006): Predicting macrofaunal species distribution in estuarine gradients using logistic regression and classification systems, Marine Ecology Progess Series 316, 69-83

Engen, S. (2007): Heterogeneous communities with lognormal species abundance distribution: Species-area curves and sustainability, Journal of Theoretical Biology 249, 791-803

EU Water Framework Directive (2000): Directive 2000/60/EC of the European Parliament and of the Council establishing a framework for the community action in the field of water Policy,

http://ec.europa.eu/environment/water/water-framework/indes_en.html

Fattorini, S. (2006): To fit or not to fit? A poorly fitting procedure produces inconsistent results when species-area relationship is used to locate hotspots, Biodiversity and Conversation 16, 2531-2538

Ferraro, S.P., Cole, F.A., Deben, W.A., Swartz, R.C. (1989): Power cost efficiency of eight macrobenthic sampling schemes in Puget Sound, Washington, USA, Canadian Journal of Fisheries and Aquatic Sciences 46, 2157-2165

Friedland, R., Neumann, T., Schernewski, G. (2012): Climate change and the Baltic Sea action plan: model simulations on the future of the western Baltic Sea, Journal of Marine Systems 105, 175-186

Fox, J. (2005): The R Commander: A Basic Statistics Graphical User Interface to R, Journal of Statistical Software 14, 1-42

Geomar: picture of Multicorer,

(http://www.geomar.de/index.php?id=518&no_cache=1&tx_geoexpedition_pi1%5bid%5d=319134)

Globalchange (2006): Relationship between Diversity and ecosystem functioning,

(http://www.globalchange.umich.edu/gctext/Inquiries/Inquiries_by_Unit/Unit_4.htm)

Glockzin, M., Zettler, M.L. (2008): Spatial macrozoobenthic distribution patterns in relation to major environmental factors- A case study from Pomeranian Bay (southern Baltic Sea), Journal of Sea research 59, 144-161

Gogina, M., Glockzin, M., Zettler, M.L. (2010): Distribution of benthic macro-faunal communities in the western Baltic Sea with regard to near-bottom environmental parameters. 1. Causal analysis, Journal of Marine Systems 79, 112-123

Gogina, M., Darr, A., Zettler, M.L. (2014): Approach to assess consequence of hypoxia disturbance events for benthic ecosystem functioning, Journal of Marine Systems 129, 203-213

Gotelli, N.J., Colwell, R.K. (2001): Quantifying biodiversity: procedures and pitfalls in the measurements and comparison of species richness, Ecology Letters 4, 379-391

Gustafsson, B.G. (2001): Quantification of water, salt, oxygen and nutrient exchange of the Baltic Sea from observations in the Arkona Basin, Continental Shelf Research 21, 1485-1500

Harte, J., Smith, A.B., Storch, D. (2009): Biodiversity scales from plots to biomes with a universal species-area curve, Ecological Letters 12, 789-797

HELCOM (2010): Manual for marine monitoring in the COMBINE programme of HELCOM, Annex C-8 Soft Bottom Macrozoobenthos

(http://www.helcom.fi/groups/monas/CombineManual/AnnexesC/en_GB/annex8)

HELCOM, (2013): Manual for Marine Monitoring in the COMBINE Programme of HELCOM**,**

(http://helcom.fi/Documents/Action%20areas/Monitoring%20and%20assessment/Manuals%20and%20Guidelines/Manual%20for%20Marine%20Monitoring%20in%20the%20COMBINE%20Programme%20of%20HELCOM.pdf)

Hubbell, S.P. (2001): The Unifield Neutral Theory of Biodiversity and Biogeograpy, Princeton University Press.

IfAÖ: picture of van Veen grab

(http://www.ifaoe.de/referenzen/benthische-organismen-habitate/projekt-8/)

ISO 16665 (2014): Water quality - Guidelines for quantitative sampling and sample processing of marine soft-bottom macrofauna ,

(http://www.iso.org/iso/catalogue_detail.htm?csnumber=54846)

Jones, G.T., Grayson, D.K., Beck; C. (1983): Artefact class richness and sample size in archaeological assemblages, Anthropological Papers 72, Museum of Anthropology, 55-73

Jørgensen, L.L., Renaud, P.E., Cochrane, S.K.J. (2011): Improving benthic monitoring by combining trawl and grab surveys, Marine Pollution Bulletin 62, 1183-1190

Karakassisa, I., Dimitriou, P. D., Papageorgioua, N., Apostolakib, E. T., Lampadarioub, N., Black, K. D. (2013): Methodological considerations on the coastal and transitional benthic indicators proposed for the Water Framework Directive, Ecological Indicators 29, 26-33

Kindt, R. (2003): Exact species richness for sample-based accumulation curve, Biodiversity and Conservation 10, 3235-3249

Kindt, R., Oksanen, J. (2015): specaccum [vegan] Species Accumulation Curves, version 2.0-10

(http://www.inside-r.org/packages/cran/vegan/docs/boxplot.specaccum)

Kirstensen, E., Delefosse, M., Quintana, C.O., Flindt, M.R., Valdemarsen, T. (2014): Influence of benthic macrofauna community shifts on ecosystem functioning in shallow estuaries, Frontiers in Marine Science 1, 41

Kohn, D.D., Walsh; D.M. (1994): Plant species richness - the effect of island size and habitat diversity, Journal of Ecology 82, 367-377

Kon, K., Tsuchtaka, Y., Sato, T., Shinagawa, H., Yamada, Y. (20015): Role of microhabitat heterogeneity in benthic faunal communities in sandy bottom sediments of Oura Bay, Shioda, Japan, Regional Studies in Marine Science, in press

Kuhrts, C., Seifert, T., Fennel, W. (2006): Modelling transport of fluff layer material in the Baltic Sea, Hydrobiologia 554, 25-30

Laine, A.O. (2002): Distribution of soft-bottom macrofauna in the deep open Baltic Sea in relation to environmental variability, Estuarine, Coastal and Shelf Science 57, 87-97

Lampadariou, N., Karakassis, I., Pearson, T. H. (2005): Cost/benefit analysis of a benthic monitoring programme of organic benthic enrichment using different sampling and analysis methods, Maine Pollution Bulletin 50, 1606-1618

