Frozen Clues: biochemistry to unravel resource partitioning among Antarctic consumers.

A. Voisin[1;2] (anthony.voisin@univ-brest.fr)
M. Dogniez[2;3;4], G. Lepoint[2], L. N. Michel[5], J. Thébault[1] and G. Schaal[1]

1. Laboratory of Environmental Marine Sciences (LEMAR), University of Brest, France
2. Laboratory of Trophic and Isotopes Ecology (LETIS), FOCUS Research Unit, University of Liège, Belgium
3. Center of Environmental Science (CMK), University of Hasselt
4. Freshwater Biology Department, Royal Belgian Institute of Natural Sciences (RBINS)
5. Animal Systematics and Diversity (ASD), FOCUS Research Unit, University of Liège, Belgium

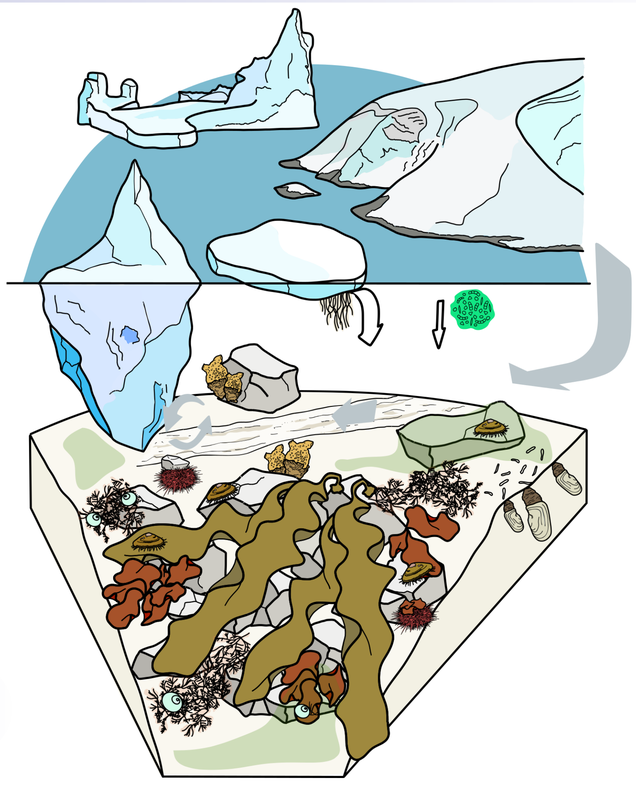
Context & Objectives

In Antarctica, benthic primary consumers rely on a variety of food sources (e.g., phytoplankton, sea-ice algae, benthic primary producers and bacteria)[1;2]. These food sources can be reflected in tissues by different molecules and trophic biomarkers[3;4].

Shifts in the environment (e.g., ice dynamic) can change food sources availability[5] and impact the diet of consumers at different scales[6].

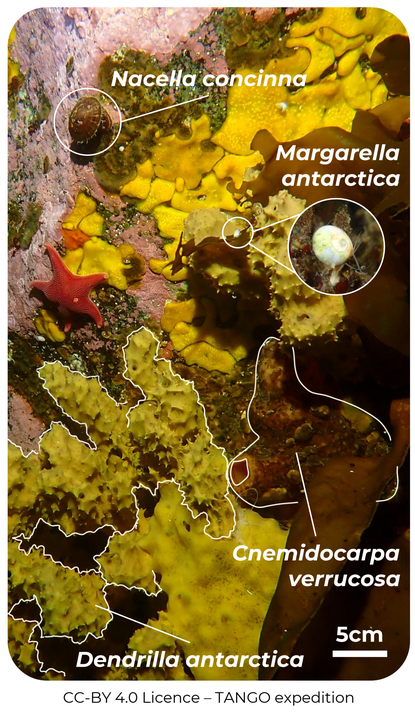
Do molecular biomarkers provide valuable insights into consumer resource use along the West Antarctic Peninsula?

WEST ANTARCTIC PENINSULA



Sampling

TANGO



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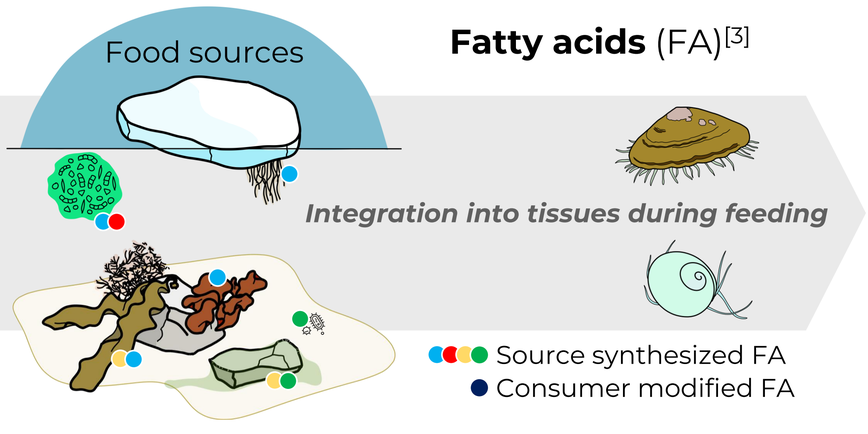
Biomarkers



