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# The role of eukaryotic microorganisms for niche partitioning of planktivorous fish

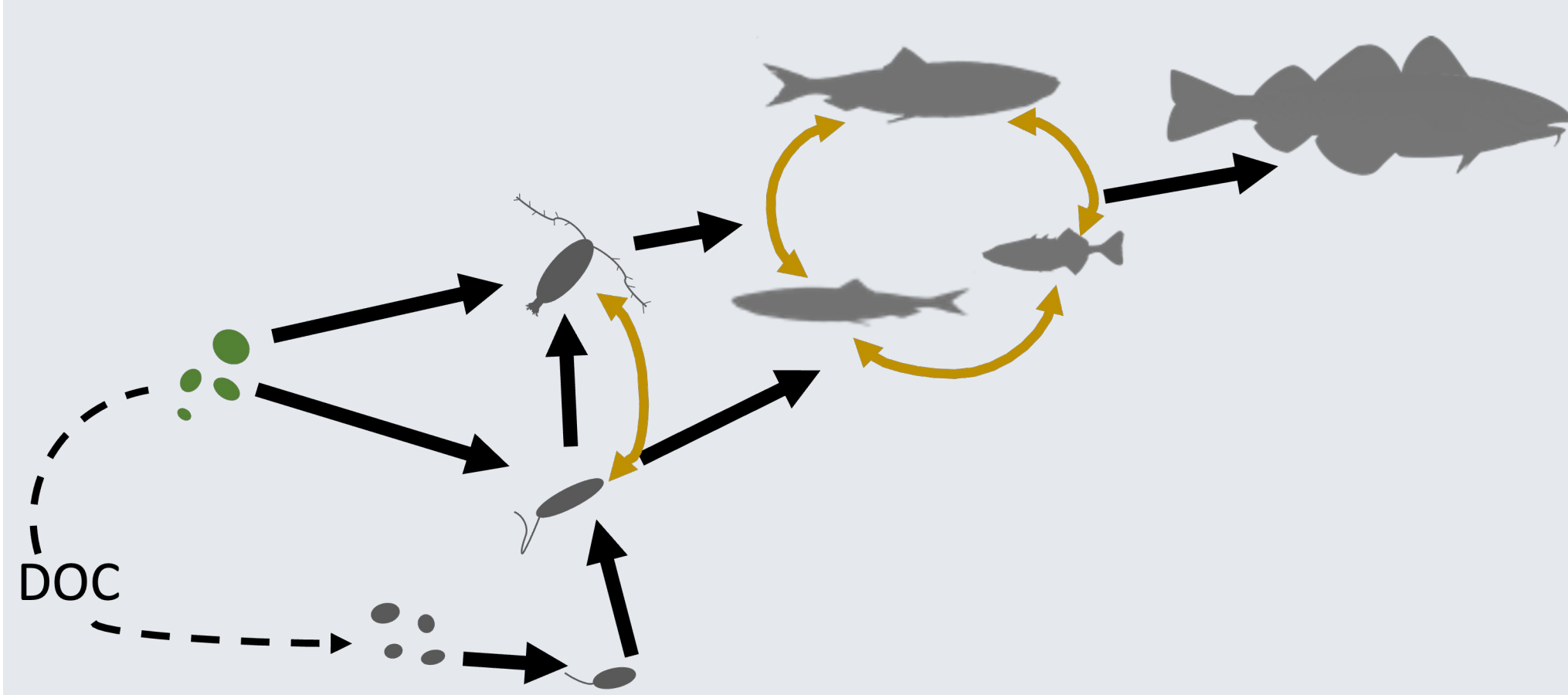


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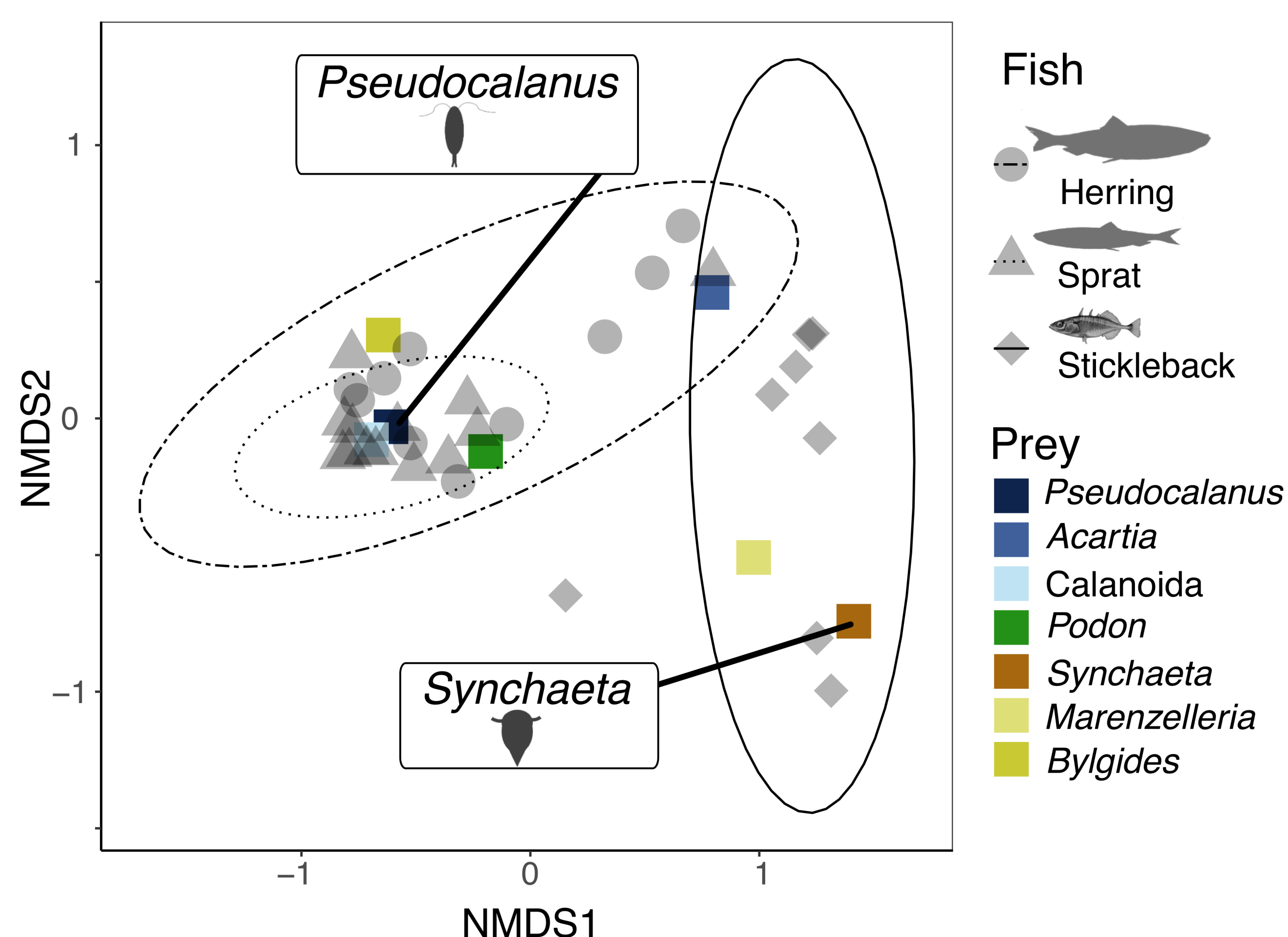
## Background

Pelagic food webs are prone to experience regime shifts due to increasing anthropogenic impacts.

In the Baltic Sea, the predatory cod population has dramatically decreased, releasing predation pressure on planktivorous mesopredators. Due to method limitations, the competition between clupeids (i.e., sprat and herring) and stickleback is assumed to be high.



**Fig. 1. Conceptual model of the pelagic food web.** Trophic interactions are represented by the black arrows and competition by orange arrows.