Lass, H.U., Mohrholz, V., Seifert, T. (2001): On the dynamics of the Pomeranian Bight, Continental Shelf Research 21, 1237-1261

Leipe, T., Eidam, J., Lampe, R., Meyer, H., Neumann, T., Osadczuk, A., Janke, W., Puff, T., Blanz, T., Gingele, F.X., Dannenberger, D., Witt, G. (1998): Das Oderhaff-Beiträge zur Rekonstruktion der holozänen geologischen Entwicklung und anthropogenen Beeinflussung des Oder-Ästuars, Meereswissenschaftliche Berichte 28, 1-61

Legendre, P., Legendre, L. (1998): Numerical ecology, Second English edition. Developments in Environmental Modelling, 20. Elsevier Science B.V., Amsterdam

Lyman, R. L., Kenneth, M.A. (2007): On the use of species-area curves to detect the effects of sample size, Journal of Archaeological Science 34, 1985-1990

MacArthur, R.H., Wilson, E.O. (1967): The Theory of Island Biogeography, Princeton University Press

Mashayekhi, M., MacPherson, B., Gras, R. (2014): Species-area relationship and a tentative interpretation of the function coefficients in an ecosystem simulation, Ecological Complexity 19, 84-95

Mikulski, Z. (1966): Wasserhaushalt der baltischen Haffe, Beiträge zur Meereskunde 19, 5-17

Miltner, A.M., Emeis, K. (2000): Origin and transport of terrestrial organic matter from the Oder lagoon to Arkona Basin, Southern Baltic Sea, Organic Geochemistry 31, 57-66

Myers, N., Mittermeier, R.A., Mitterweier, C.G., da Fonseca, G.A.B., Kent, J. (2000): Biodiversity hotspots for conservation priorities, Nature 403, 853-858

Neumann, G., Bublitz, G. (1968): Seegrunduntersuchungen im westlichen Teil der Oder-Bucht, Beitrag Meereskunde 24/25, 81-109

Neumann, T., Leipe, T., Brand, T., Shimmield, G. (1996): Accumulation of heavy metals in the Oder estuary and is off-shore basins, Chemie der Erde 56, 207-222

Ojaveer, E., Kalejs, M. (2008): On ecosystem-based regions in the Baltic Sea, Journal of Marine Systems 74,672-685

Oksanen, J., Guillaume, F.B., Kindt, K., Legendre, P., Minchin, P.R., O'Hara, R.B., Simpson, G.L., Solymos, P., Stevens, H.H., Wagner, H. (2015): vegan: Community Ecology Package, R package version 2.2-1

Oliveira, R.B.S., Mugnai, R., Castro, C.M., Baptista, D.F. (2011): Determining subsampling effort for the development of a rapid bioassessment protocol using benthic macroinvertebrates in streams of Southeastern Brazil, Environmental Monitoring and Assessment 175, 75-85

Tauber, F. (2012): Meeresbodensedimente in der deutschen Ostsee/Seabed sediments in the German Baltic Sea, Hamburg, Rostock: Bundesamt für Seeschifffahrt und Hydrographie. 9 Map Sheets,

(http://www.bsh.de/de/Produkte/Karten/Geologische_Karten/index.jsp)

Tett, P., Gowen, R.J., Painting, S.J.,Elliott, M., Forster, R., Gilpin, L.C.; Huxham, M., McQuatters-Gollop, A.L., Malcom; S.J., Sau-Picart, S., Platt, T., Racault, M.F., Sathyendranath, S., van der Molen, J., Wilkinson, M. (2013): Framework for understanding marine ecosystem health, Marine Ecology Progress Series 494, 1-27

Olenin, S. (1997): Benthic zonation of Eastern Gotland Basin, Netherlands Journal of Aquatic Ecology 30, 265-282

Omstedt, A., Meuller, L., Nyberg, L. (1997): Interannual, seasonal and regional variations of precipitation and evaporation over the Baltic Sea, The American Biology 26, 484-492

Palmer, M.W., White, P.S. (1994): Scale dependence and the species-area relationship, The American Naturalist 144, 717,740

Pastuszak, M., Sitek, S., Grelowski, A. (1998): The exceptional Oder flood in summer 1997. Nutrient concentrations in the Swina Strait during the years 1996-1997 - with emphasis on the flood event, Deutsche Hydrographische Zeitschrift 50, 183-202

Paterson, D.M., Defew; E.C., Jabour, J. (2012): Ecosystem functionand co-evolution of terminology in marine science and management, Marine Biodervisity and Ecosystem Functioning 1, 1-240

Pearson, T., Rosenberg, R. (1978): Macrobentic succession in relation to organic enrichment and pollution of the marine environment, Oceanography and Marine Biology 16, 229-311

Pigolotti, S., Cencini, M. (2009): Speciation-rate dependence in species-area relationships, Journal of Theoretical Biology 260, 83-89

Pinna, M.; Basset, A. (2004): Influence of summer drought on spatial patterns in three River Tirso (Sardinia, Italy) sub-basins, Hydrobiologia 522, 311-319

Pinna, M., Marini, G., Mancinelli, G., Basset, A. (2014): Influence of sampling effort on ecological descriptors and indicators in perturbed and unperturbed conditions: A study case using benthic macroinvertebrates in Mediterranean transitional, Ecological Indicators 37, 27-39

Plotkin, J.B., Potts, M.D., Leslie, N., Manokaran, N., Lafreankie, J., Ashton, P.S. (2000): Species-area curves, spatial aggregation, and habitat specialization in tropical forests, Journal of Theoretical Biology 207, 81-99

Ponti, M., Vadrucci, M.R.; Orfanidis, S., Pinna, M. (2009): Biotic indices for ecological status of transitional water ecosystems, Transitional Waters Bulletin 3, 32-90

Riddle, M. J. (1989): Precision of the mean and the design of benthos sampling programmes: caution advised, Marine Biology 103, 225-230

Rosenzweig, M.L. (1995): Species Diversity in Space and Time, Cambridge University Press

Ruhmor, H. (1990): Soft bottom macrofauna: Collection and treatment of samples (ICES), Techniques in Marina Environmental Science

Rumohr, H., Karakassis, I., Jensen, J. N. (2001): Estimating species richness, abundance and diversity with 70 macrobenthic replicates in the Western Baltic Sea, Marine Ecology Progress Series 214, 103-110

Schinke, H., Matthäus, W. (1998): On the causes of major Baltic inflows - an analysis of long time series, Continental Shelf Research 18, 67-97

Schreiner, S.M: (2003): Six types of species-area curves, Global Ecology Biogeography 12, 441-447

Schumacher, B. (2003): Literature Review an Report – Surface sediment sampling technologies, Tetra Tech EM Inc.

