

METAGENOMICS SHOTGUN SEQUENCING TO IDENTIFY FOOD WEB STRUCTURES IN MARINE FISH SPECIES: PREY & PREDATORS

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1. Introduction

Metagenomics has the potential to revolutionise our understanding of marine food webs by analysing DNA from the stomach contents of organisms. The technique reveals intricate details of their diets, hence providing a detailed picture of the marine food chain and its complex interactions. For a deeper understanding of marine ecosystem dynamics and to predict the potential impacts of environmental changes, we performed a whole-genome metagenome assessment of the stomach content of six marine fish species, paving the way for new discoveries in marine ecology.

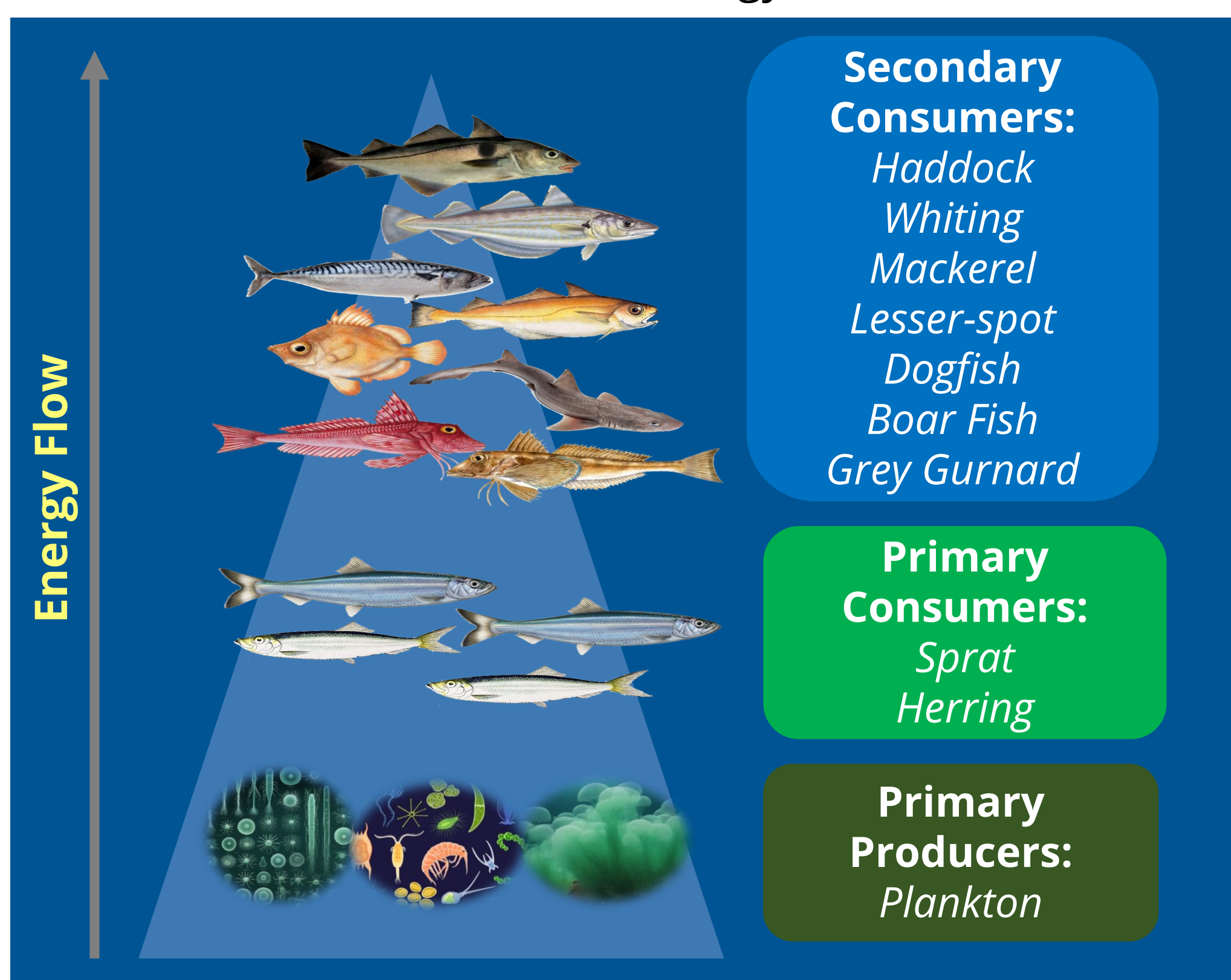


