

# Unraveling organic matter fluxes in coastal Antarctica using compound-specific analysis of amino acid $\delta^{15}\text{N}$

Loïc N. MICHEL<sup>1</sup>, Marcel VAN DER MEER<sup>2</sup>, Gilles LEPOINT<sup>1</sup> & Philip RIEKENBERG<sup>2</sup>



<sup>1</sup> Freshwater and Oceanic sSciences Unit of reSearch (FOCUS), University of Liège, Liège, Belgium

<sup>2</sup> Department of Marine Microbiology and Biogeochemistry (MMB), Royal Netherlands Institute of Sea Research (NIOZ), Texel, The Netherlands



Royal Netherlands Institute for Sea Research

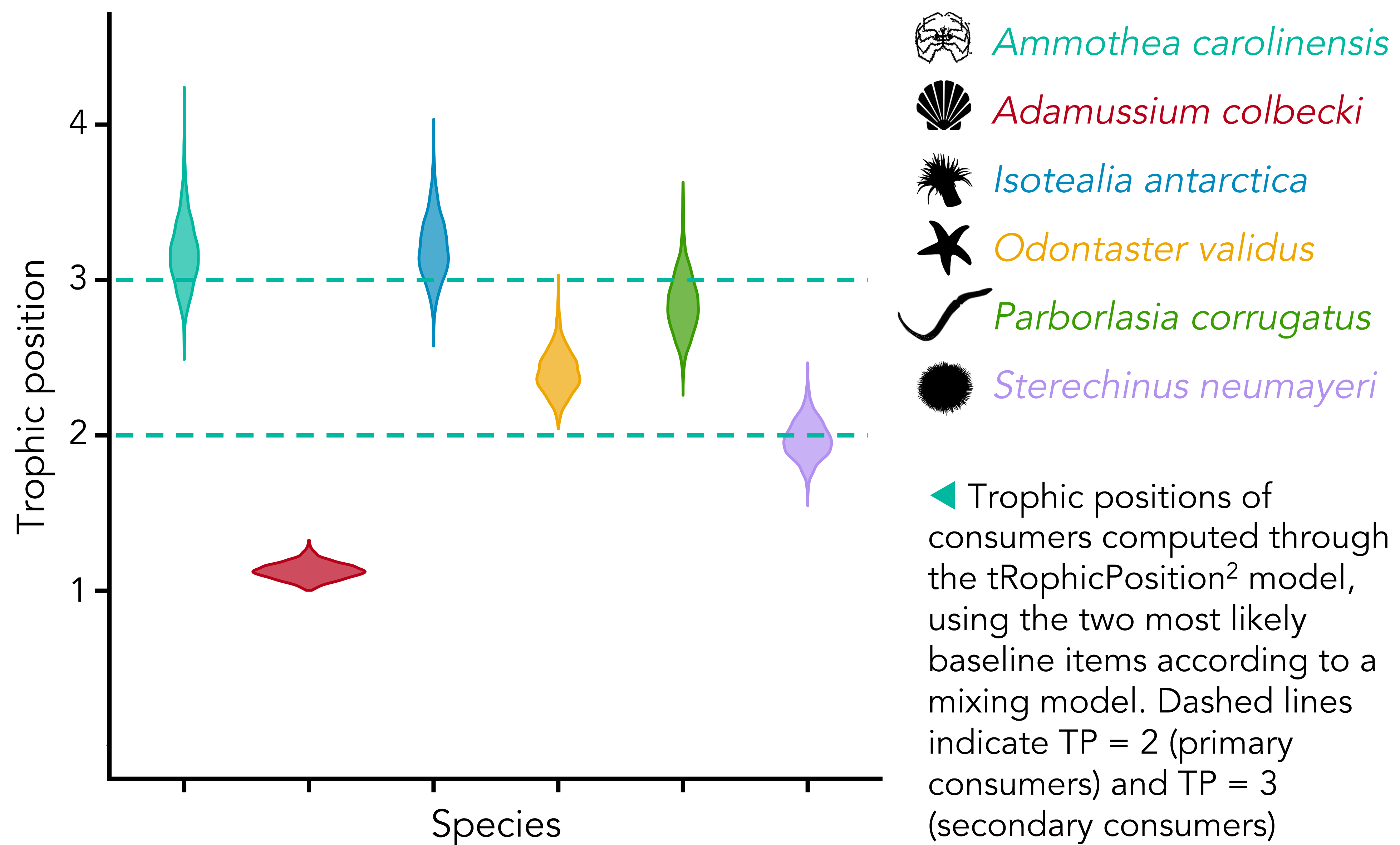
## Context & objectives

Global change causes strong and contrasted environmental modifications in coastal Antarctica. Understanding how these changes impact ecosystem functioning is a major priority.

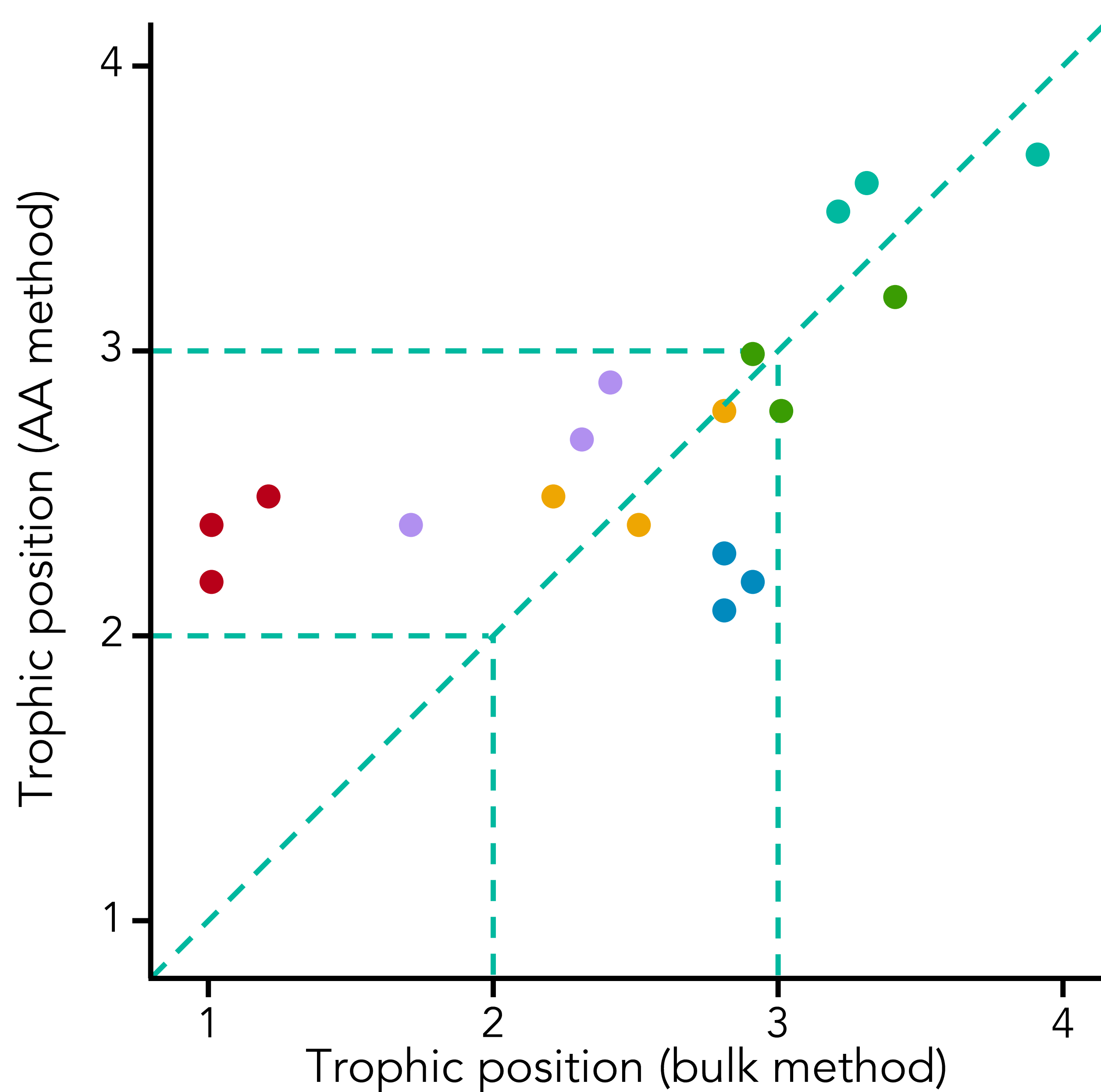
Trophic positions (TP) provide simple ways to assess organisms' functional roles and estimate energy flow through ecological communities, while taking into account complex processes such as omnivory.