Fatty acids (FA)[3]

Consumers

Fatty acid content (%)

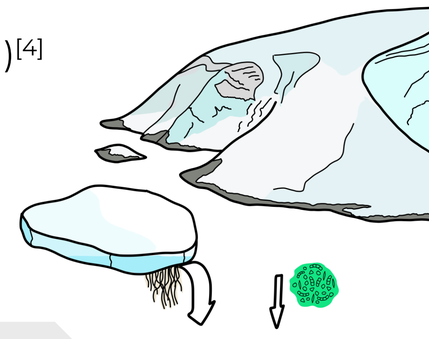
lipidocean Marine lipid analytic platform UBO CNRS IRD IFREMER

IPSL LOCEAN

Highly branched isoprenoids(HBI)[4]

Sea-ice diatoms
➲ Diene (HBI II)

Open water phytoplankton
➲ Triene (HBI III)



Integration in sediments & tissues

HBI II / HBI III ratio

Results

obtained by gas chromatography analyses

1 Diversity of food sources consumed

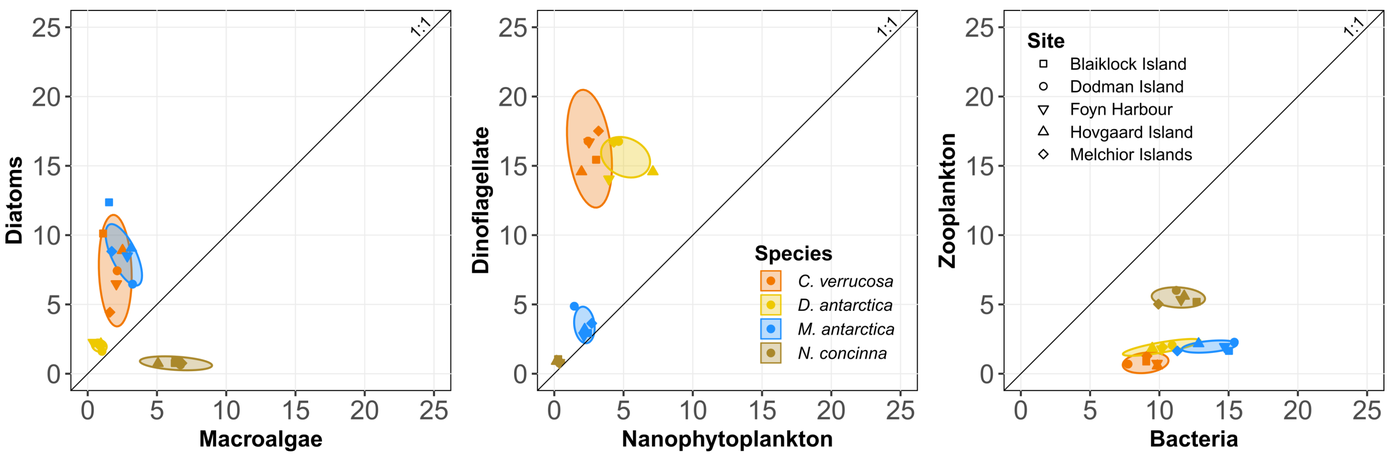


Fig. 1: Proportion of food sources biomarker (% of total fatty acid), based on Table 1. Points are mean values for each site and species. Ellipses represent the core variability at a level of 40%.

Higher proportion of macroalgal markers in *N. concinna*.

High proportion of diatoms markers in *M. antarctica* and *C. verrucosa*.

Filter feeders had high proportion of dinoflagellate and *D. antarctica* had higher nanophytoplankton.

Very low zooplankton but high bacteria proportion in all consumers, specially for *M. antarctica*.

Table 1: Fatty acids used as trophic biomarkers in polar benthic food webs[5].

Biomarker for	FA
Macroalgae	20:4n-6
Diatoms	16:1n-7 16:4n-1 16:3n-4
Nanophytoplankton (e.g., cryptophyte)	18:3n-3 18:4n-3
Dinoflagellate	22:6n-3
Bacteria	Odd num ante/iso 18:1n-7
Zooplankton	Σ 20:1 + 22:1

2 Sympagic contribution (i.e., sea-ice algae)

Higher ratios:

Foyn Harbour
Blaiklock Island

➲ Coherent with higher mean sea ice cover.

