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EXPLORING BIODIVERSITY REFUGIA: PATTERNS OF MEROPLANKTON BIODIVERSITY IN THE VICINITY OF RESTORED OYSTER REEFS

INTRODUCTION

Meroplankton communities are important components of **reef-associated biodiversity**, because they determine the distribution of benthic life history stages & lead to replenishment or potential recovery of benthic populations. However, little is known about **how restoration of reef habitats in the North Sea influences meroplankton biodiversity**.

OBJECTIVES

We initiated a case study in the **marine protected area** [Natura 2000 site] 'Borkum Reef Ground' (BRG) in the German Bight, North Sea, where European flat oyster pilot reefs for restoration are located[1]. This makes BRG an ideal region to **identify reef-associated biodiversity**. We ask if **specific patterns of meroplankton biodiversity develop in the vicinity of the restored reefs**, i.e. whether the reefs develop refugia & provide habitats for other species.
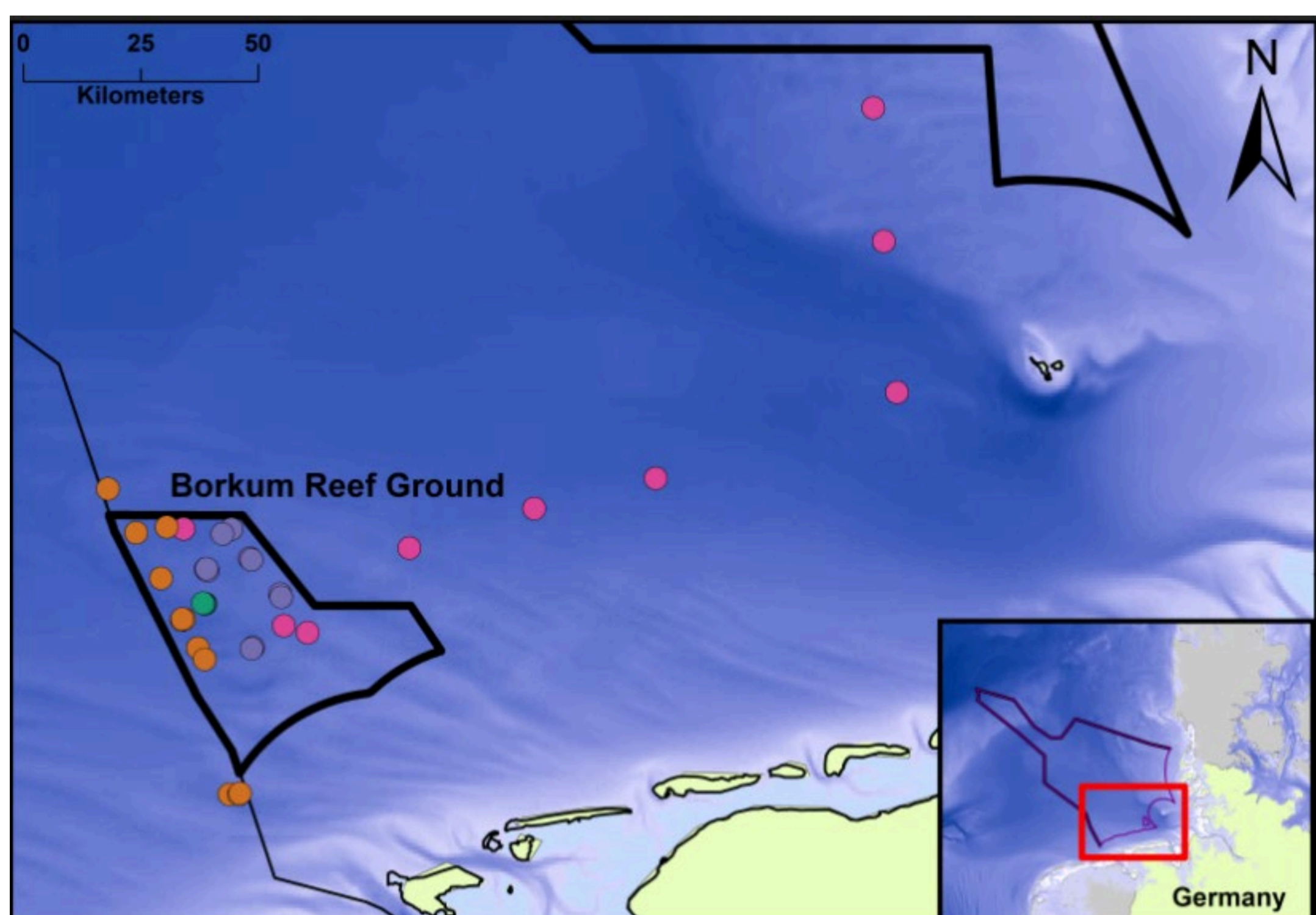
METHODS

Fig. 1: Study area showing sampling sites.