Figure 1: Generalised trophic pyramid for a marine ecosystem

2. Methodology

Sampling and Data Collection

- Periodical fish surveys (2018) in the Irish and Celtic Seas by AFBI and Marine Institute (MI).
- Biological data collection (location, weight, length, date/time, size class, etc.)



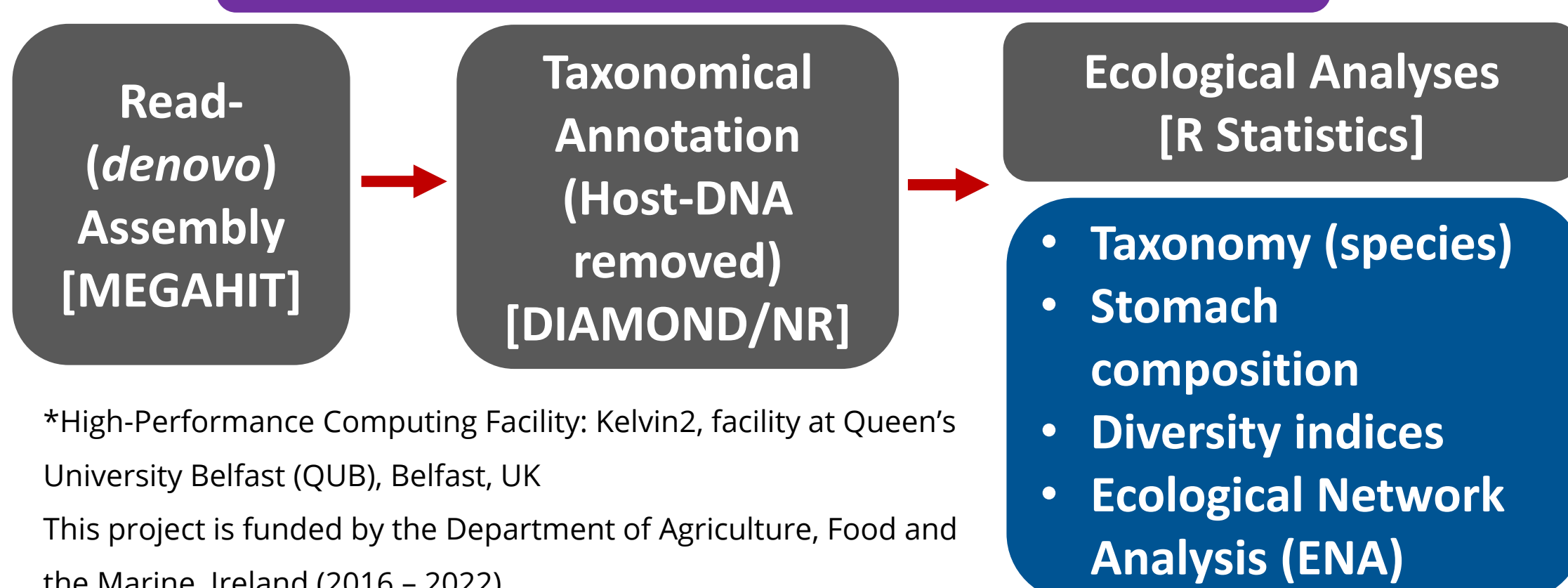
Sampling: Gut Sections



Primary:
Herring (HER, n=97)
Sprat (SPR, n=44)

Secondary:
Whiting (WHG, n=45)
Lesser-spot Dogfish (LSD, n=67)
Grey Gurnard (GUG, n=35)
Mackerel (MAC, n=32)

Bioinformatic Pipeline



*High-Performance Computing Facility: Kelvin2, facility at Queen's University Belfast (QUB), Belfast, UK
This project is funded by the Department of Agriculture, Food and the Marine, Ireland (2016 – 2022).