Sola, J. C., Urcelay, A., Miner, A., Ibanez, M. (1989): Quantitative sampling methodology of sediments in Bidasoa estuary, Topics in marine Biology 53, 585-589

Song, Y., Wang, P., Li, G., Zhou, D. (2014): Relationships between functional diversity and ecosystem functioning: A review, Acta Ecologica Sinica 34, 85-91

Strong, J.A., Andonegi, E., Bizsel, K.C., Danovaro R., Elliott M., Franco A., Garces, E., Little, S. , Mazik, K., Moncheva, S., Papadopoulou, N., Patrício, J., Queiros, A.M., Smith, C., Stefanova, K., Solaun, O. (2015): Marine biodiversity and ecosystem function relationships: The potential for practical monitoring applications, Estuarine, Coastal and Shelf Science 161, 46-64

Tilman, D., Knops, J., Wedin, D., Reich, P., Ritchie, M., Siemann, E. (1997): The influence of functional diversity and composition on ecosystem processes, Science 277, 1300-1302

Tittensor, D.P. (2007): Human impacts on the species-area relationship in marine fish assemblages, Ecology Letters 10, 760-772

Tukey, J.W. (1977): Exploratory data analysis, Addison-Wesley 1977

Törnroos, A., Bonsdorff, E., Bremner, J., Blomqvist, M., Josefson, A.B.; Garcia, C., Warzocha, J. (2015): Marine benthic ecological functioning over decreasing taxonimic richness, Journal of Sea Research 98, 49-56

Ulrich, W., Buszko, J. (2007): Sampling design and the shape of species-area curves on the regional scale, ACTA Oecologica 31, 54-59

U.S. Environmental Protection Agency (2001): Methods for Collection, Storage and Manipulation of Sediments for Chemical and Toxicological Analyses: Technical Manual, Office of Water, Washington, D.C. EPA/823/B-01/002

U.S. Geological Survey (1997): National Field Manual for the Collection of Water-Quality, U.S. Geological Survey Techniques of Waters. Resources Investigations 9, 1-9

Whittaker, R.H., (1960): Vegetation of the Siskiyou Mountains, Oregon and California, Ecological Monographs 30, 279-338

Yasuhara, M., Grimm, M., Brandao, S. N., Jöst, A., Okahashi, H., Iwatani, H., Ostmann, A., Marinez Arbizu, P. (2014): Deep−sea benthic ostracodes from multiple core and epibenthic sledge samples in Icelandic waters, Polish Polar Research 35, 341-360

Zettler, M.L., Schiedek, D., Bobertz, B. (2007): Benthic biodiversity indices versus salinity gradient in the southern Baltic Sea, Marine Pollution Bulletin 55, 258-270

Zettler, M.L., Proffitt, C.E., Darr, A., Degraer, S., Devriese, L., Greathead, C., Kotta, J., Magni, P., Martin, G., Reiss, H., Speybroeck, J., Tagliapietra, D., Van Hoey, G., Ysebaert, T. (2013): On the myths of indicator species: issues and further consideration in the use of static concepts for ecological applications,PLoS ONE 8(10): e78219

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Eigenständigkeitserklärung

Hiermit erkläre ich, Natalie Katharina Steiner, dass ich die Masterarbeit “Influence of the sampling strategy on the descrition of benthic ecosystem functioning” eigenständig verfasst habe und keine anderen, als die angegebenen Hilfsmittel verwendet habe. Die Stellen der Arbeit, die dem Wortlaut oder Sinn anderen Werken entnommen sind, wurden unter Angabe der Quelle kenntlich gemacht.

Rostock, den 16. September 2015

Natalie Katharina Steiner

Appendix

1. Table of the sampling positions

Tab. x. 1. Sampling positions of the sampling stations at Arkona Basin and Oder Bank by Multicorer and van Veen grab. Positions are given in E°min,dec and N°min,dec.

Sample	Position E°min,dec	Position N°min,dec
AB_MUC1	13°50,9395	54°53,1648
AB_MUC2	13°50,9395	54°53,1648
AB_MUC3	13°50,9821	54°53,0960
AB_MUC4	13°50,9821	54°53,0960
AB_MUC5	13°51,0299	54°53,1228
AB_MUC6	13°51,0299	54°53,1228
AB_MUC7	13°51,0382	54°53,1593
AB_MUC8	13°51,0382	54°53,1593
AB_MUC9	13°51,0244	54°53,1661
AB_MUC10	13°51,0244	54°53,1661
AB_MUC11	13°50,8529	54°53,0933
AB_MUC12	13°50,8529	54°53,0933
AB_vV1	13°50,9866	54°53,1531
AB_vV2	13°50,9972	54°53,1521
AB_vV3	13°50,9914	54°53,1465
AB_vV4	13°50,9935	54°53,1325
AB_vV5	13°51,0076	54°53,1417
AB_vV6	13°51,0076	54°53,1218
AB_vV7	13°51,0089	54°53,1101
AB_vV8	13°51,0069	54°53,0943
AB_vV9	13°51,0217	54°53,0840
AB_vV10	13°51,0158	54°53,0771
OB_MUC1	14°3,6375	54°26,4507
OB_MUC2	14°3,6375	54°26,4507
OB_MUC3	14°3,6763	54°26,4263
OB_MUC4	14°3,6763	54°26,4263
OB_MUC5	14°3,7138	54°26,4043
OB_MUC6	14°3,7138	54°26,4043
OB_MUC7	14°3,6382	54°26,3978
OB_MUC8	14°3,6382	54°26,3978
OB_MUC9	14°3,6691	54°26,3806
OB_MUC10	14°3,6691	54°26,3806
OB_MUC11	14°3,5846	54°26,4366
OB_MUC12	14°3,5846	54°26,4366
OB_vV1	14°3,6372	54°26,3665
OB_vV2	14°3,6279	54°26,3641
OB_vV3	14°3,6141	54°26,3696
OB_vV4	14°3,6757	54°26,3875
OB_vV5	14°3,6873	54°26,4023
OB_vV6	14°3,6863	54°26,3864
OB_vV7	14°3,7066	54°26,3723
OB_vV8	14°3,6911	54°26,3675
OB_vV9	14°3,6695	54°26,3686
OB_vV10	14°3,6660	54°26,3634

2. Table of the average values of species number, abundance and biomass

Tab. x. 2. Table of the average values of the species number, abundance per sample and m² and biomass per sample and m² for the station (AB, OB), the gear type (MUC, vV) and sample number.

