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Detecting hot-spots of bivalve biomass in the south-western Baltic Sea

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ABSTRACT

Bivalves are among the most important taxonomic groups in marine benthic communities in nutrient cycling via benthic–pelagic coupling and as food source for higher trophic levels. Additionally, bivalve species combine several autecological features with potential value for assessment and management purposes. Therefore, the demand for quantitative distribution maps of bivalves is high both in research with focus on functional ecology of marine benthos and in policy.

In our study, we modelled and mapped the distribution of biomass of soft- and hard-bottom bivalves in the south-western Baltic Sea using Random Forest algorithms. Models were achieved for ten of the most frequent of overall 29 identified species. The distribution of bivalve biomass was mainly influenced by the abiotic parameters salinity, water depths, sediment characteristics and the amount of detritus as a proxy for food availability. Three hot-spots of bivalve biomass dominated by different species were detected: the oxygen-rich deeper parts of the Kiel Bay dominated by *Arctica islandica*, the shallow areas close to the mouth of the river Oder dominated by *Mya arenaria* and the hard-substrates around Rügen Island and the shallow Adlergrund dominated by *Mytilus* spp. The attained maps provide a good basis for further functional and applied analysis.

1. Introduction

Bivalves are regarded as an essential part of the benthic community in marine and brackish water systems (Gosling, 2003). Especially in brackish water systems where several important phyla of marine invertebrates do not occur due to reduced salinity bivalves are more relevant. For instance in the south-western Baltic Sea bivalves often provide more than 80% of the benthic macrofauna biomass in soft-bottom communities (Kube et al., 1996). Bivalves are an important food source for benthivore fishes (Brey et al., 1990; Siaulys et al., 2012), sea-birds (Lewis et al., 2007) and species of other higher trophic levels of the food-web. Especially in soft-bottoms they play a predominant role in benthic–pelagic coupling by filtering the water column for nourishment and deposing pseudofaeces onto or into the sediment (e.g. Graf, 1992; Norkko et al., 2001).

Additionally, bivalve species combine several autecological features with potential value for assessment and management purposes. Most adult bivalves are, once settled, more or less sessile and therefore reflect the environmental conditions in the area where they were found. The Ocean Quahog *Arctica islandica* is among the most long-lived invertebrate species world-wide (Ridgway and Richardson, 2010), in addition the lifespan of other species like *Astarte elliptica* may exceed 20 years (Trutschler and Samtleben, 1988). Therefore, not only do these species provide information on recent environmental conditions but also the state of their population structure may give information on the conditions during the last decades.

However, the calculation of the different functions of benthic bivalves and the application of these information are up to now limited by the imprecise knowledge of the distribution of benthic invertebrate species. Within the last decade, habitat suitability modelling became a common tool in benthic ecology (e.g. Glockzin et al., 2009; Gogina and Zettler, 2010; Reiss et al., 2011). First attempts focussed on the prediction of the probability of occurrence as the distribution of benthic invertebrates heavily varies in spaces and time. Studies predicting the abundance or the biomass of marine benthic invertebrates are still rare and the target species were often selected with regard to favoured food sources of commercial fish species (Siaulys et al., 2012; Wei et al., 2010).

However, as the intended linkage with key functions of the benthic ecosystem, e.g. the filtering capacity and its impact on the pelagic community, requires the usage of individual biomass as parameter (e.g. in Riisgard and Seerup, 2004), the development of quantitative distribution maps of macrobenthic invertebrate species is heavily demanded. Also the application of the recently developed HELCOM Underwater-Biotope Classification System HUB for the Baltic Sea requires the mapping of the biomass of dominant species (HELCOM, 2013a). Therefore, our aim was to provide quantitative distribution maps of the most frequent bivalve species in the German part of the Baltic Sea and to identify hot spots of bivalve biomass.

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2. Material and methods

2.1. Study area

Due to the highly variable environment, the south-western Baltic represents a demanding area for this kind of studies. Nevertheless, the distribution of benthic invertebrates and their relation to abiotic parameters has already been subject to several studies (Forster and Zettler, 2004; Glockzin and Zettler, 2008; Gogina et al., 2010).

The life conditions for bivalves in the south-western Baltic Sea are affected by declining salinity from 20 to 25 in the Kiel Bay in the western part of the study area towards 7 in the Pomeranian Bay in the eastern part (Fig. 1). Water exchange between the western Baltic and the Baltic Proper is inhibited by several sills like Darss and Drodgen Sill. Temporal variability in salinity is high especially in the western part of the study area towards the Darss Sill.

The composition of surface sediments mainly results from postglacial processes. Shallow areas along the shore and on top of the offshore glacial elevations are characterized by a mosaic of rocks, till, gravel and coarser sands. Substrate gets generally finer with increasing water depth. Muddy sediments dominate in the basins and deeper part of trenches. These substrates are widely enriched with organic load. Additional parameters influencing the distribution and condition of benthic bivalves are water temperature and food availability. An important food source is the inflow of freshwater from the larger rivers such as Trave, Warnow and Oder. Seasonal oxygen depletion events, which occur especially in the deeper areas of the Kiel Bay, and Bay of Mecklenburg and in the Arkona basin (Friedland et al., 2012), have negative effects on the population of soft-bottom bivalves (Arntz, 1981).