4. Preliminary Findings

- Each fish species exhibited a distinct gut content: species from Arthropoda, Cnidaria, Hemichordate, Mollusca, Nematoda, and Platyhelminthes.
- Despite the difficulty in removing host DNA, prey species were successfully identified.
- The absence of comprehensive reference data for marine fish genomes hinders species-level identification.
- The metagenomic method proves to be an effective tool for broadening our understanding of species interactions within aquatic trophic networks.

3. Results

3a. Ecological Diversity Measures

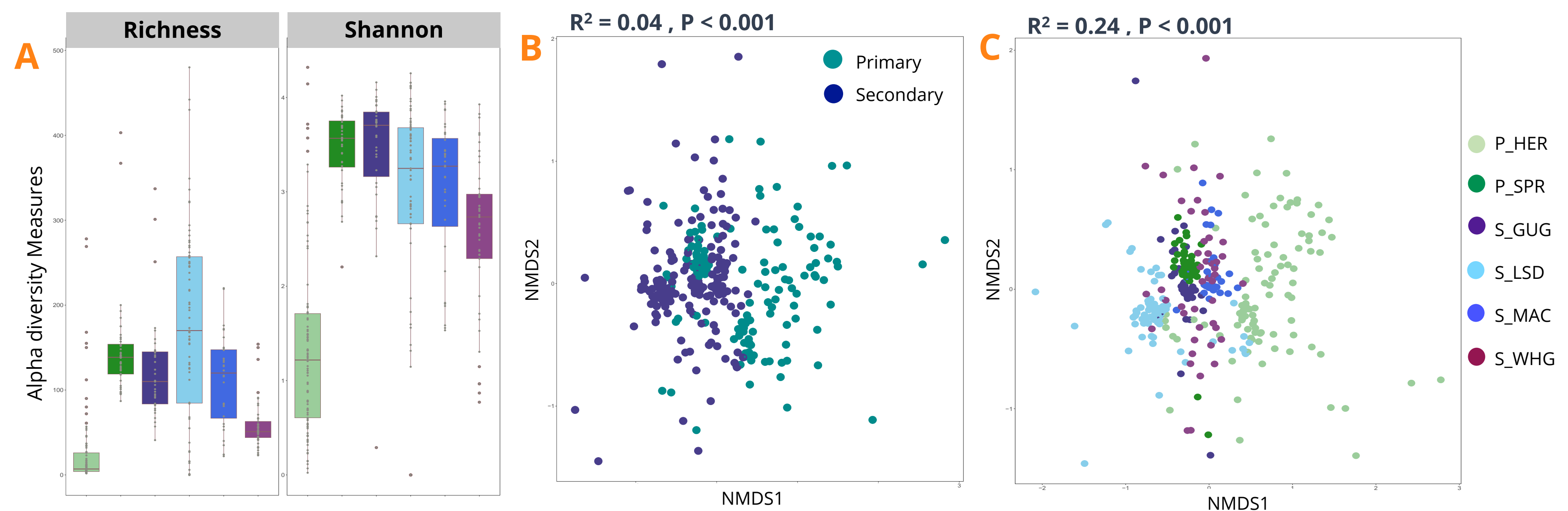
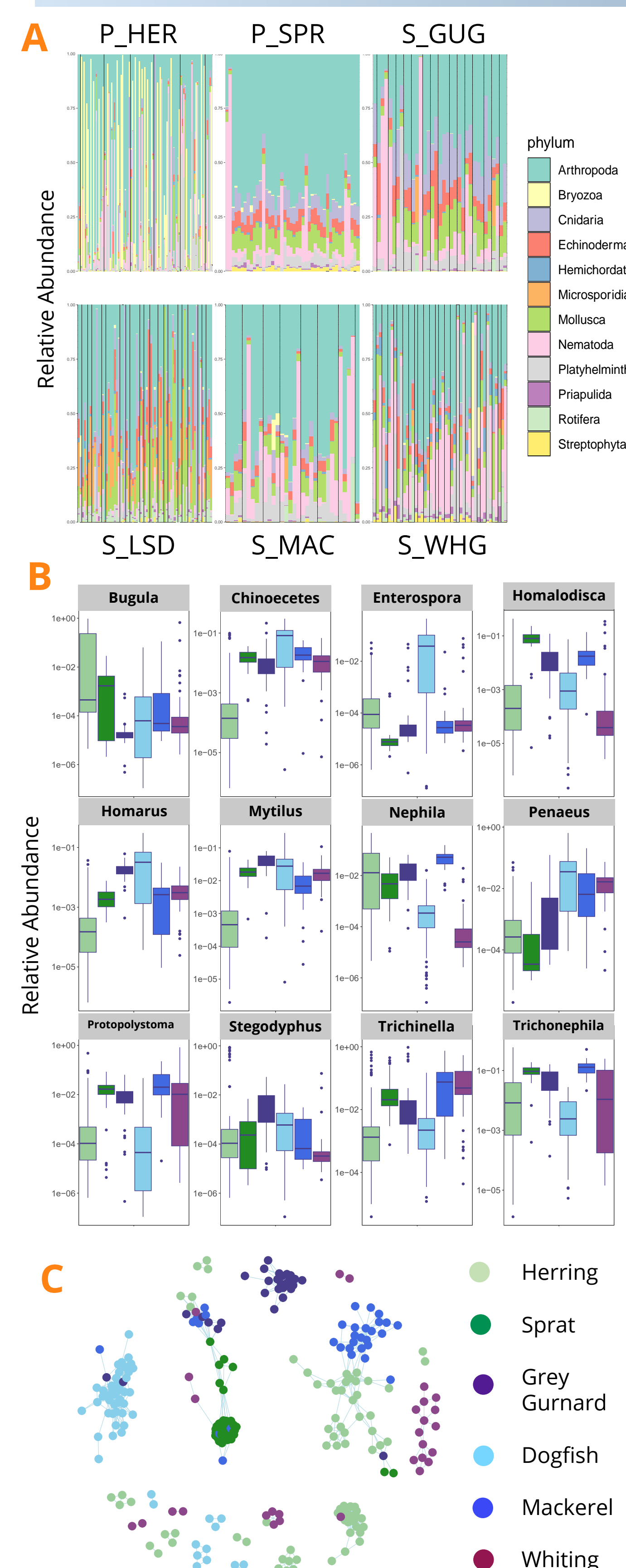