Station	Gear	Sample	Species	Abz.	Abz./m²	ww	ww/m²
AB	MUC[0.00785m²]	1	3	6	764.33	0.0288	3.67
AB	MUC[0.00785m²]	2	2	8	1019.11	0.0600	7.65
AB	MUC[0.00785m²]	3	3	7	891.72	0.0409	5.21
AB	MUC[0.00785m²]	4	4	4	509.55	0.1048	13.35
AB	MUC[0.00785m²]	5	1	3	382.17	0.0412	5.25
AB	MUC[0.00785m²]	6	1	3	382.17	0.0301	3.84
AB	MUC[0.00785m²]	7	2	4	509.55	0.0102	1.30
AB	MUC[0.00785m²]	8	2	2	254.78	0.4569	58.20
AB	MUC[0.00785m²]	9	6	10	1273.89	0.0945	12.03
AB	MUC[0.00785m²]	10	3	7	891.72	0.0710	9.04
AB	MUC[0.00785m²]	11	3	4	509.55	0.3438	43.79
AB	MUC[0.00785m²]	12	5	6	764.33	0.0360	4.59
AB	vV[0.09765m²]	1	7	16	163.85	0.1294	1.32
AB	vV[0.09765m²]	2	8	28	286.74	1.1336	11.61
AB	vV[0.09765m²]	3	5	12	122.89	0.0471	0.48
AB	vV[0.09765m²]	4	11	34	348.18	2.3794	24.37
AB	vV[0.09765m²]	5	6	9	92.17	0.3247	3.33
AB	vV[0.09765m²]	6	11	49	501.79	20.5550	210.50
AB	vV[0.09765m²]	7	6	10	102.41	0.1778	1.82
AB	vV[0.09765m²]	8	7	30	307.22	0.4534	4.64
AB	vV[0.09765m²]	9	6	29	296.98	2.9977	30.70
AB	vV[0.09765m²]	10	9	24	245.78	0.9864	10.10
OB	MUC[0.00785m²]	1	8	121	15414.01	1.1459	145.97
OB	MUC[0.00785m²]	2	10	78	9936.31	1.0317	131.42
OB	MUC[0.00785m²]	3	8	110	14012.74	2.0718	263.93
OB	MUC[0.00785m²]	4	7	96	12229.30	1.2939	164.83
OB	MUC[0.00785m²]	5	6	112	14267.52	0.5885	74.96
OB	MUC[0.00785m²]	6	8	143	18216.56	1.6369	208.52
OB	MUC[0.00785m²]	7	7	109	13885.35	1.7520	223.18
OB	MUC[0.00785m²]	8	7	149	18980.89	1.7016	216.77
OB	MUC[0.00785m²]	9	7	131	16687.90	1.0279	130.95
OB	MUC[0.00785m²]	10	6	113	14394.90	2.3001	293.01
OB	MUC[0.00785m²]	11	10	186	23694.27	5.0924	648.71
OB	MUC[0.00785m²]	12	6	67	8535.03	1.8658	237.68
OB	vV[0.09765m²]	1	10	1152	11797.24	13.3522	136.73
OB	vV[0.09765m²]	2	11	1327	13589.35	13.3283	136.49
OB	vV[0.09765m²]	3	9	1745	17869.94	19.7391	202.14
OB	vV[0.09765m²]	4	11	1468	15033.28	21.0536	215.60
OB	vV[0.09765m²]	5	12	1809	18525.35	27.1081	277.60
OB	vV[0.09765m²]	6	12	1729	17706.09	27.0897	277.42
OB	vV[0.09765m²]	7	9	1251	12811.06	18.8582	193.12
OB	vV[0.09765m²]	8	13	1566	16036.87	18.8850	193.39
OB	vV[0.09765m²]	9	11	1882	19272.91	28.2892	289.70
OB	vV[0.09765m²]	10	11	1549	15862.78	15.8507	162.32

3.Table of the raw data generated in this study

Tab. x. 3. The table shows each species found at each station, gear type and sample number under specification of the abundance [ind] per sample and m² and the wet weigh [g]t per sample and m².