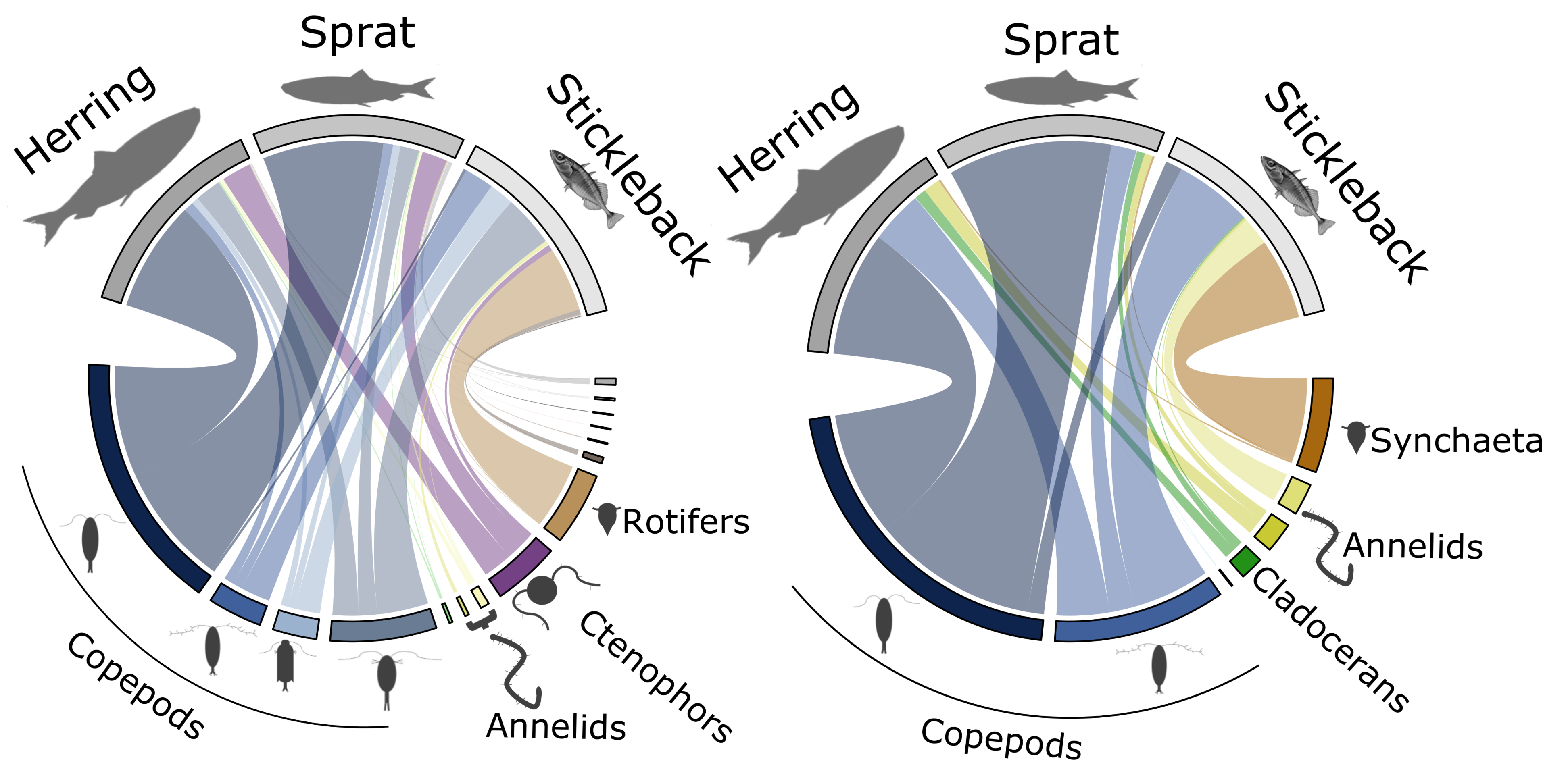


**Fig. 3. NMDS plot of the COI gut content sequences.** The prey taxa are represented with the coloured squares and prey contributing for most of the dissimilarity between fish species are shown with their names. The ellipses represent the t-distribution of the fish species.

## Neglected microorganisms are important for fish diet

Using the traditional microscopy approach, only prey with hard parts are identified. Here, we show that soft-bodied organisms, such as rotifers, may play an important role in niche partitioning of planktivorous fish in the pelagic Baltic Sea.

Ongoing research investigates the importance of soft-bodied prey at larger spatial scale and for different fish life stages.