Figure 2: Alpha-diversity: A) Richness (Observed number of groups) and Shannon diversity of fish types and Bray-Curtis distance-based Non-metric multidimensional scaling (NMDS) plot illustrating the diversity between B) Food web consumer levels C) fish types.

- Richness:** The highest and the lowest number of prey items were detected in Lesser-spot dogfish and Herring guts, respectively.
- Shannon Diversity:** Secondary consumers and Sprat exhibited a higher variety of prey species in their diets compared to Herring.
- Beta diversity:** NMDS reveals distinct dietary patterns, separating secondary from primary consumers. Apart from Herrings, which differ, other fish show comparable diets within their respective trophic level.

3b. Stomach Composition & Ecological Network Analysis



- Phylum-level:** Primary consumers exhibit distinct feeding preferences, including species from Arthropoda and Mollusca, among others. Secondary consumers, (predators), exhibit a diverse diet that includes species such as Arthropods, cnidarians, and Echinoderms.
- Genus-level:** Primary consumers primarily feed on *Bugula*, a type of seaweed. Predators, on the other hand, have a diet consisting of various arachnids (e.g. *Nephila* and *Trichnephila*), crustaceans (e.g. *Homarus*, *Penaeus* and *Chionoecetes*), insects (e.g. *Homalodisca* and *Vespula*), as well as a variety of Platyhelminthes and nematode worms.
- ENA - Feeding habits:** show the interactions among primary producers – primary consumers (Herring, Sprat) and secondary consumers (predators).
- Prey-predator relationship:** between Herring and Mackerel, alongside the interlinks among secondary consumers like Sprat, Mackerel, Dogfish, and Gurnard, delineates the energy transfer through various trophic levels in the ecosystem under study.

Figure 3: The contig-based taxonomic composition gut content at the A) Phylum and B) Genus-level of highly abundant macrofaunal groups C) Ecological network illustrating the association between the gut content of fish types.