Station_gear	Sample	Taxon	Abz.	Abz./m²	ww	ww/m²
AB_MUC	1	*Arctica islandica*	2	254.78	0.0121	82.44
AB_MUC	1	*Macoma balthica*	3	382.17	0.0140	71.38
AB_MUC	1	*Pontoporeia femorata*	1	127.39	0.0027	375.94
AB_MUC	2	*Macoma balthica*	4	509.55	0.0360	55.52
AB_MUC	2	*Pontoporeia femorata*	4	509.55	0.0240	83.30
AB_MUC	3	*Arctica islandica*	3	382.17	0.0178	168.16
AB_MUC	3	*Diastylis rathkei*	1	127.39	0.0050	598.80
AB_MUC	3	*Pontoporeia femorata*	3	382.17	0.0181	166.11
AB_MUC	4	*Arctica islandica*	1	127.39	0.0041	970.87
AB_MUC	4	*Diastylis rathkei*	1	127.39	0.0048	831.60
AB_MUC	4	*Macoma balthica*	1	127.39	0.0024	1687.76
AB_MUC	4	*Nephtys ciliata*	1	127.39	0.0935	42.79
AB_MUC	5	*Macoma balthica*	3	382.17	0.0412	121.42
AB_MUC	6	*Macoma balthica*	3	382.17	0.0301	199.20
AB_MUC	7	*Nephtys caeca*	2	254.78	0.0068	1026.39
AB_MUC	7	*Peringia ulvae*	2	254.78	0.0034	2052.79
AB_MUC	8	*Alitta succinea*	1	127.39	0.4391	18.22
AB_MUC	8	*Diastylis rathkei*	1	127.39	0.0179	448.18
AB_MUC	9	*Abra alba*	2	254.78	0.0590	152.46
AB_MUC	9	*Arctica islandica*	1	127.39	0.0015	5882.35
AB_MUC	9	*Macoma balthica*	3	382.17	0.0232	388.60
AB_MUC	9	*Nephtys hombergii*	1	127.39	0.0016	5590.06
AB_MUC	9	*Peringia ulvae*	1	127.39	0.0011	8411.21
AB_MUC	9	*Pontoporeia femorata*	2	254.78	0.0081	1118.01
AB_MUC	10	*Macoma balthica*	3	382.17	0.0020	5128.21
AB_MUC	10	*Nephtys hombergii*	1	127.39	0.0498	200.68
AB_MUC	10	*Pontoporeia femorata*	3	382.17	0.0192	521.38
AB_MUC	11	*Arctica islandica*	1	127.39	0.0032	3448.28
AB_MUC	11	*Macoma balthica*	2	254.78	0.3366	32.68
AB_MUC	11	*Pontoporeia femorata*	1	127.39	0.0040	2777.78
AB_MUC	12	*Arctica islandica*	1	127.39	0.0042	2884.62
AB_MUC	12	*Diastylis rathkei*	1	127.39	0.0010	12500.00
AB_MUC	12	*Macoma balthica*	1	127.39	0.0007	17647.06
AB_MUC	12	*Nephtys ciliata*	1	127.39	0.0223	539.08
AB_MUC	12	*Pontoporeia femorata*	2	254.78	0.0080	1507.54
AB_vV	1	*Diastylis rathkei*	2	20.48	0.0016	613.50
AB_vV	1	*Dipolydora quadrilobata*	1	10.24	0.0006	1587.30
AB_vV	1	*Heteromastus filiformis*	1	10.24	0.0023	440.53
AB_vV	1	*Macoma balthica*	2	20.48	0.0013	769.23
AB_vV	1	*Mya arenaria*	4	40.96	0.0039	256.41
AB_vV	1	*Nephtys ciliata*	2	20.48	0.0918	10.90
AB_vV	1	*Pontoporeia femorata*	4	40.96	0.0279	35.88

AB_vV	2	*Abra alba*	7	71.68	0.5181	3.86
AB_vV	2	*Arctica islandica*	2	20.48	0.0057	348.43
AB_vV	2	*Macoma balthica*	2	20.48	0.2799	7.15
AB_vV	2	*Nephtys hombergii*	2	20.48	0.2431	8.23
AB_vV	2	*Phyllodoce mucosa*	1	10.24	0.0104	192.12
AB_vV	2	*Pontoporeia femorata*	12	122.89	0.0583	34.33
AB_vV	2	*Scoloplos (Scoloplos)*	1	10.24	0.0036	560.22
AB_vV	2	*Trochochaeta*	1	10.24	0.0146	137.17
AB_vV	3	*Arctica islandica*	5	51.20	0.0276	108.58
AB_vV	3	*Diastylis rathkei*	2	20.48	0.0043	702.58
AB_vV	3	*Macoma balthica*	3	30.72	0.0025	1181.10
AB_vV	3	*Nephtys hombergii*	1	10.24	0.0117	255.75
AB_vV	3	*Peringia ulvae*	1	10.24	0.0010	3157.89
AB_vV	4	*Abra alba*	3	30.72	0.4647	8.61
AB_vV	4	*Arctica islandica*	1	10.24	0.0061	661.16
AB_vV	4	*Bylgides sarsi*	1	10.24	0.0039	1033.59
AB_vV	4	*Heteromastus filiformis*	1	10.24	0.0042	947.87
AB_vV	4	*Macoma balthica*	16	163.85	0.7109	5.63
AB_vV	4	*Nephtys ciliata*	1	10.24	1.0673	3.75
AB_vV	4	*Nephtys hombergii*	3	30.72	0.0842	47.49
AB_vV	4	*Peringia ulvae*	2	20.48	0.0021	1913.88
AB_vV	4	*Phyllodoce mucosa*	1	10.24	0.0016	2580.65
AB_vV	4	*Pontoporeia femorata*	3	30.72	0.0176	226.89
AB_vV	4	*Scoloplos (Scoloplos)*	2	20.48	0.0169	236.83
AB_vV	5	*Alitta succinea*	1	10.24	0.3061	16.33
AB_vV	5	*Arctica islandica*	1	10.24	0.0011	4385.96
AB_vV	5	*Diastylis rathkei*	2	20.48	0.0026	1960.78
AB_vV	5	*Macoma balthica*	1	10.24	0.0008	6172.84
AB_vV	5	*Peringia ulvae*	2	20.48	0.0033	1533.74
AB_vV	5	*Pontoporeia femorata*	2	20.48	0.0109	459.98
AB_vV	6	*Abra alba*	2	20.48	0.1028	58.35
AB_vV	6	*Ampharete acutifrons*	1	10.24	0.0113	530.04
AB_vV	6	*Arctica islandica*	5	51.20	18.8029	0.32
AB_vV	6	*Diastylis rathkei*	1	10.24	0.0006	9677.42
AB_vV	6	*Macoma balthica*	8	81.93	1.3666	4.39
AB_vV	6	*Nephtys caeca*	1	10.24	0.0021	2884.62
AB_vV	6	*Nephtys ciliata*	1	10.24	0.0811	73.99
AB_vV	6	*Peringia ulvae*	2	20.48	0.0018	3370.79
AB_vV	6	*Pontoporeia femorata*	21	215.05	0.1313	45.71
AB_vV	6	*Scoloplos (Scoloplos)*	7	71.68	0.0545	110.05
AB_vV	7	*Abra alba*	1	10.24	0.0300	233.57
AB_vV	7	*Arctica islandica*	2	20.48	0.0075	937.08
AB_vV	7	*Macoma balthica*	1	10.24	0.0007	10294.12
AB_vV	7	*Nephtys caeca*	2	20.48	0.1060	66.07
AB_vV	7	*Nephtys ciliata*	1	10.24	0.0159	440.25
AB_vV	7	*Pontoporeia femorata*	3	30.72	0.0178	393.26
AB_vV	8	*Abra alba*	2	20.48	0.2994	26.72
AB_vV	8	*Arctica islandica*	2	20.48	0.0039	2046.04
AB_vV	8	*Bylgides sarsi*	1	10.24	0.0014	5755.40