G1: Restored oyster reef,
G2: Vicinity, west of reef,
G3: Vicinity, east of reef, < 10 km distance,
G4: Distance, easterly direction, > 10 km from restored reefs.

The overall current flows from BRG in an easterly to northeasterly direction.

We sampled meroplankton in the vicinity of restored European flat oyster reefs (G1) & in areas with increasing distance & bearing from the reefs (G2-G4) in the German Bight (Fig. 1). Sampling was conducted on board of three cruises in June-July 2022 using oblique Baby Bongo (100 µm mesh size) hauls and a pump-hose system. Samples were fixed in ethanol. In the lab, DNA was extracted, the COI region was amplified using the Leray XT[2] & Geller primers[3] & paired-end sequenced on Illumina Miseq. Bioinformatics analyses were performed using dada2 pipeline[4]. Taxonomic assignment was performed using a combination of the RDP classifier[5] with MetaZooGene database[6] & Blast[7] with NCBI GenBank[8].

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RESULTS

We detected a total of **146 meroplankton species** belonging to nine phyla (Fig. 2). **All four regions shared 46 (31.5%) species** (Fig. 3).
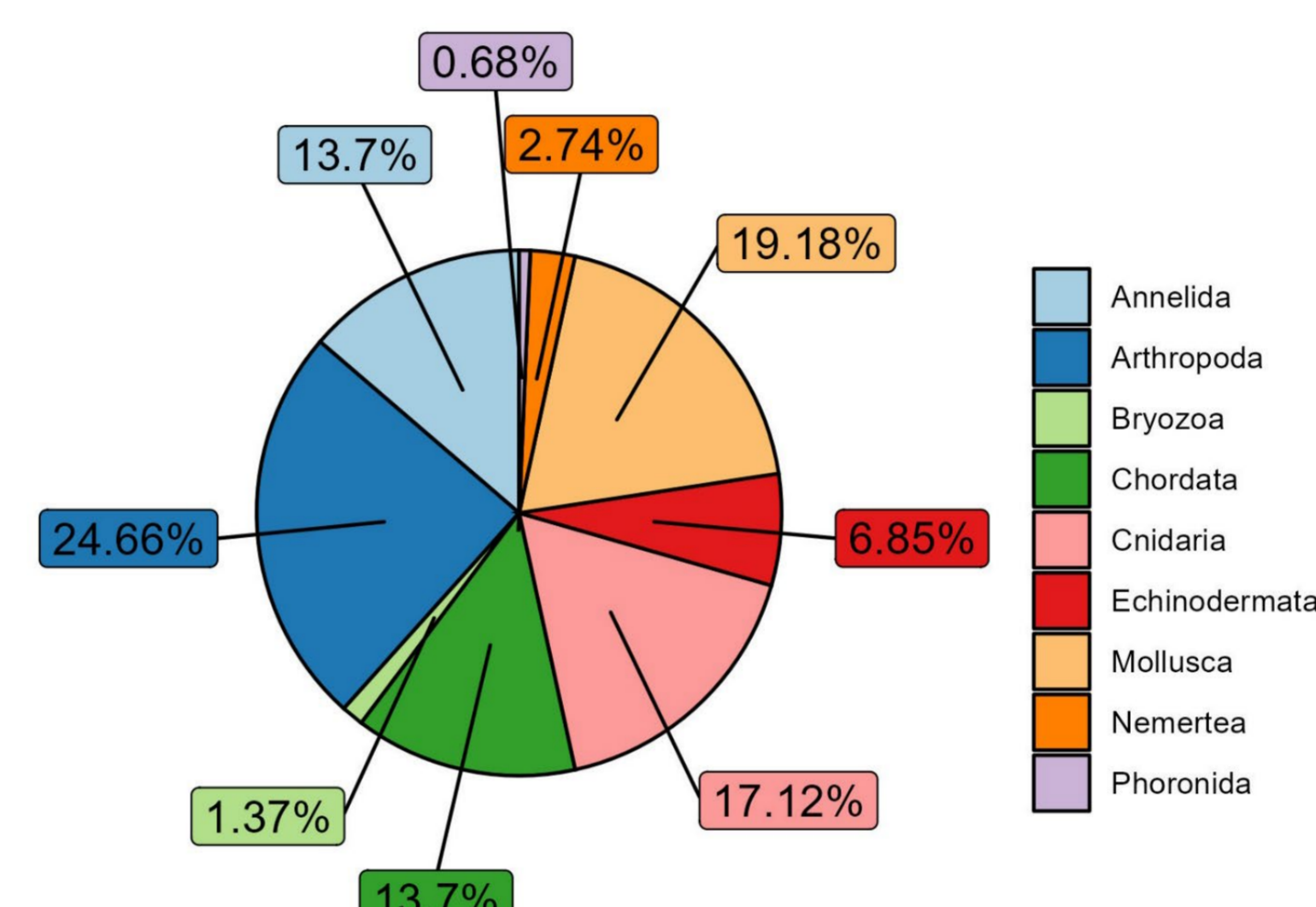