In a previous study<sup>1</sup>, we studied trophic position in Antarctic zoobenthos sampled during an extreme high sea ice event. We used traditional bulk organic matter  $\delta^{15}\text{N}$  analysis in consumer tissue and baseline items. TP estimates (►) were strikingly low for some taxa (omnivores *O. validus* & *P. corrugatus*), sometimes conceptually unlikely so (*A. colbecki*).

Here, we used a more novel tracer (compound-specific analysis of amino acids  $\delta^{15}\text{N}$ ) to reassess those results.



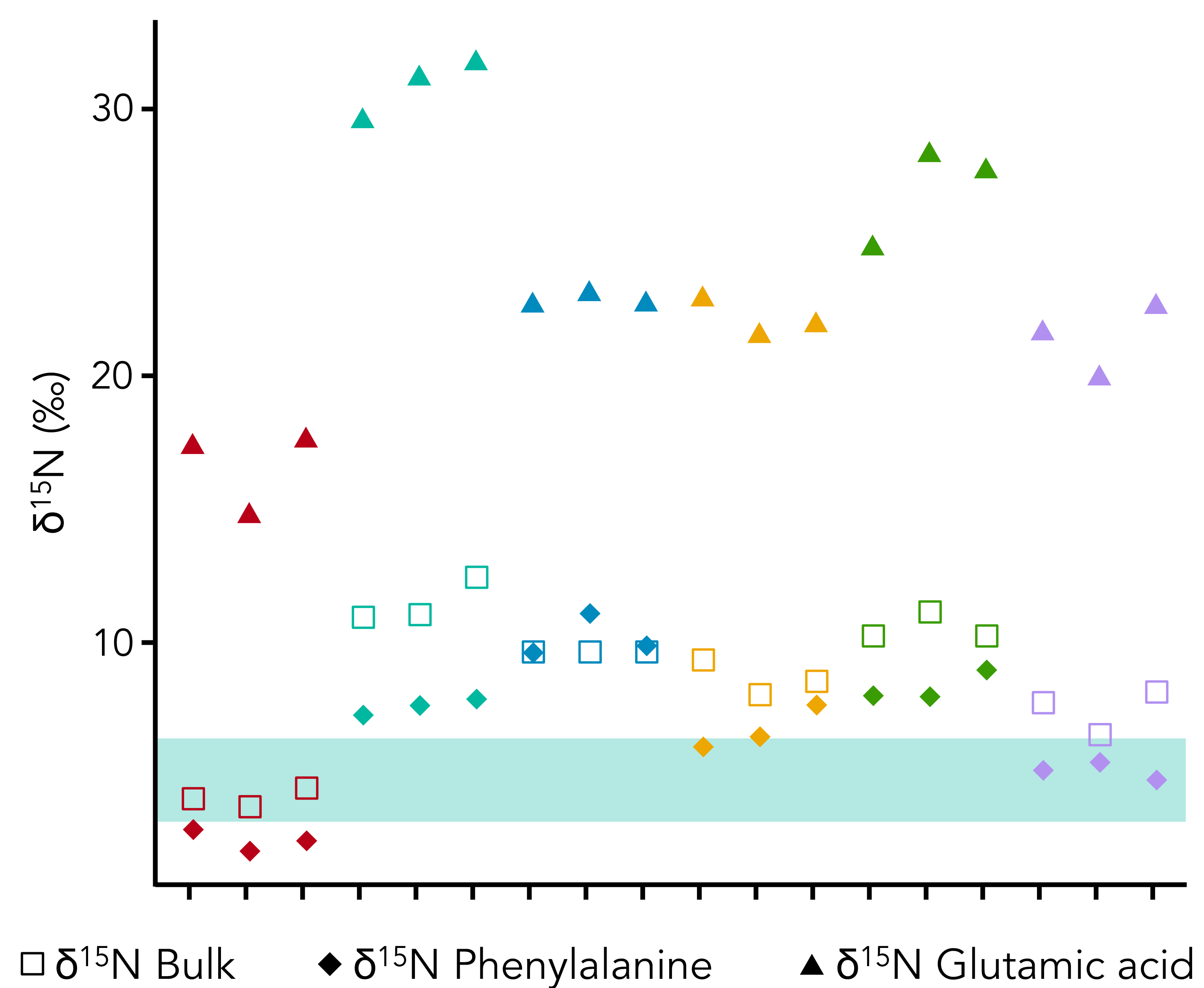
## Key findings



▲ Correspondence between consumer trophic position computed using bulk<sup>3</sup> and amino acid<sup>4</sup>  $\delta^{15}\text{N}$ . Dashed lines indicate TP = 2, TP = 3, and the identity line. See figure above for color codes.

Good congruence for 3 species including *O. validus* and *P. corrugatus*, corroborating findings from the original paper.

TP estimates using AA  $\delta^{15}\text{N}$  are notably higher (TP > 2) for *A. colbecki*, slightly higher for *S. neumayeri*, but lower for *I. antarctica*.



▲  $\delta^{15}\text{N}$  of bulk tissue, phenylalanine (source amino acid) and glutamic acid (trophic amino acid) in sampled zoobenthos. Green area: bulk  $\delta^{15}\text{N}$  in sampled producers / baseline items. See figure above for color codes.