AB_vV	8	*Macoma balthica*	7	71.68	0.0414	193.42
AB_vV	8	*Nephtys ciliata*	2	20.48	0.0333	240.60
AB_vV	8	*Nephtys hombergii*	1	10.24	0.0054	1481.48
AB_vV	8	*Pontoporeia femorata*	15	153.61	0.0687	116.47
AB_vV	9	*Abra alba*	1	10.24	0.1433	62.82
AB_vV	9	*Arctica islandica*	1	10.24	2.2146	4.06
AB_vV	9	*Arctica islandica*	4	40.96	0.0253	355.45
AB_vV	9	*Macoma balthica*	6	61.44	0.0244	368.55
AB_vV	9	*Nephtys hombergii*	2	20.48	0.5078	17.72
AB_vV	9	*Pontoporeia femorata*	15	153.61	0.0823	109.36
AB_vV	10	*Abra alba*	3	30.72	0.1611	62.08
AB_vV	10	*Arctica islandica*	2	20.48	0.0150	668.90
AB_vV	10	*Bylgides sarsi*	1	10.24	0.0023	4273.50
AB_vV	10	*Diastylis rathkei*	1	10.24	0.0013	7633.59
AB_vV	10	*Macoma balthica*	10	102.41	0.3029	33.02
AB_vV	10	*Nephtys hombergii*	2	20.48	0.2732	36.60
AB_vV	10	*Pontoporeia femorata*	3	30.72	0.0108	923.36
AB_vV	10	*Scoloplos (Scoloplos)*	1	10.24	0.0051	1945.53
AB_vV	10	*Trochochaeta*	1	10.24	0.2147	46.59
OB_MUC	1	*Cerastoderma glaucum*	7	891.72	0.4485	2.23
OB_MUC	1	*Enchytraeidae*	1	127.39	0.0001	8333.33
OB_MUC	1	*Hediste diversicolor*	4	509.55	0.1957	5.11
OB_MUC	1	*Macoma balthica*	1	127.39	0.0782	12.79
OB_MUC	1	*Marenzelleria viridis*	1	127.39	0.0768	13.02
OB_MUC	1	*Mya arenaria*	61	7770.70	0.2454	4.07
OB_MUC	1	*Mytilus edulis*	2	254.78	0.0055	181.49
OB_MUC	1	*Peringia ulvae*	44	5605.10	0.0957	10.45
OB_MUC	2	*Cerastoderma glaucum*	10	1273.89	0.1950	10.26
OB_MUC	2	*Corophium volutator*	1	127.39	0.0119	167.50
OB_MUC	2	*Enchytraeidae*	1	127.39	0.0007	2857.14
OB_MUC	2	*Hediste diversicolor*	4	509.55	0.1000	19.99
OB_MUC	2	*Macoma balthica*	1	127.39	0.2274	8.79
OB_MUC	2	*Marenzelleria viridis*	4	509.55	0.3409	5.87
OB_MUC	2	*Mya arenaria*	26	3312.10	0.1031	19.39
OB_MUC	2	*Peringia ulvae*	22	2802.55	0.0472	42.40
OB_MUC	2	*Pygospio elegans*	6	764.33	0.0042	477.33
OB_MUC	2	*Tubificidae*	3	382.17	0.0012	1652.89
OB_MUC	3	*Cerastoderma glaucum*	17	2165.61	0.4096	7.32
OB_MUC	3	*Hediste diversicolor*	2	254.78	0.0029	1020.41
OB_MUC	3	*Macoma balthica*	2	254.78	1.2871	2.33
OB_MUC	3	*Marenzelleria viridis*	2	254.78	0.0769	39.01
OB_MUC	3	*Mya arenaria*	37	4713.38	0.1909	15.71
OB_MUC	3	*Mytilus edulis*	2	254.78	0.0035	867.05
OB_MUC	3	*Peringia ulvae*	47	5987.26	0.1000	30.00
OB_MUC	3	*Tubificidae*	1	127.39	0.0009	3191.49
OB_MUC	4	*Cerastoderma glaucum*	14	1783.44	0.2322	17.23
OB_MUC	4	*Hediste diversicolor*	3	382.17	0.1787	22.38
OB_MUC	4	*Macoma balthica*	3	382.17	0.6184	6.47
OB_MUC	4	*Marenzelleria viridis*	3	382.17	0.0937	42.70