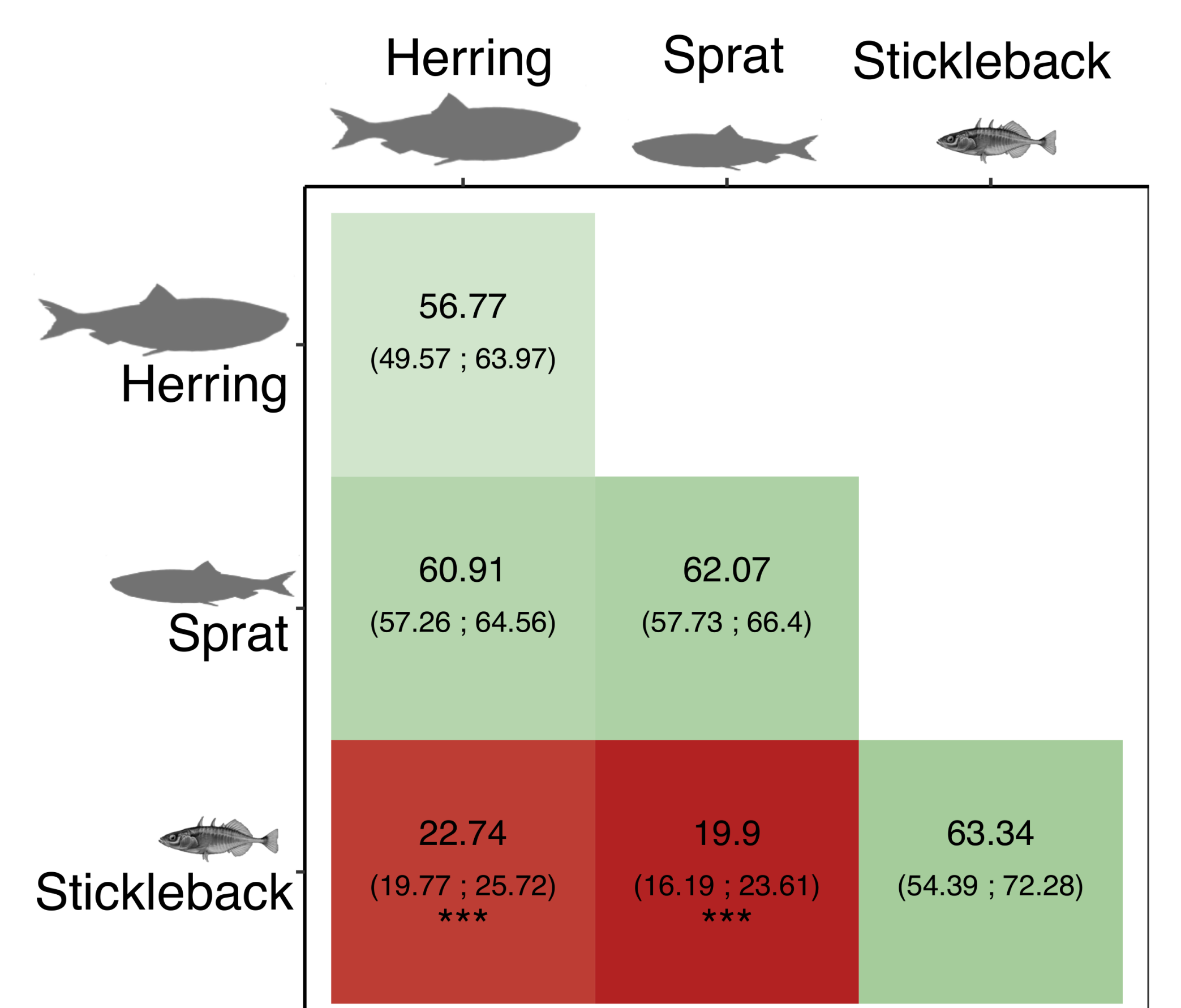


**Fig. 2. Diet composition of the three dominant planktivorous fish in the southern Baltic Sea.** Predators are shown on top and prey in the bottom of the circle plot based on 18S rRNA (left) and COI (right) gene metabarcoding.

## Are pelagic mesopredators competing for the same resources?

Using DNA metabarcoding on the 18S rRNA and COI genes we found that:

1. The copepods *Temora*, *Centropages*, and *Acartia* were consumed by the three fish species (**Fig. 2**).
2. The copepod *Pseudocalanus* was an important prey for sprat and herring (**Fig. 2 and 3**).
3. The rotifer *Synchaeta* was only preyed upon by stickleback (**Fig. 2**).
4. *Pseudocalanus*, *Temora*, *Synchaeta*, and the ctenophore *Mertensia* contributed for most of the dissimilarity between fish species (**Fig. 3**).
5. Clupeid's niche overlapped at more than 60% and was different than stickleback's niche (**Fig. 4**).



**Fig. 4. Diet overlap between and across the three fish species based on the 18S rRNA gene sequences.** Bray-Curtis similarity Index (95% CI) are shown. Significant niche partitioning is shown with asterisks (\*\*\* = P < 0.001).