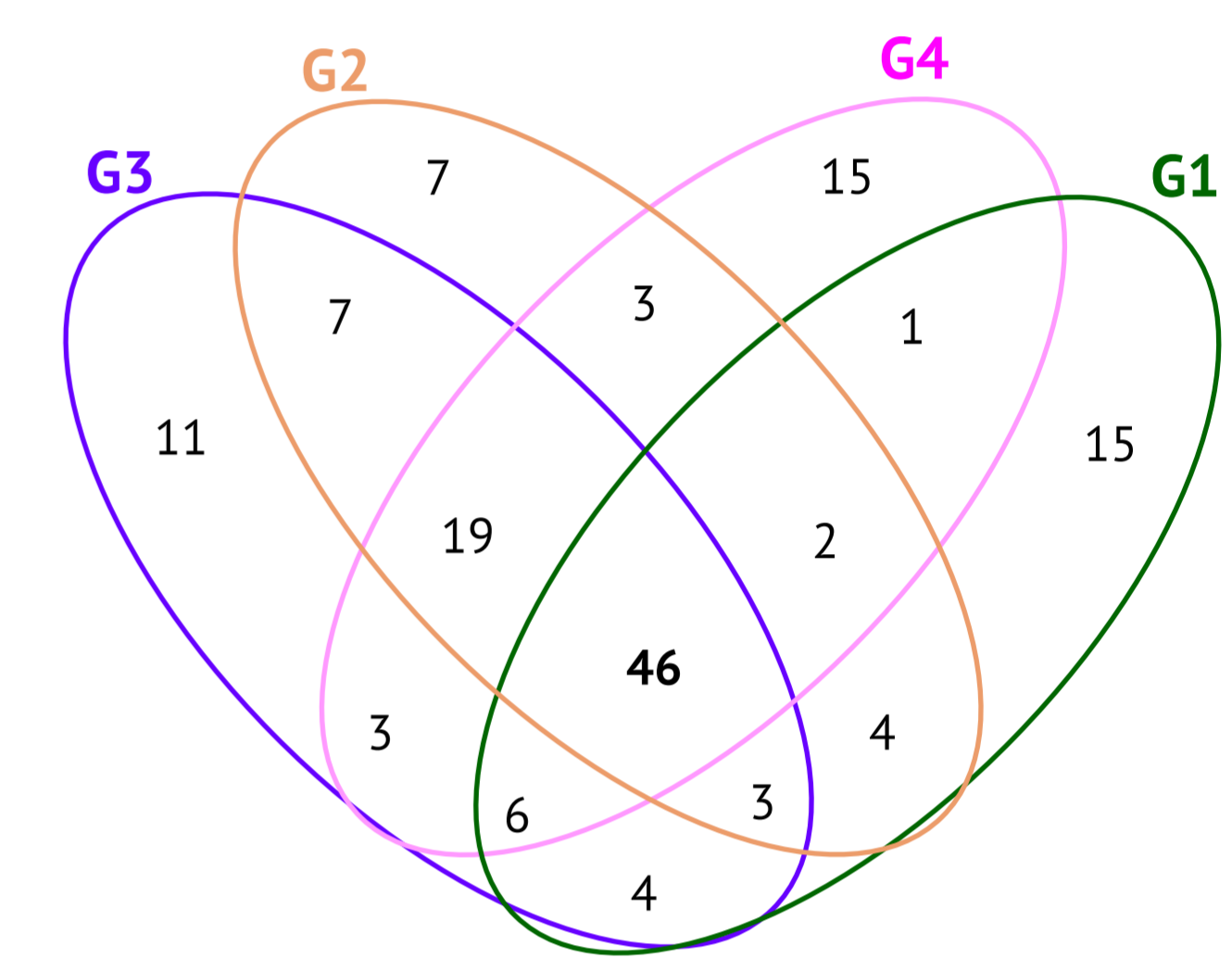**Fig. 2.** Proportion of species per phylum