OB_MUC	4	*Mya arenaria*	33	4203.82	0.0973	41.11
OB_MUC	4	*Peringia ulvae*	36	4585.99	0.0719	55.66
OB_MUC	4	*Pygospio elegans*	4	509.55	0.0018	2222.22
OB_MUC	5	*Cerastoderma glaucum*	13	1656.05	0.1929	25.92
OB_MUC	5	*Hediste diversicolor*	4	509.55	0.1514	33.02
OB_MUC	5	*Mya arenaria*	41	5222.93	0.1495	33.44
OB_MUC	5	*Peringia ulvae*	49	6242.04	0.0922	54.21
OB_MUC	5	*Pygospio elegans*	3	382.17	0.0011	4424.78
OB_MUC	5	*Tubificidae*	2	254.78	0.0012	4032.26
OB_MUC	6	*Cerastoderma glaucum*	37	4713.38	1.2387	4.84
OB_MUC	6	*Hediste diversicolor*	2	254.78	0.0284	211.27
OB_MUC	6	*Macoma balthica*	1	127.39	0.0143	420.46
OB_MUC	6	*Marenzelleria viridis*	5	636.94	0.0873	68.76
OB_MUC	6	*Mya arenaria*	47	5987.26	0.1537	39.04
OB_MUC	6	*Mytilus edulis*	2	254.78	0.0184	325.73
OB_MUC	6	*Neomysis integer*	1	127.39	0.0076	785.34
OB_MUC	6	*Peringia ulvae*	48	6114.65	0.0886	67.76
OB_MUC	7	*Cerastoderma glaucum*	16	2038.22	0.3317	21.10
OB_MUC	7	*Hediste diversicolor*	1	127.39	0.0013	5511.81
OB_MUC	7	*Macoma balthica*	3	382.17	0.8615	8.13
OB_MUC	7	*Marenzelleria viridis*	4	509.55	0.1374	50.93
OB_MUC	7	*Mya arenaria*	45	5732.48	0.3557	19.68
OB_MUC	7	*Peringia ulvae*	39	4968.15	0.0640	109.41
OB_MUC	7	*Pygospio elegans*	1	127.39	0.0004	16279.07
OB_MUC	8	*Cerastoderma glaucum*	32	4076.43	0.6798	11.77
OB_MUC	8	*Hediste diversicolor*	1	127.39	0.0023	3493.45
OB_MUC	8	*Macoma balthica*	2	254.78	0.4996	16.01
OB_MUC	8	*Marenzelleria viridis*	2	254.78	0.1406	56.91
OB_MUC	8	*Mya arenaria*	45	5732.48	0.2443	32.74
OB_MUC	8	*Peringia ulvae*	64	8152.87	0.1326	60.32
OB_MUC	8	*Pygospio elegans*	3	382.17	0.0025	3225.81
OB_MUC	9	*Cerastoderma glaucum*	23	2929.94	0.5615	16.03
OB_MUC	9	*Macoma balthica*	1	127.39	0.1576	57.11
OB_MUC	9	*Marenzelleria viridis*	2	254.78	0.0612	147.08
OB_MUC	9	*Mya arenaria*	30	3821.66	0.0972	92.60
OB_MUC	9	*Mytilus edulis*	2	254.78	0.0098	921.19
OB_MUC	9	*Peringia ulvae*	72	9171.97	0.1397	64.41
OB_MUC	9	*Pygospio elegans*	1	127.39	0.0010	9473.68
OB_MUC	10	*Cerastoderma glaucum*	29	3694.27	1.0762	9.29
OB_MUC	10	*Hediste diversicolor*	2	254.78	0.0196	510.20
OB_MUC	10	*Macoma balthica*	1	127.39	0.5227	19.13
OB_MUC	10	*Marenzelleria viridis*	8	1019.11	0.4815	20.77
OB_MUC	10	*Mya arenaria*	37	4713.38	0.1318	75.87
OB_MUC	10	*Peringia ulvae*	36	4585.99	0.0683	146.48
OB_MUC	11	*Cerastoderma glaucum*	33	4203.82	2.1009	5.24
OB_MUC	11	*Hediste diversicolor*	7	891.72	0.1189	92.48
OB_MUC	11	*Macoma balthica*	2	254.78	0.8776	12.53
OB_MUC	11	*Marenzelleria viridis*	2	254.78	0.0077	1428.57
OB_MUC	11	*Mya arenaria*	53	6751.59	1.8140	6.06

OB_MUC	11	*Mytilus edulis*	1	127.39	0.0145	760.19
OB_MUC	11	*Peringia ulvae*	81	10318.47	0.1527	72.05
OB_MUC	11	*Pygospio elegans*	5	636.94	0.0044	2511.42
OB_MUC	11	*Tubificidae*	2	254.78	0.0018	6145.25
OB_MUC	12	*Cerastoderma glaucum*	12	1528.66	0.2094	57.32
OB_MUC	12	*Hediste diversicolor*	2	254.78	0.2547	47.11
OB_MUC	12	*Macoma balthica*	2	254.78	1.1730	10.23
OB_MUC	12	*Marenzelleria viridis*	2	254.78	0.0201	596.13
OB_MUC	12	*Mya arenaria*	18	2292.99	0.1407	85.28
OB_MUC	12	*Peringia ulvae*	31	3949.04	0.0679	176.63
OB_vV	1	*Cerastoderma glaucum*	215	2201.74	5.7519	0.17
OB_vV	1	*Hediste diversicolor*	29	296.98	0.2620	3.82
OB_vV	1	*Macoma balthica*	31	317.46	3.9162	0.26
OB_vV	1	*Marenzelleria viridis*	12	122.89	0.1732	5.77
OB_vV	1	*Mya arenaria*	476	4874.55	2.5380	0.39
OB_vV	1	*Mytilus edulis*	1	10.24	0.0016	609.76
OB_vV	1	*Peringia ulvae*	357	3655.91	0.6895	1.45
OB_vV	1	*Pygospio elegans*	21	215.05	0.0140	71.48
OB_vV	1	*Tubificidae*	10	102.41	0.0056	178.25
OB_vV	2	*Cerastoderma glaucum*	184	1884.28	5.3534	0.37
OB_vV	2	*Eteone longa*	1	10.24	0.0008	2380.95
OB_vV	2	*Hediste diversicolor*	51	522.27	0.3417	5.85
OB_vV	2	*Macoma balthica*	24	245.78	3.7248	0.54
OB_vV	2	*Marenzelleria viridis*	13	133.13	0.1366	14.64
OB_vV	2	*Mya arenaria*	526	5386.58	2.7097	0.74
OB_vV	2	*Mytilus edulis*	4	40.96	0.0141	141.94
OB_vV	2	*Peringia ulvae*	465	4761.90	1.0129	1.97
OB_vV	2	*Pygospio elegans*	39	399.39	0.0255	78.40
OB_vV	2	*Tubificidae*	20	204.81	0.0088	228.31
OB_vV	3	*Cerastoderma glaucum*	287	2939.07	8.1296	0.37
OB_vV	3	*Hediste diversicolor*	24	245.78	0.4642	6.46
OB_vV	3	*Macoma balthica*	24	245.78	6.8997	0.43
OB_vV	3	*Marenzelleria viridis*	16	163.85	0.1927	15.57
OB_vV	3	*Mya arenaria*	516	5284.18	2.1932	1.37
OB_vV	3	*Mytilus edulis*	11	112.65	0.0262	114.46
OB_vV	3	*Peringia ulvae*	836	8561.19	1.8149	1.65
OB_vV	3	*Pygospio elegans*	21	215.05	0.0133	225.23
OB_vV	3	*Tubificidae*	10	102.41	0.0054	557.62
OB_vV	4	*Cerastoderma glaucum*	402	4116.74	10.6627	0.38
OB_vV	4	*Hediste diversicolor*	43	440.35	0.5099	7.84
OB_vV	4	*Macoma balthica*	20	204.81	6.4012	0.62
OB_vV	4	*Marenzelleria viridis*	19	194.57	0.3876	10.32
OB_vV	4	*Mya arenaria*	436	4464.93	1.9434	2.06
OB_vV	4	*Mytilus edulis*	11	112.65	0.1123	35.63
OB_vV	4	*Peringia ulvae*	490	5017.92	1.0110	3.96
OB_vV	4	*Pygospio elegans*	21	215.05	0.0121	329.76
OB_vV	4	*Streblospio shrubsolii*	3	30.72	0.0018	2185.79
OB_vV	4	*Tubificidae*	23	235.54	0.0115	346.92
OB_vV	5	*Cerastoderma glaucum*	276	2826.42	7.9000	0.63