Sampled taxa likely rely on different food web baselines, as suggested by differences in  $\delta^{15}\text{N}_{\text{Phe}}$ .

*A. colbecki* (filter feeder): active selection of low  $\delta^{15}\text{N}$  items? *I. antarctica* (omnivore/predator): dependence on microbially reworked OM<sup>5</sup>?

## Take home message

The correspondence between classic and novel methods of TP estimation was species-specific.

Compound-specific AA  $\delta^{15}\text{N}$  analysis confirmed the low trophic positions of omnivores *O. validus* and *P. corrugatus*, which could have implications for secondary production. This corroborates initial findings regarding how unusually high sea ice cover might influence ecosystem functioning.

Besides TP estimation, AA  $\delta^{15}\text{N}$  provided invaluable info about food web structure, emphasizing the interest of this tracer in coastal Antarctica, whose remoteness, intense seasonality and extreme conditions limit insights from traditional methods.

## References

<sup>1</sup>Michel et al. 2019 Sci. Rep. 9: 8062. <sup>2</sup>Quezada et al. 2019 Meth. Ecol. Evol. 9: 1592-99. <sup>3</sup>Post 2002 Ecology 83: 703-18. <sup>4</sup>Chikaraishi et al. 2009 Limnol. Oceanogr. Meth. 7: 740-50. <sup>5</sup>McCarthy et al. 2007 Geochim. Cosmochim. Acta 71: 4727-44.