Fig. 3. Number of unique & shared species in and between regions

There were **no significant differences in species richness between regions** (ANOVA: $F_{3,70}=0.83$, p = 0.48; Fig. 4). However, multivariate analysis revealed a high degree of patchiness (within-group dissimilarities > 66%), with each region having a **distinct species assemblage** (between-group dissimilarity > 70%, PERMANOVA: $F_{3,70}=2.53$, p<0.001), & some overlap among regions (Fig. 5). About 25% of the variability in species composition was described by the first two PCoA axes.
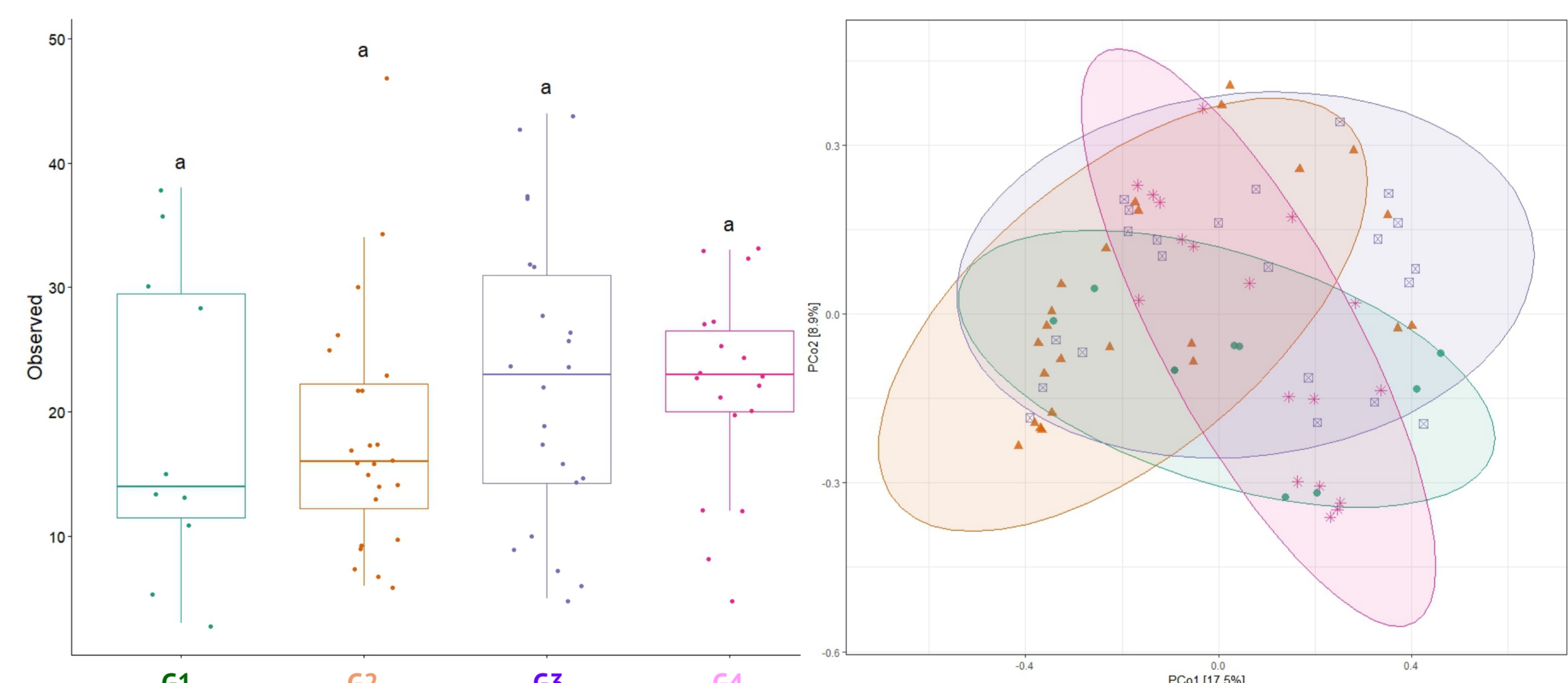

Fig. 4: Species richness per region

Fig. 5: Species composition of the individual regions

13 indicator species were identified for the four regions, with seven significantly associated to **G1**, one to **G2**, two to **G3** and three to **G4**.

Ostrea edulis (Bivalvia) - **European flat oyster**

Ectopleura larynx (Hydrozoa)
Jassa herdmani (Amphipoda)
Lutraria angustior (Bivalvia)

Pusillina inconspicua (Gastropoda)
Embletonia pulchra (Gastropoda)
Philocheras bispinosus (Decapoda)

Malmgrenia lunulata (Polychaeta)

Pomatoschistus minutus (Teleostei)
Mytilus galloprovincialis (Bivalvia)

Amphiura filiformis (Ophiuroidea)
Ophiura albida (Ophiuroidea)
Trachurus trachurus (Teleostei)

DISCUSSION

We found **high meroplankton patchiness** in the samples, as reflected in the high within-group dissimilarities. The **European flat oyster** was identified as an **indicator species of G1**, the restored reef, only. The communities at the habitats in the vicinity (**G2**, **G3**) of the restored reef did not [yet?] show a significant influence from the restoration. The distant **G4** represented the typical sand bottom fauna (& fish). Similar species richness but dissimilar species assemblages reflect differences in the occurrence of benthic life history stages at each region.