OB_vV	5	*Corophium volutator*	1	10.24	0.0087	574.05
OB_vV	5	*Hediste diversicolor*	83	849.97	1.3005	3.84
OB_vV	5	*Macoma balthica*	27	276.50	12.5533	0.40
OB_vV	5	*Marenzelleria viridis*	21	215.05	0.1532	32.65
OB_vV	5	*Mya arenaria*	749	7670.25	3.8321	1.30
OB_vV	5	*Mytilus edulis*	1	10.24	0.0020	2475.25
OB_vV	5	*Peringia ulvae*	604	6185.36	1.3276	3.77
OB_vV	5	*Pygospio elegans*	12	122.89	0.0057	871.08
OB_vV	5	*Streblospio shrubsolii*	2	20.48	0.0011	4385.96
OB_vV	5	*Tubificidae*	33	337.94	0.0239	209.64
OB_vV	6	*Cerastoderma glaucum*	364	3727.60	10.6646	0.56
OB_vV	6	*Enchytraeidae*	1	10.24	0.0003	18750.00
OB_vV	6	*Hediste diversicolor*	53	542.75	0.6381	9.40
OB_vV	6	*Macoma balthica*	25	256.02	7.0393	0.85
OB_vV	6	*Marenzelleria viridis*	33	337.94	0.4143	14.48
OB_vV	6	*Mya arenaria*	569	5826.93	6.9715	0.86
OB_vV	6	*Mytilus edulis*	5	51.20	0.1002	59.89
OB_vV	6	*Peringia ulvae*	638	6533.54	1.2375	4.85
OB_vV	6	*Pygospio elegans*	22	225.29	0.0118	510.20
OB_vV	6	*Streblospio shrubsolii*	3	30.72	0.0013	4724.41
OB_vV	6	*Tubificidae*	16	163.85	0.0109	551.47
OB_vV	7	*Cerastoderma glaucum*	202	2068.61	7.1344	0.98
OB_vV	7	*Hediste diversicolor*	39	399.39	0.6189	11.31
OB_vV	7	*Macoma balthica*	23	235.54	2.7526	2.54
OB_vV	7	*Marenzelleria viridis*	25	256.02	0.4708	14.87
OB_vV	7	*Mya arenaria*	600	6144.39	7.1524	0.98
OB_vV	7	*Mytilus edulis*	2	20.48	0.0298	234.82
OB_vV	7	*Peringia ulvae*	336	3440.86	0.6834	10.24
OB_vV	7	*Pygospio elegans*	21	215.05	0.0157	445.86
OB_vV	7	*Tubificidae*	3	30.72	0.0004	17948.72
OB_vV	8	*Bathyporeia pilosa*	1	10.24	0.0024	3361.34
OB_vV	8	*Cerastoderma glaucum*	315	3225.81	9.1357	0.88
OB_vV	8	*Enchytraeidae*	2	20.48	0.0004	19047.62
OB_vV	8	*Hediste diversicolor*	48	491.55	0.7867	10.17
OB_vV	8	*Macoma balthica*	23	235.54	4.2496	1.88
OB_vV	8	*Marenzelleria viridis*	18	184.33	0.2628	30.44
OB_vV	8	*Mya arenaria*	707	7240.14	3.5922	2.23
OB_vV	8	*Mytilus edulis*	5	51.20	0.0247	324.02
OB_vV	8	*Peringia ulvae*	389	3983.61	0.7992	10.01
OB_vV	8	*Pygospio elegans*	40	409.63	0.0210	381.50
OB_vV	8	*Streblospio shrubsolii*	2	20.48	0.0011	7017.54
OB_vV	8	*Tubificidae*	16	163.85	0.0092	873.36
OB_vV	9	*Cerastoderma glaucum*	277	2836.66	11.3140	0.80
OB_vV	9	*Enchytraeidae*	2	20.48	0.0003	34615.38
OB_vV	9	*Hediste diversicolor*	54	553.00	0.8899	10.11
OB_vV	9	*Macoma balthica*	36	368.66	9.7558	0.92
OB_vV	9	*Marenzelleria viridis*	15	153.61	0.2260	39.82
OB_vV	9	*Mya arenaria*	837	8571.43	4.8520	1.85
OB_vV	9	*Mytilus edulis*	3	30.72	0.0119	757.58

OB_vV	9	*Peringia ulvae*	611	6257.04	1.2132	7.42
OB_vV	9	*Pygospio elegans*	22	225.29	0.0144	627.18
OB_vV	9	*Streblospio shrubsolii*	1	10.24	0.0005	17647.06
OB_vV	9	*Tubificidae*	24	245.78	0.0114	790.17
OB_vV	10	*Cerastoderma glaucum*	221	2263.18	5.5205	1.81
OB_vV	10	*Crangon crangon*	1	10.24	0.4032	24.80
OB_vV	10	*Enchytraeidae*	1	10.24	0.0001	76923.08
OB_vV	10	*Hediste diversicolor*	27	276.50	0.4556	21.95
OB_vV	10	*Macoma balthica*	18	184.33	4.7332	2.11
OB_vV	10	*Marenzelleria viridis*	36	368.66	0.5167	19.35
OB_vV	10	*Mya arenaria*	679	6953.41	3.1433	3.18
OB_vV	10	*Peringia ulvae*	513	5253.46	1.0425	9.59
OB_vV	10	*Pygospio elegans*	38	389.14	0.0295	338.75
OB_vV	10	*Streblospio shrubsolii*	1	10.24	0.0003	33333.33
OB_vV	10	*Tubificidae*	14	143.37	0.0059	1709.40