2.2. Sampling and generation of data

Overall, 917 sampling events were included in the analysis. Samples were taken on behalf of different projects between 2004 and 2012. Standard procedure included the sampling of three replicates at each station using a van-Veen grab (70–75 kg; 0.1 m^2; 10–15 cm penetration depth). Samples were washed through 1 mm mesh-size following HELCOM-guidelines (HELCOM, 2013b) and preserved in 4% buffered formaldehyde-seawater solution. All macrobenthic organisms were sorted, identified to the lowest possible taxonomic level, counted and weighted (fresh mass). The blue mussels were not identified on species level as *Mytilus edulis*, *Mytilus trossulus* and, to a large extent, hybrids between these species occur sympatric in the study area (Riginos and Cunningham, 2005; Väinölä and Hvilsom, 1991; Väinölä and Strelkov, 2011). It was assumed that due to the hybridization and the sympatric occurrence the ecological requirements of all blue mussels in the study area are more or less comparable.

Ash-free dry mass (afdm) was calculated from fresh mass using conversion factors generated from own measurements. Biomass (afdm) is presented and used in models in $g*m^{-2}$ for the larger bivalve species, but in $mg*m^{-2}$ for smaller species. Ash-free dry mass (afdm) was chosen as response variable instead of wet weight to ignore inorganic weights like shells. The conversion factor from wet weight to afdm is about 1: 0.05–0.1, i.e. wet weight is approximately 10–20

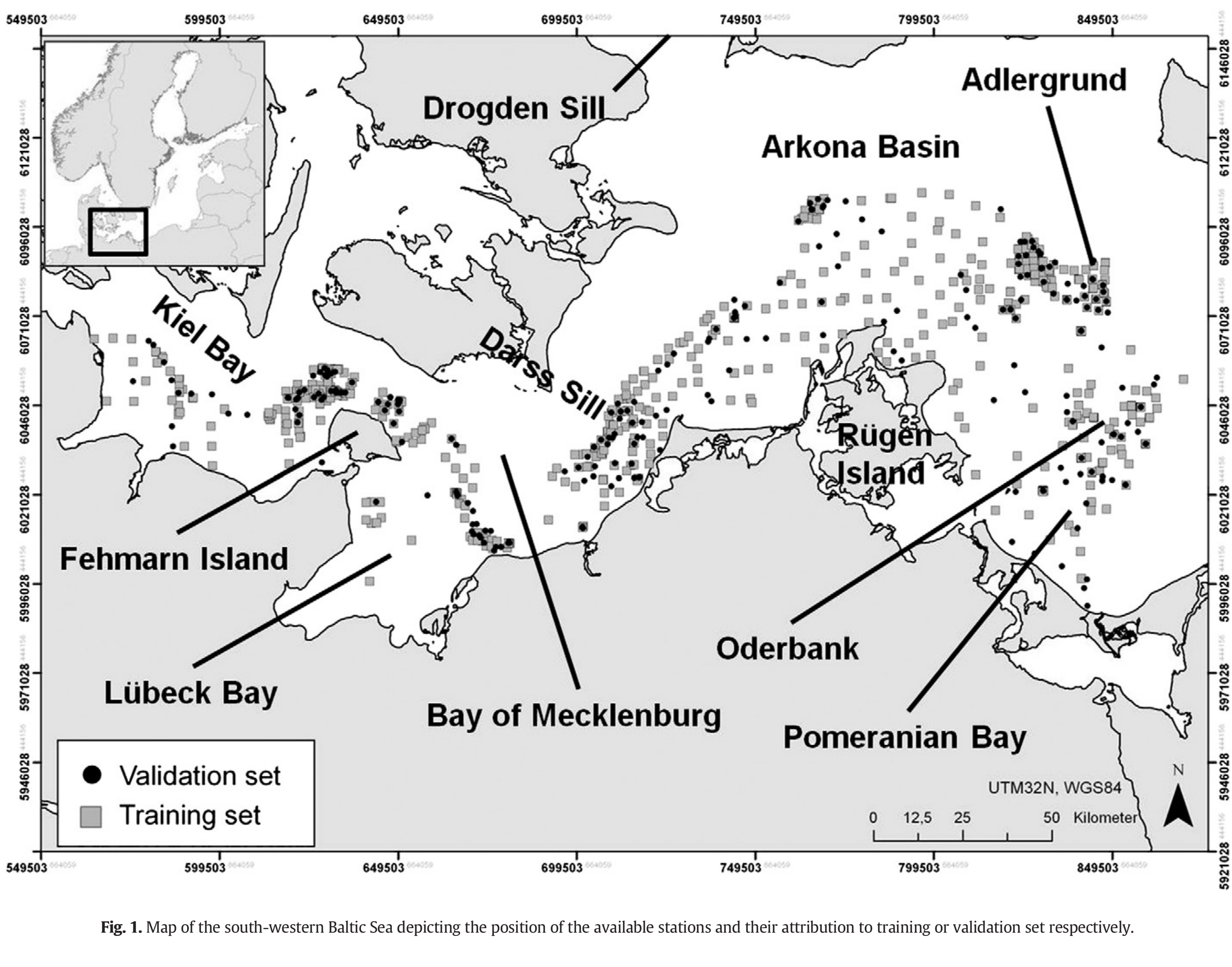

Fig. 1. Map of the south-western Baltic Sea depicting the position of the available stations and their attribution to training or validation set respectively.