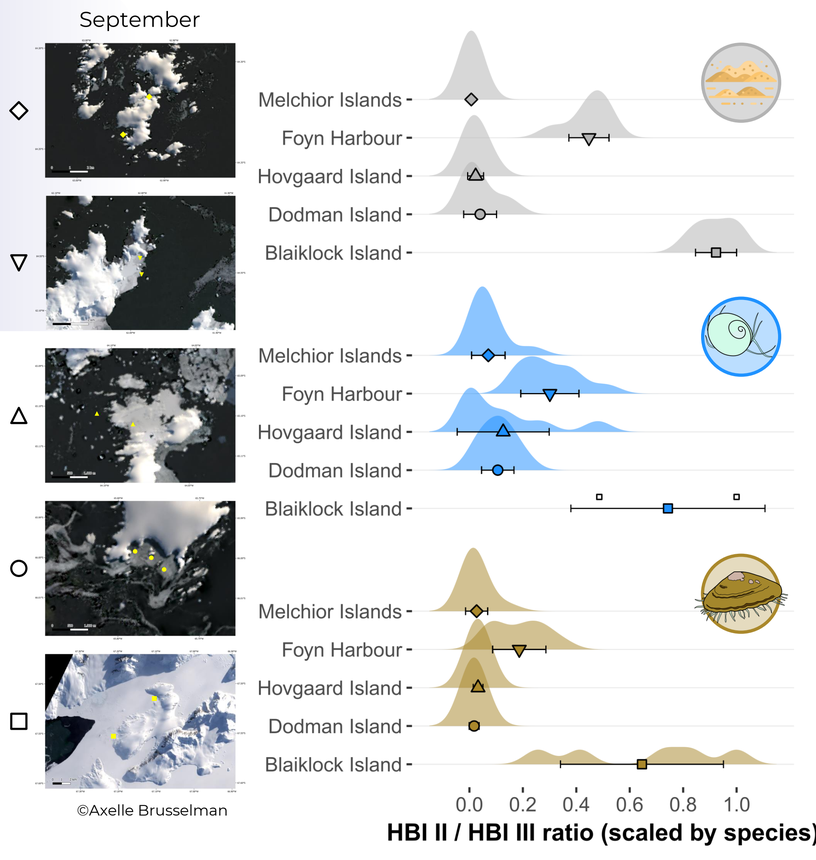


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Fig. 2: Density plot of HBI ratio. The mean and standard deviation were computed for site. Lack of density plot is related to an insufficient number of replicates.

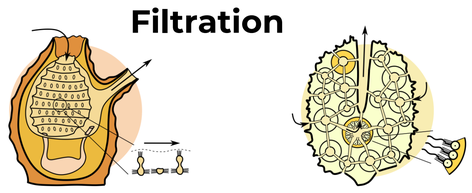
Discussion

Fatty acids revealed functional differences in the feeding mechanisms of organisms:

- ➲ Filter feeders diet function of particle size[7;8].
  - Ascidian capable of feeding on larger particles (e.g., diatoms).
  - Porifera (e.g., leuconoid Demosponge) having smaller pore size and filtration capability.
- ➲ Grazers diet influence by radula structure[9].
  - Rhipidoglossa radula: sweeping the substrate to feed on epibionts (e.g., microphytobenthos).
  - Docoglossa radula: digging in materials to feed, getting organic matter from diverse sources (e.g., macroalgae and epibionts).

HBI ➲ sea-ice diatom consumption linked to sea-ice cover[4].

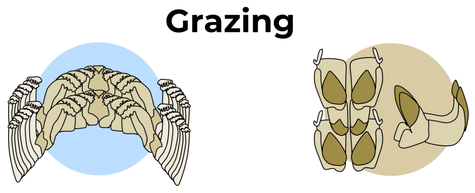
Filtration



Pharyngeal chamber (size range 1µm – 1mm)

Choanocyte chamber (size range 0.1µm – 100µm)

Grazing



Rhipidoglossa radula (*M. antarctica*)

Docoglossa radula (*N. concinna*)

Conclusions

Biomarker analysis highlighted species diet and trophic plasticity, reflecting a functional response to environmental change along the West Antarctic Peninsula.

Fatty acids and HBI complementarity helped to overcome the inherent limitations of each biomarker.

It raised new questions about species' physiology and development, which might be able to change their molecular content to cope with changes.

References

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Acknowledgments

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